Die Bodenkultur: Journal of Land Management, Food and Environment
Volume 77, Issue 1, 42–52, 2026. 10.2478/boku-2026-0004
ISSN: 0006-5471 online, https://reference-global.com/journal/BOKU

Integrative Multi-Trait Analysis of Potatoes (*Solanum tuberosum* L.) Somaclones in a Tropical Highland Environment

Integrative Multi-Trait-Analyse von Kartoffel-Somaklonen (*Solanum tuberosum* L.) in einer tropischen Hochlandumgebung

Muhammad Ridwan Fauzi[1], Haris Maulana[2]*, Hanny Hidayati Nafi'ah[1], Andrew Yoel[3], Ika Roostika[2], Dwinita Wikan Utami[2], Kusmana[2], Tri Handayani[2], Asih Kartasih Karjadi[2], Alina Akhdiya[2], Rina C. Hutabarat[2]

[1] Faculty of Agriculture, Universitas Garut, Jl. Prof. kh. Cecep Syarifudin no. 52A, Garut, West Java 44151, Indonesia
[2] Research Center for Horticulture, National Research and Innovation Agency, Jl. Raya Jakarta - Bogor KM 46, Cibinong, Bogor, West Java 16911, Indonesia
[3] Faculty of Agriculture, Universitas Padjadjaran, Jl. Raya Bandung - Sumedang Km. 21, Jatinangor, Sumedang, West Java 45363, Indonesia
* Corresponding author: hari061@brin.go.id

Received: 7 May 2026, received in revised form: 30 June 2026, accepted: 2 July 2026

Summary

Potatoes (*Solanum tuberosum* L.) play a vital role in ensuring global food security. Population growth, market demand, and the need for high-quality crop yields have driven the adoption of efficient technologies to identify somaclones with superior yield potential. This study was conducted with the primary objectives of identifying variance in potato morphological traits and yield, identifying relationships between measured traits, and selecting superior somaclones using multi-trait analysis. The experiment was conducted in Pangalengan, West Java, Indonesia, using a randomized block design with three replications. The analysis results showed significant differences among somaclones for all observed traits. The correlation analysis showed that tuber weight per plot (yield) had a significant positive correlation with various growth parameters and yield components. The increase in tuber weight per plot was in line with the increase in economic tuber weight, number of economic tubers, stem diameter, and plant height. In addition, leaf dimensions, including leaf length and width, also contributed significantly to the achievement of tuber weight per plot in each observation area unit. Furthermore, the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) analysis proved successful in identifying three superior potato somaclones, namely G3, G4, and G7, with G7 being the most superior somaclone. The achieved selection accuracy was very high (86.4%), with heritability values ranging from 76.1% to 94.9%. Selected somaclones can be used for further potato breeding programs.

Keywords: Heritability, MGIDI, multi-traits, potato, selection

Zusammenfassung

Kartoffeln (*Solanum tuberosum* L.) spielen eine entscheidende Rolle für die globale Ernährungssicherheit. Bevölkerungswachstum, Marktnachfrage und der Bedarf an qualitativ hochwertigen Ernten haben die Anwendung effizienter Technologien zur Identifizierung von Somaklonen mit überlegenem Ertragspotenzial vorangetrieben. Ziel dieser Studie war es, die Varianz morphologischer Merkmale und des Ertrags von Kartoffeln zu ermitteln, Zusammenhänge zwischen den gemessenen Merkmalen aufzudecken und mithilfe einer Mehrmerkmalsanalyse überlegene Somaklonen auszuwählen. Das Experiment wurde in Pangalengan, Westjava, Indonesien, in einem randomisierten Blockdesign mit drei Wiederholungen durchgeführt. Die Analyseergebnisse zeigten signifikante Unterschiede zwischen den Genotypen hinsichtlich aller beobachteten Merkmale. Die Korrelationsanalyse ergab eine signifikante positive Korrelation zwischen dem Knollengewicht pro Parzelle (Ertrag) und verschiedenen Wachstumsparametern sowie Ertragskomponenten. Der Anstieg des Knollengewichts pro Parzelle korrelierte mit dem Anstieg des wirtschaftlich nutzbaren Knollengewichts, der Anzahl wirtschaftlich nutzbarer Knollen, des Stammdurchmessers und der Pflanzenhöhe. Darüber hinaus trugen die Blattdimensionen, einschließlich Blattlänge und -breite, signifikant zum Knollengewicht pro Parzelle in jeder Beobachtungseinheit bei. Die MGIDI-Analyse identifizierte erfolgreich drei überlegene Kartoffelgenotypen (G7, G3 und G4). Die erzielte Selektionsgenauigkeit war sehr hoch (86,4 %), die Heritabilitätswerte lagen zwischen 76,1 % und 94,9 %. Ausgewählte Somaklone können für weitere Kartoffelzüchtungsprogramme verwendet werden.

Schlagwörter: Vererbbarkeit, MGIDI, Mehrfachmerkmale, Kartoffel, Selektion

Open Access. © 2026 Muhammad Ridwan Fauzi, Haris Maulana, Hanny Hidayati Nafi'ah, Andrew Yoel, Ika Roostika, Dwinita Wikan Utami, Kusmana, Tri Handayani, Asih Kartasih Karjadi, Alina Akhdiya, Rina C. Hutabarat, published by BOKU University (www.boku.ac.at). CC BY-NC-ND
This work is licensed under the Creative Commons Attribution-NonCommercial-NoDerivatives 3.0 License.
https://doi.org/10.2478/boku-2026-0004

1. Introduction

Potatoes (*Solanum tuberosum* L.) occupy a strategic position in the global agricultural system as the fourth major food source after wheat, rice, and corn. In addition to their high economic potential, potatoes are recognized as a solution for sustainable food diversification due to their nutritional composition rich in complex carbohydrates, fiber, vitamins, and bioactive compounds (Camire et al., 2021). Efficient biomass production per unit area and short cropping cycle provide significant comparative advantages over other food crops in strengthening global food stability (Haverkort and Struik, 2015).

This crop is generally cultivated in highland areas with cool temperatures that support growth and tuber formation. However, in tropical environments, potato plants are exposed to unique climatic conditions such as sharp diurnal temperature fluctuations and increased solar radiation. These conditions significantly affect physiological processes, photosynthetic activity, and biomass allocation (Mølmann and Johansen, 2025). Temperature variations at high elevations often alter growth responses and limit the expansion of cultivation to lower elevations, making understanding the environmental context crucial for shaping crop performance.

Given the complexity of plant responses to environmental variation, understanding genotype performance requires an analytical approach capable of integrating multiple agronomic and physiological traits. Traditional univariate analysis often fails to capture the interrelationships between traits that collectively determine adaptation. From a modern breeding perspective, multivariate analysis tools such as the Multi-Trait Genotype–Ideotype Distance Index (MGIDI) offer a powerful framework for synthesizing layered trait information into meaningful biological insights (Olivoto and Nardino, 2022). MGIDI enables researchers to evaluate the overall integration of traits, going beyond the effects of single traits.

Table 1. Somaclones used in the experiment
Tabelle 1. Im Experiment verwendete Somaklone

No.	Code	Genotypes	Initial variety	Note
1	G1	G48	Granola	Mutant
2	G2	G21	Granola	Mutant
3	G3	R17	Repita	Mutant
4	G4	V35	Vega	Mutant
5	G5	Nadia	-	Check
6	G6	Granola	-	Check
7	G7	Medians	-	Check

Although MGIDI has been successfully applied to various commodities to support genotype evaluation (Pallavi et al., 2024; Alam et al., 2024; Putri et al., 2026), its application to tropical highland potato production systems remains very limited. Therefore, this study aims to elucidate the biological performance and trait integration of potato genotypes in a tropical highland environment through an integrative multi-trait analysis that highlights the relationships between genotype, traits, and environment.

2. Materials and method

2.1. Plant materials

This study used seven potato somaclones that consisted of four mutant and three commercial varieties that served as controls. The controls were superior commercial varieties widely cultivated by farmers in various regions. The mutant potato clones evaluated in this study were derived from induced mutations of commercial potatoes using gamma ray irradiation. The irradiation process was performed on stem cuttings obtained from plantlets at a dose of 30 Gy, utilizing the Gammacell 220 irradiator at the Center for Isotopes and Radiation Application, National Nuclear Energy Agency (PAIR BATAN), Pasar Jumat, South Jakarta. Following irradiation, the stem cuttings were subcultured every 4 weeks on a half-strength Murashige and Skoog (1/2 MS) medium supplemented with 0.5 ppm kinetin. These cultures were maintained in an incubation room at a temperature of 18–23°C under fluorescent lighting with an intensity of 1500 lux for a 16-h photoperiod. Specific details regarding the characteristics of all genotypes used in this experiment are provided in Table 1.

2.2. Experimental design

The field experiment was conducted for 4 months from August to November 2024 in Pangalengan, West Java, Indonesia. The test site is located at an altitude of 1,470 m above sea level (masl), with coordinates 7° 18' 41" S, 107° 58' 37" E. This field experiment was designed using a randomized block design with four replications for each somaclone. Each experimental unit (plot) has dimensions of 5 × 3 m. Climate data during the study period is presented in Figure 1.

The soil type at the experimental field is Andosols. During the experiment, chicken manure was applied at a rate of 10 t/ha and a compound nitrogen–phosphorus–potassium (NPK)

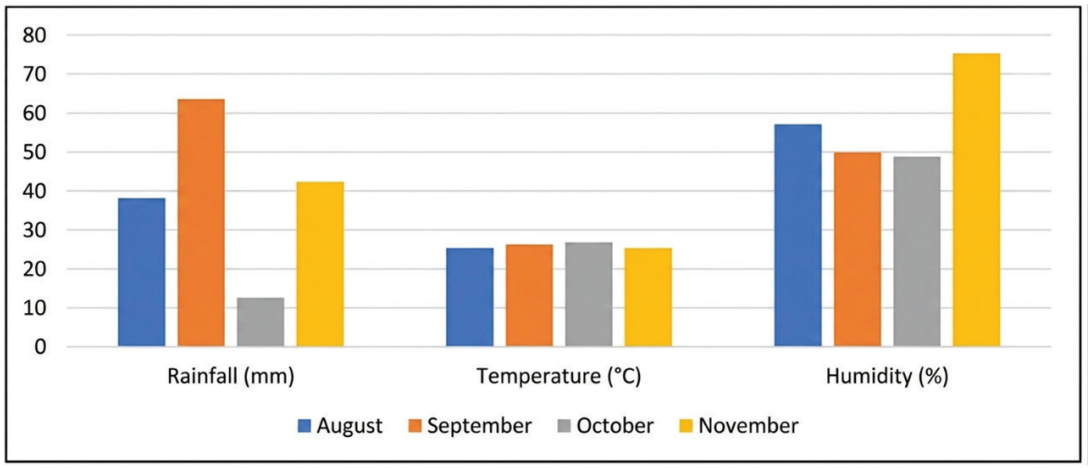


Figure 1. Weather conditions during the study
Abbildung 1. Wetterbedingungen während der Studie

fertilizer (Mutiara (16–16–16)) at a rate of 750 kg/ha. The NPK fertilizer contained 16% nitrogen (N), 16% phosphorus (expressed as P_2O_5), and 16% potassium (expressed as K_2O). The irrigation system relied on rainwater throughout the experiment, with regular watering done every 2 days during the dry season. Weeds were removed manually every 2 weeks.

2.3. Data collection

Vegetative characters observed included leaf length (LL) (cm), leaf width (LW) (cm), stem diameter (SD) (mm), and plant height (PH) (cm) measured at the growth phase of 40 days after planting (DAP). Measurement of yield and productivity components such as economic amount of tuber/marketable tuber (EAT), economic tuber weight (ETW), and tuber weight per plot/yield (TWP) was carried out at the harvest time (110 DAP). The harvest of each genotype was weighed using a digital scale and then converted to determine the productivity value in tons per hectare (t/ha).

2.4. Data analysis

The collected data were analyzed using R programming software in Google Colab. Based on various morphological and yield traits, all collected data were analyzed using R programming software in Google Colab. The „Agricloae" package was used to perform analysis of variance (ANOVA) for each trait separately. The Pearson's rank correlation algorithm was used to construct correlation plots to evaluate the strength and direction of association between variables. Principal component analysis (PCA) was performed using the Google Colab packages „Ggally," „factoextra," and „ggfortify." To visualize the PCA results, a two-way matrix containing the genotypes and their associated traits was used, focusing on the first two principal components (PCs). To show the distribution of these traits, the eigenvectors of each PC were used.

Heritability (h_b^2) is calculated using the following equation:

$$h_b^2 = \frac{\sigma_g^2}{\sigma_p^2} \times 100$$

The MGIDI index for the seven potato genotypes was calculated using the method suggested by Olivoto and Nardino (2021) to determine the best performing genotype. The following equation is used for this calculation:

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

In this equation, γ_{ij} represents the j^{th} score of the i^{th} genotype and represents the j^{th} score of the ideotype. The index is calculated for each genotype ($i = 1, 2, ..., t$), where t is the total number of genotypes and j ranges from 1 to f, which is the number of characters.

To assess the strengths and weaknesses of the genotypes under study, crucial assessment techniques are used. The proportion of the MGIDI of the i^{th} genotype explained by the j^{th} factor (ω_{ij}) was used to show the strengths and weaknesses of each genotype. The calculation for ω_{ij} is:

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

D_{ij} indicates the genetic distance between the i^{th} genotype and the ideal genotype with respect to the MGIDI, and ω calculations were performed using the "mgidi" and "gamam" functions available in the "metan" package (Olivoto and Lúcio, 2020) in R software. These calculations allow to measure how closely each genotype aligns with the ideal genotype for a given character, providing valuable insights into the performance of the genotype regarding the character of interest. A low value ω_{ij} indicates that the genotype in that particular character is highly aligned with the ideal genotype, indicating strong performance in that particular character.

Table 2. Results of analysis of variance (ANOVA) on all tested characters of the 12 genotypes
Tabelle 2. Ergebnisse der Varianzanalyse (ANOVA) aller getesteten Merkmale der 12 Genotypen

Traits	Means	Sign.	CV (%)
Leaf length (LL) (cm)	21.248 ± 1.11	***	5.22
Leaf width (LW) (cm)	4.369 ± 0.86	**	19.60
Stem diameter (SD) (mm)	7.185 ± 0.64	***	8.90
Plant height (PH) (cm)	265.84 ± 3.69	***	1.38
Economic amount of tuber (EAT)	429.2 ± 7.27	***	1.69
Economic tuber weight (ETW)	2.6701 ± 0.57	***	21.30
Tuber weight per plot (TWP)	268.12 ± 8.00	**	2.98

$^{**}p < 0.01$, $^{***}p < 0.001$, Sign. = Significance level, CV = coefficient of variation

3. Results

3.1. ANOVA for all tested characters

ANOVA showed that all morphological and yield characters tested were significantly different among potato genotypes in tropical highland environments ($p < 0.01$ and $p < 0.001$), including LL, LW, SD, PH, number of economic tubers, ETW, and TWP (Table 2). The coefficient of variation (CV) values indicating a relatively low level of trait diversity (<10%) include LL, SD, PH, number of economically viable tubers, and TWP. Moderate CV values (10–20%) are indicated by leaf width (LW), while high CV values are indicated by economic tuber weight (21.3%) (Table 2).

3.2. Relationships between measured traits

The correlation analysis results showed that several traits had a significant positive correlation, including EAT with PH, TWP, LW, LL, SD, and ETW. Furthermore, PH correlated with EAT and TWP (Figure 2). The darker the blue color for each trait, the higher the correlation value. These results suggest that targeting genotypes that exhibit favorable values for these traits may be beneficial for finding genotypes with better yields.

PCA was conducted to determine the traits that contributed the most to potato genotypic diversity. Each trait in the PC reflects its contribution to total diversity. Positive and negative loading values were used to differentiate between groups; traits with high absolute values (either positive or negative) contributed significantly to diversity within a component, while values close to zero indicated an insignificant contribution (Maulana et al., 2023). Based on the results of PCA given in Table 3, two PCs were obtained with eigenvalues greater than 1, namely PC1 and PC2. These two components cumulatively explained 86.4% of the total potato genotypic diversity, thus being sufficiently representative in describing the observed trait variation.

The first PC (PC1) had an eigenvalue of 4.82 with a diversity contribution of 68.8%, indicating that PC1 was the most dominant component in explaining potato genotype diversity. Characters with high loading values (>0.5) on PC1 included LL, LW, SD, PH, number of economic tubers, ETW, and TWP. The high positive loading values for these traits indicate that PC1 is closely related to vegetative growth and yield components. Genotypes with high PC1 scores tend to have more vigorous plant growth, characterized by larger leaves, thicker stems, taller plants, and higher tuber production in terms of both quantity and weight.

The second PC (PC2) had an eigenvalue of 1.23 and contributed 17.5% to the variance. Although its contribution was

Table 3. PCA character values that influence potato genotype diversity
Tabelle 3. PCA-Charakterwerte, die die Genotypendiversität von Kartoffeln beeinflussen

Traits	PC1	PC2
Leaf length	**0.81**	−0.49
Leaf width	**0.91**	−0.04
Stem diameter	**0.88**	−0.20
Plant height	**0.76**	**0.53**
Economic amount of tuber	**0.61**	**0.66**
Economic tuber weight	**0.94**	0.16
Tuber weight per plot	**0.81**	−0.42
Eigenvalue	4.82	1.23
Variability (%)	68.8	17.5
Cumulative (%)	68.8	86.4

Note: Numbers in bold indicate a discriminant of >0.5 or <−0.5 that contributed to variance

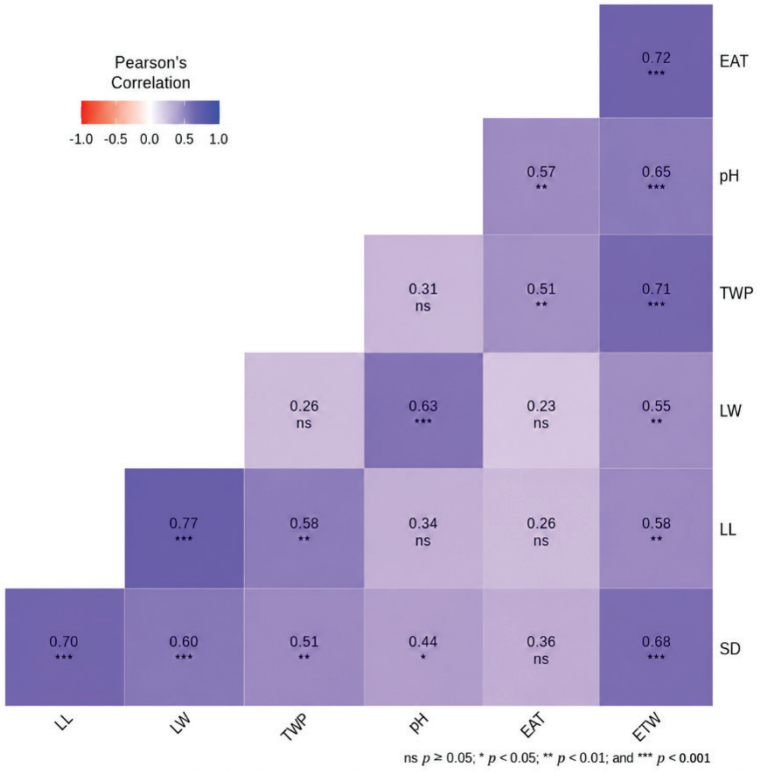


Figure 2. Visualization of Pearson's correlation coefficient matrix for quantitative charactersof the potato genotypes
Abbildung 2. Visualisierung der Pearson-Korrelationskoeffizientenmatrix für die quantitative Merkmale der Kartoffelgenotypen

smaller than PC1, PC2 still provided additional information on potato genotype variation. The characters that made a relatively larger contribution to PC2 were the number of economical tubers and PH, with the number of economical tubers having the highest positive loading value. This indicates that PC2 plays a greater role in differentiating genotypes based on yield patterns, particularly regarding the number of tubers produced, and indicates a difference in tendencies between vegetative growth traits and yield distribution.

The first two principal components (PC1 and PC2) explained 68.9% and 17.5% of the total variance, respectively, accounting for a cumulative variance of 86.4% (Figure 3). This high cumulative proportion indicates that the first two principal components adequately represent the variability among the evaluated traits. The PCA biplot illustrates the relationships among traits based on the angles between their vectors. Plant height (PH), ear attachment trait (EAT), and ear total weight (ETW) were represented by vectors with small angles between them, indicating strong positive correlations among these traits. Similarly, leaf width (LW), stem diameter (SD), total weight per plant (TWP), and leaf length (LL) also formed a cluster of closely aligned vectors, suggesting positive associations among these variables. Furthermore, the biplot revealed genotype–trait associations, with genotype G7 closely associated with the EAT vector, whereas genotypes G3 and G4 were positioned in the direction of the ETW vector, indicating superior performance for this trait.

3.3. Heritability and multi-trait selection in potatoes

Factor analysis (FA) showed that two main factors (FA1 and FA2) successfully explained 86.4% of the total variability in potato traits, indicating that most of the phenotypic variation can be represented through a simpler factor structure (Table 4). Vegetative traits such as LL, LW, SD, and PH showed high loadings on FA1 (e.g., LL = –0.95; LW = –0.75; SD = –0.83), indicating that FA1 reflects the components of vegetative growth and photosynthetic potential. This is biologically consistent because leaf size and SD are closely related to the plant's ability to capture light, photosynthetic rate, and biomass formation (Devaux and Haverkort, 2008). Meanwhile, yield traits such as EAT, ETW, and TWP tend to have high loadings on FA2 (e.g., EAT = 0.99; ETW = 0.92; TWP = 0.16), so that FA2 can

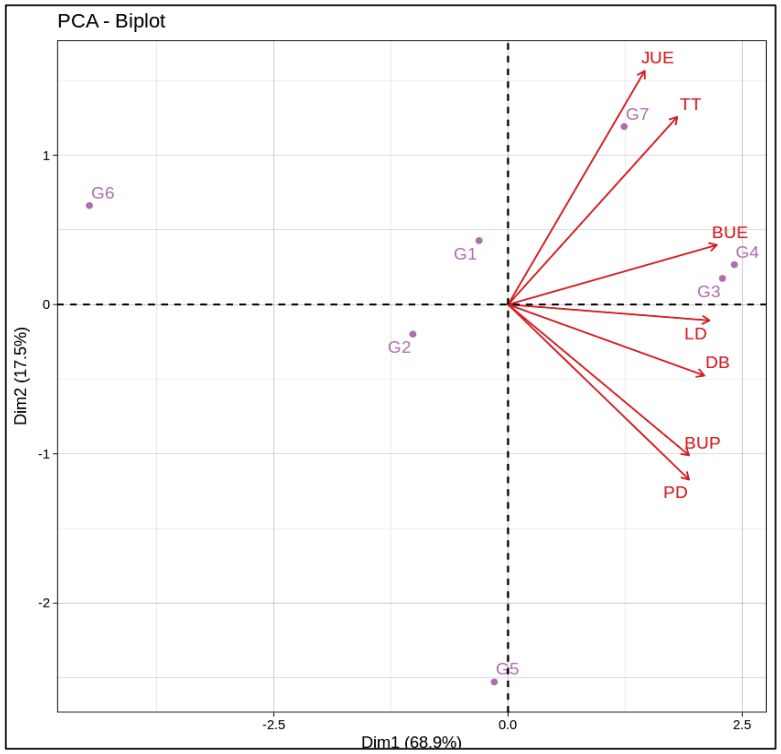


Figure 3. PCA biplot on all genotypes and measured traits
Abbildung 3. PCA-Biplot aller Genotypen und gemessenen Merkmale

be interpreted as a component of assimilate allocation and tuber formation efficiency. In the context of tropical highlands, tuber formation is influenced by the dynamics of the transition from the vegetative to reproductive phases that are influenced by temperature and radiation, so the separation of these factors is biologically plausible.

More specifically, high heritability values (>76%) for all traits indicate that variation between genotypes is more dominant than environmental variation, so that these characters are stable enough to describe genotype differences in tropical highland environments. However, high communality values (>0.82) for almost all traits indicate that the factor model successfully captures most of the variance of each trait, so that the biological interpretation of FA1 and FA2 is reliable. In the context of plant ecology, this factor structure supports the idea that adaptation of potato genotypes to tropical highland environments involves two main dimensions: (1) vegetative growth ability that determines the source of assimilates and (2) the efficiency of assimilate allocation to tubers as a sink. This approach is in line with the idea that understanding genotype performance in tropical environments must consider the integration of many traits, not just a single character (Olivoto and Nardino, 2022).

Identification of genotypes approaching ideotype through MGIDI resulted in three main genotypes that exceeded or were on the red line, namely G7, G4, and G3 (Figure 4A), where G7 was the best genotype. Genotype G1 was approaching the selection threshold, indicated by the red line, indicating the possibility that the genotype might have special char-

Table 4. Selection differentials for seven characters tested on potato genotypes
Tabelle 4. Selektionsdifferenziale für sieben an Kartoffelgenotypen getestete Merkmale

Variables	FA1	FA2	Sense	h2 (%)	Communality	Uniqueness
LL	−0.95	0.10	Increase	94.1	0.92	0.08
LW	−0.75	0.52	Increase	82.9	0.83	0.17
SD	−0.83	0.38	Increase	94.3	0.83	0.17
PH	−0.28	0.89	Increase	76.1	0.87	0.13
EAT	−0.09	0.90	Increase	94.9	0.82	0.18
ETW	−0.65	0.71	Increase	87.7	0.92	0.08
TWP	−0.91	0.16	Increase	87.5	0.85	0.15
Cumulative (%)	68.8	86.4				

FA = factor analysis; h2 = heritability

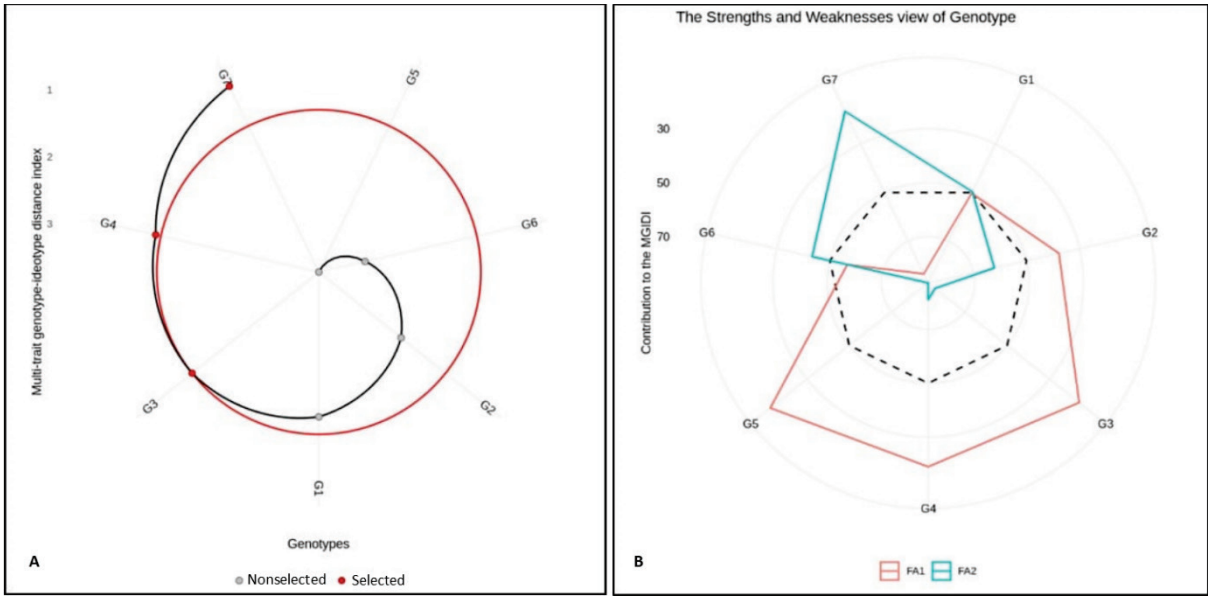


Figure 4. Multiple Genotype–Ideotype Distance Index (MGIDI). A. Somaclones ranking, B. Strengths and weaknesses view
Abbildung 4. Multipler Genotyp-Ideotyp-Distanzindex (MGIDI), A. Somaklon-Rangliste, B. Stärken- und Schwächenübersicht

acteristics. Meanwhile, genotype G5 was on the trajectory, indicating that it was the genotype furthest from the desired criteria. The desired character values for most of the characters being investigated were indicated by the selected mutations. Visualization of the strengths and weaknesses of a genotype can be assessed with MGIDI (Figure 4B). The selected genotypes are expected to exhibit high factor loadings for the traits represented by each principal factor. Genotype G7 was primarily associated with FA2, reflecting high loadings for plant height (PH), economic amount of tuber (EAT), and economic tuber weight (ETW), whereas it exhibited low loadings on FA1, indicating a weak contribution to the traits represented by this factor. In contrast, genotypes G5, G4, and G3 were primarily associated with FA1, showing high loadings for leaf length (LL), leaf width (LW), stem diameter (SD), and tuber weight per plot (TWP), while exhibiting low loadings on FA2.

4. Discussion

This analysis showed that all tested morphological and yield traits were significantly different between potato genotypes in tropical highland environments ($p < 0.01$ and $p < 0.001$), including LL, LW, SD, PH, number of economically viable tubers, ETW, and TWP. The existence of morphological and phenotypic diversity is a fundamental prerequisite in plant breeding activities, serving as an important basis for determining the criteria and implementing character selection (Yadav et al., 2025). This finding is consistent with the results of previous research reporting that potato mutant genotypes induced by gamma rays show substantial differences (Maulana et al., 2024). These significant differences can be explained by three main factors: differences in the genotypes themselves, environmental influences, and genotype–environment interactions (Ebem et al., 2021).

These results reflect significant morphological diversity in vegetative growth responses and biomass allocation to tubers. Physiologically, variations in leaf size and SD indicate differences in genotypes' capacity to capture and utilize solar radiation and regulate photosynthetic rates, which are important factors in tropical highland conditions characterized by high daily temperature fluctuations and strong light intensities (Devaux and Haverkort, 2008; Molahlehi et al., 2013). Significant differences in PH also have implications for canopy architecture, which influences light-use efficiency and interleaf competition for environmental resources.

The CV is used to assess the relative level of diversity and precision of the data. In this study, CV values were divided into three criteria: low, indicated by LL, SD, PH, EAT, and TWP; medium, indicated by LW; and high, indicated by ETW. Traits classified as low and medium show relatively low and homogeneous variation, thus providing good validity for vegetative traits. Conversely, traits with high CV

values (>20%) exhibit higher diversity but are still within acceptable limits for complex traits. Yield traits (including ETW) are generally more sensitive to environmental factors such as temperature and soil moisture; therefore, higher CV values are often found in agronomic analyses (Tokatlidis et al., 2023; Lee et al., 2023).

Identifying traits with high correlations is crucial for improving the efficiency of the selection process (Ahmadikhah et al., 2008). This study found that all traits had significant positive correlations, including EAT with PH, TWP, LW, LL, SD, and ETW. This correlation provides an opportunity to utilize these traits as effective indirect selection criteria to identify genotypes with high yield potential (Joshi et al., 2020). Variation in yield traits indicates that genotypes respond differently to resource allocation from the vegetative to reproductive phases. Therefore, the significant ANOVA results for all these traits support the use of a multi-trait approach such as MGIDI to integrate information on multiple plant traits simultaneously to evaluate genotype performance comprehensively and biologically meaningfully (Olivoto and Nardino, 2022). Overall, this high level of genetic variation is a prerequisite for predicting the superior potential of future potato genotypes (Gowda et al., 2025).

The value for each character in each PC indicates the character's contribution to diversity. PC1 and PC2 explain the main variation pattern and account for 86.3% of the total variation (Table 3). The PCA biplot serves to visualize the correlation coefficient between characters. This correlation can be interpreted through the angle between the vectors representing the tested characters; a small angle indicates a strong positive correlation (Maulana et al., 2023). Based on the biplot interpretation, this condition indicates that genotypes that show minimal angular variation among important character vectors can be key in formulating effective selection strategies. This directly leads to the identification of genotypes with high and stable tuber yield potential. These results also indicate that all characters contribute to genotypic diversity on PC1. Meanwhile, only the PH and EAT characters significantly contribute to genotypic diversity on PC2.

The PCA biplot (Figure 3) serves as a visual tool that helps understand the complex relationships between traits and individuals (genotypes) (Khan et al., 2021; Maulana et al., 2023). By observing the position and direction of the trait vectors and genotype points on the biplot, patterns and relationships hidden in the data can be identified. The EAT trait has a strong affinity with PH and ETW. Similarly, LW is close to SD, TWP, and LL. This proximity indicates a strong positive vector angle correlation between these traits, indicating a significant interrelated contribution to diversity. Interpretation of genotype positions on the biplot also provides insight into trait dominance. For example, the position of Genotype 7 (G7), which is very close to the EAT trait vector angle, indicates that this genotype has high dominance or superior performance for that trait.

Quantitative genetic approaches have been recognized for their effectiveness in selecting the best genotypes, but conventional methods are often limited to studies involving only a few traits (Maulana et al., 2023). To address this, this study applied the Multi-Trait Index Analysis by Distance (MGIDI) (Olivoto and Nardino, 2021). The results of FA showed that two main factors (FA1 and FA2) successfully explained 68.8% of the total variability. Vegetative traits such as LL, LW, SD, and PH showed high loadings on FA1, which reflects the components of vegetative growth and photosynthetic potential. This is biologically consistent because leaf size and SD are closely related to plant ability to capture light, photosynthetic rate, and biomass formation (Devaux and Haverkort, 2008). Previous studies have shown that environmental stress reduces shoot biomass, thereby limiting dry matter allocation to tubers (Gervais et al., 2021; Chang et al., 2018). In this study, the high rainfall recorded in September may have influenced shoot growth and biomass partitioning, suggesting that including shoot dry matter and climate data at different DAP could improve the interpretation of potato responses under tropical conditions. Meanwhile, FA2 is interpreted as an assimilate allocation component because it is dominated by yield traits such as EAT and ETW. Biologically, this separation of factors reflects the dynamics of transition from the vegetative to the reproductive phase influenced by temperature and radiation in tropical highlands.

Specifically, high heritability values (>76%) for almost all traits indicate that variation between genotypes is more dominant than environmental variation, making these traits relatively stable (Olivoto and Nardino, 2022). In this study, the very high heritability value for the number of tubers per plant (>87%) is crucial. This characteristic allows for efficient selection of superior genotypes in early generations, ultimately saving up to two growing seasons in a breeding program cycle. This factor structure supports the idea that potato adaptation to highlands involves two main dimensions: vegetative growth capacity (source) and efficient assimilate allocation to tubers (sink).

The MGIDI analysis successfully identified G7, G4, and G3 as the genotypes closest to the ideal criteria (Figure 4A). The G7 genotype (Median cultivar) was selected due to its highest productivity and disease resistance, which is crucial

considering that farmers still rely on the susceptible Granola cultivar. Utilizing G7 could be a strategic solution to reduce dependence on seed imports by up to 40%. Furthermore, G4 and G3 demonstrated superior TWP, supported by optimal leaf morphology and SD for assimilate accumulation. The unique characteristics of G4 and G3, which even exceed the ideal criteria, make them important targets for future breeding programs.

The flexibility of the MGIDI method has been demonstrated through its application to various commodities such as wheat, soybeans, corn, rice, and potato (Pour-Aboughadareh and Poczai, 2021; Nasution et al., 2025; Putri et al., 2026). The MGIDI selection accuracy in this study reached 72.4%, comparable to the success rates in rice (91.2%) and corn (85.7%) (Yue et al., 2022), thus confirming the reliability of this method. Although G7, G4, and G3 show great potential, this study was conducted at only one location. Therefore, validation through multi-location testing is urgently needed to confirm the stability and adaptability of these promising genotypes before they are widely recommended as new superior varieties.

5. Conclusions

ANOVA showed significant differences for all observed traits. The correlation analysis showed that TWP (yield) had a significant positive correlation with various growth parameters and yield components. The increase in TWP was in line with the increase in ETW, number of economic tubers, SD, and PH. In addition, leaf dimensions, including LL and LW, also contributed significantly to the achievement of TWP in each observation area unit. The MGIDI analysis successfully identified the highest heritability for the number of economical tubers (94.9%) and accumulated PCA variance of 86.3%. The MGIDI analysis successfully identified three superior potato genotypes (G7, G3, and G4) with the desired trait profiles.

Acknowledgments

A high appreciation is given to the field assistance team during the trial, and thanks to the National Research and Innovation Agency and Hikmah Farm for providing field research facilities to conduct this research. This research was funded by a research grant from the National Research and Innovation Agency (Rumah Program ORPP).

Author Contribution

Conceptualization: H.M., I.R., H.H.N., methodology: H.M., I.R., software: H.M., M.R.F., A.Y., validation: H.M., I.R., H.H.N., K., D.W.U., T.H., A.K.K., formal analysis: M.R.F., A.Y., K., investigation: M.R.F., K., T.H., A.K.K., A.A., R.C.H., resources: H.M., I.R., data curation: M.R.F., T.H., K., A.K.K., A.A., R.C.H., writing-original draft: H.M., M.R.F., writing-review and editing: I.R., H.H.N., A.Y., K., D.W.U., A.A., T.H., A.K.K., R.C.H., visualization: M.R.F., A.Y., supervision: H.M., project administration: H.M., funding acquisition: H.M. All co-authors reviewed the final version and approved the manuscript before submission.

Conflict of interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

References

Ahmadikhah, A., Nasrollanejad, S., Alishah, O., 2008. Quantitative studies for investigating variation and its effect on heterosis of rice. International Journal of Plant Production 2(4), 297–307.

Alam, Z., Akter, S., Khan, M. A. H., Amin, M. N., Karim, M. R., Rahman, M. H. S., Rashid, M. H., Rahman, M. A., Mokarroma, N., Sabuz, A. A., Alam, M. J., Roy, T. K., Rahaman, E. H. M. S., Ali, M. A., Chanda, D., Sarker, U., 2024. Multivariate analysis of yield and quality traits in sweet potato genotypes (*Ipomoea batatas* L.). Scientia Horticulturae 328, 112901. Doi: 10.1016/j.scienta.2024.112901

Camire, M. E., Kubow, S., Donnelly, D. J., 2021. Potatoes and human health. Critical Reviews in Food Science and Nutrition 61(10), 1642–1662. DOI: 10.1080/10408390903041996

Chang, D. C., Jin, Y. I., Nam, J. H., Cheon, C. G., Cho, J. H., Kim, S. J., Yu, H. S., 2018. Early drought effect on canopy development and tuber growth of potato cultivars with different maturities. Field Crops Research 215, 156–162. DOI: 10.1016/j.fcr.2017.10.008

Devaux, A., Haverkort, A. J., 2008. The effects of shifting planting dates and mulching on late blight (*Phytophthora*

infestans) and drought stress of potato crops grown under tropical highland conditions. Experimental Agriculture 23(3), 325–333. DOI: 10.1017/S001447970001721X

Ebem, E. C., Afuape, S. O., Chukwu, S. C., Ubi, B. E., 2021. Genotype × environment interaction and stability analysis for root yield in sweet potato [*Ipomoea batatas* (L.) Lam]. Frontiers in Agronomy 3, 665564. DOI: 10.3389/fagro.2021.665564

Gowda, K. H., Amarananjundeswara, H., Fakrudin, B., Vasudeva, K. R., Kattegoudar, J., Doddabasappa, B., 2025. Genetic variability, heritability and divergence analysis for growth, yield and nutritional quality parameters in potato (*Solanum tuberosum* L.). International Journal of Advanced Biochemistry Research 9(2), 633–647. DOI: 10.33545/26174693.2025.v9.i2i.3854

Gervais, T. G., Creelman, A., Li, X.-Q., Bizimungu, B., De Koeyer, D., Dahal, K., 2021. Potato response to drought stress: Physiological and growth basis. Frontiers in Plant Science 12, 698060. DOI: 10.3389/fpls.2021.698060

Haverkort, A. J., Struik, P. C., 2015. Yield levels of potato crops: Recent achievements and future prospects. Field Crops Research 182, 76–85. DOI: 10.1016/j.fcr.2015.06.002

Joshi, L. P., Sharma, S., Poudel, A., Kandel, B. P., 2020. Varietal evaluation and genetic variability in rice (*Oryza sativa* L.) genotypes of the Mid-hill region of Nepal. Vietnam Journal of Agricultural Sciences 3(2), 580–592. DOI:10.31817/VJAS.2020.3.2.02

Khan, M. M. H., Rafii, M. Y., Ramlee, S. I., Jusoh, M., Al-Mamun, M., 2021. Genetic analysis and selection of Bambara groundnut (*Vigna subterranea* [L.] Verdc.) landraces for high yield revealed by qualitative and quantitative traits. Scientific Reports 11(1), 7597. DOI: 10.1038/s41598-021-87039-8

Lee, S., Kim, J., Park, H., 2023. Stability analysis of crop yield across multiple environments using statistical indicators. Agriculture 13(2), 256. DOI: 10.3390/agriculture13020256

Maulana, H., Maxiselly, Y., Yuwariah, Y., Ruswandi, D., 2023. Heritability and selection using GGE biplots and the sustainability index (SI) of maize genotypes under different cropping systems in upland. Sustainability 15(8), 6824. DOI: 10.3390/su15086824

Maulana, H., Nafi'ah, H. H., Solihin, E., Ruswandi, D., Arifin, M., Amien, S., Karuniawan, A., 2022. Combined stability analysis to select stable and high yielding sweet potato genotypes in multi-environmental trials in West Java, Indonesia. Agriculture and Natural Resources 56(4), 761-772. DOI: 10.34044/J.ANRES.2022.56.4.10

Maulana, H., Widaningsih, N.A., Kusmana, Jaenudin, U., Utami, D. W., Akhdiya, A., Handayani, T., Karjadi, A.K., Maharijaya, A., Sobir, Roostika, I., 2024. Selection of superior potato (*Solanum tuberosum* L.) by combined stability analysis for future breeding strategies. Agriculture 70 (2), 72–86. DOI: 10.2478/agri-2024-0006

Molahlehi, L., Steyn, J. M., Haverkort, A. J., 2013. Potato crop response to genotype and environment in a subtropical highland agro-ecology. Potato Research 56(3), 237–258. DOI: 10.1007/s11540-013-9241-1

Mølmann, J. A. B., Johansen, T. J., 2025. Influence of growth temperature on development and yield in potato cultivars. Potato Research 68, 2939–2950. DOI: 10.1007/s11540-025-09854-0

Nafi'ah, H.H., Fajarfika, R., Fatimah, R., Maulana, H., Yoel, A., 2025. Comparison of soil microbial composition and fertility in rhizosphere of healthy and Fusarium wilt-affected sweet potato plants. Biodiversitas 26(2), 941–950. DOI: 10.13057/biodiv/d260243

Nasution, K. Y., Melati, P., Dewi, A. K., Maryono, M. Y., Dwimahyani, I., Solim, M. H., Yuliasti, Harsanti, L., Widiarsih, S., Sitaresmi, T., Maulana, H., Suwarno, W. B., Sobrizal, 2025. Yield stability and multitrait selection of advanced mutant rice genotypes across diverse environments in Indonesia. Advances in Agriculture 2025, 9092588. DOI: 10.1155/aia/9092588

Olivoto, T., Lúcio, A.D., 2020. metan: An R package for multi-environment trial analysis. Methods in Ecology and Evolution 11(6), 783–789. DOI: 10.1111/2041-210X.13384

Olivoto, T., Nardino, M., 2021. MGIDI: toward an effective multivariate selection in biological experiments. Bioinformatics 37(10), 1383–1389. DOI: 10.1093/bioinformatics/btaa981

Olivoto, T., Nardino, M., 2022. MGIDI: a powerful tool to analyze plant multivariate data. Plant Methods 18, 121. DOI: 10.1186/s13007-022-00952-5

Pallavi, M., Maruthi Prasad, B. P., Shanthi, P., Reddy, V. L. N., Nirmal Kumar, A. R., 2024. Multi trait genotype–ideotype distance index (MGIDI) for early seedling vigour and yield related traits to identify elite lines in rice (*Oryza sativa* L.). Electronic Journal of Plant Breeding 15(1), 120–131. DOI: 10.37992/2024.1501.020

Pour-Aboughadareh, A., Poczai, P., 2021. A dataset on multi-trait selection approaches for screening desirable wild relatives of wheat. Data in Brief 39, 107541. DOI: 10.1016/j.dib.2021.107541

Putri, R.A., Maulana, H., Roostika, I., Nafi'ah, H.H. Yoel, A., Kusmana, Handayani, T., Karjadi, A.K., Nurdiana, D.,

2026. Selection of promising potato (*Solanum tuberosum* L.) Genotypes using the multi-traits genotype-ideotype distance index (MGIDI). SABRAO Journal of Breeding and Genetics 58 (2), 676–687. DOI: 10.54910/sabrao2026.58.2.18

Tokatlidis, I. S., Koutis, K., Tamoutsidis, E., 2023. Coefficient of variation and its use in plant breeding and agronomic experiments. Agronomy 13(1), 176. DOI: 10.3390/agronomy13010176

Uddin, M. S., Billah, M., Afroz, R., Rahman, S., Jahan, N., Hossain, M.G., Bagum, S. A., Uddin, M. S., Khaldun, A. B. M., Azam, M. G., Hossain, N., Akanda, M. A. L., Alhomrani, M., Gaber, A., Hossain, A., 2021. Evaluation of 130 eggplant (*Solanum melongena* L.) genotypes for future breeding program based on qualitative and quantitative traits, and various genetic parameters. Horticulturae 7(10), 376. DOI: 10.3390/horticulturae7100376

Yadav, L. P., Gangadhara, K., Singh, A. K., Yadav, V., Apparao, V. V., Pawar, A., Kumar, S., Janani, P., Sahil, A., Kumar, P., Khapte, P. S., Meena, N. K., Jinger, D., Rane, J., 2025. Genetic variability, morphological diversity, and antioxidant potential in gynoecious Coccinia accessions: Implications for breeding and biofortification. BMC Plant Biology 25, 844. DOI: 10.1186/s12870-025-06335-x

Yue, H., Wei, J., Xie, J., Chen, S., Peng, H., Cao, H., Bu, J., Jiang, X., 2022. A study on genotype-by-environment interaction analysis for agronomic traits of maize genotypes across Huang-huai-hai region in China. Phyton-International Journal of Experimental Botany 91(1), 57–81. DOI: 10.32604/phyton.2022.017308