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GENETIC PARAMETERS AND BREEDING STRATEGIES TO ENHANCE YIELD IN LOCAL SWEET POTATO (*Ipomoea batatas* (L.) Lam.) GERMPLASM FROM SOUTHEAST SULAWESI

PARAMETER GENETIK DAN STRATEGI PEMULIAAN UNTUK PENINGKATAN HASIL PADA PLASMA NUTFAH UBI JALAR (*Ipomoea batatas* (L.) Lam.) LOKAL ASAL SULAWESI TENGGARA

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ABSTRACT

Sweet potato (*Ipomoea batatas* (L.) Lam.) is an important food crop with strategic value for food security, dietary diversification, and the sustainability of rural livelihoods in Indonesia. Local sweet potato germplasm from Southeast Sulawesi represents a valuable genetic resource for breeding high-yielding and stress-resilient varieties. This study aimed to evaluate genetic diversity, heritability, trait correlations, and the direct and indirect contributions of agronomic traits to yield in 20 local sweet potato clones originating from Southeast Sulawesi. The experiment utilized a Randomized Complete Block Design (RCBD) with three replications, measuring 14 agronomic and physiological traits. The study was conducted under lowland tropical humid agroecosystem conditions in the Kendari area. Data were analyzed using analysis of variance, broad-sense heritability estimation, Pearson correlation, stepwise regression, and path analysis. Significant genetic variation was observed for all evaluated traits, with heritability values ranging from 58.43% to 97.08%. Tuber weight and tuber number per plant were identified as the primary yield determinants, whereas internode length exhibited a significant negative effect. Stepwise regression and path analysis confirmed that tuber weight had the strongest direct effect on yield, followed by tuber number. The integrative analytical approach applied in this study provides a comprehensive understanding of causal relationships among agronomic traits. These findings indicate that selection based on tuber weight and number of tubers per plant, combined with regulation of excessive vegetative growth, may enhance yield efficiency and support the development of high-yielding, locally adapted sweet potato varieties for tropical agroecosystems.

Key words: Agronomy, Path analysis, Heritability, Genetic diversity, Breeding strategy

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ABSTRAK

Ubi jalar (*Ipomoea batatas* (L.) Lam.) merupakan tanaman pangan penting yang memiliki nilai strategis dalam mendukung ketahanan pangan, diversifikasi konsumsi, dan keberlanjutan mata pencaharian masyarakat pedesaan di Indonesia. Plasma nutfah lokal ubi jalar dari Sulawesi Tenggara merupakan sumber daya genetik yang berharga untuk pemuliaan varietas berdaya hasil tinggi dan toleran terhadap cekaman. Penelitian ini bertujuan untuk mengevaluasi keragaman genetik, heritabilitas, korelasi antarkarakter, serta kontribusi langsung dan tidak langsung sifat agronomi terhadap hasil pada 20 klon ubi jalar lokal asal Sulawesi Tenggara. Percobaan disusun menggunakan Rancangan Acak Kelompok Lengkap dengan tiga ulangan, dan sebanyak 14 karakter agronomi dan fisiologis diamati. Penelitian dilaksanakan pada kondisi agroekosistem tropis lembap dataran rendah di wilayah Kendari. Data dianalisis menggunakan analisis ragam, estimasi heritabilitas arti luas, korelasi Pearson, regresi stepwise, dan analisis lintasan. Hasil penelitian menunjukkan adanya keragaman genetik yang signifikan pada seluruh karakter yang diamati, dengan nilai heritabilitas berkisar antara 58,43% hingga 97,08%. Bobot umbi dan jumlah umbi per tanaman secara konsisten teridentifikasi sebagai penentu utama hasil, sedangkan panjang ruas menunjukkan pengaruh negatif yang nyata. Regresi stepwise dan analisis lintasan mengonfirmasi bahwa bobot umbi memiliki pengaruh langsung terbesar terhadap hasil, diikuti oleh jumlah umbi per tanaman. Pendekatan analisis integratif ini memberikan pemahaman komprehensif mengenai hubungan kausal antar karakter. Temuan ini mengindikasikan bahwa seleksi berbasis bobot umbi dan jumlah umbi per tanaman, disertai pengendalian pertumbuhan vegetatif yang berlebihan, berpotensi meningkatkan efisiensi hasil serta mendukung pengembangan varietas ubi jalar unggul yang adaptif terhadap agroekosistem tropis.

Kata kunci: Agronomi, Analisis lintasan, Heritabilitas, Keragaman genetik, Strategi pemuliaan

INTRODUCTION

Sweet potato (*Ipomoea batatas* (L.) Lam.) is a strategic crop for supporting food security, dietary diversification, and rural economic development in Indonesia. Agricultural statistics indicate that national sweet potato production has experienced fluctuations associated with changes in harvested area and productivity (Pusat Data dan Sistem Informasi Pertanian, 2023). At the regional level, Southeast Sulawesi recorded a production of 13,272 tons from 1,079 ha with an average productivity of 123.00 quintals ha^{-1} during the January–August 2018 period (BPS Provinsi Sultra, 2018). In Kendari City, a sharp decline in sweet potato production was reported in 2022, mainly due to decreasing harvested area and productivity (BPS Kota Kendari, 2023). These trends highlight the urgent need to develop superior, locally adapted sweet potato varieties.

Local sweet potato germplasm represents a rich source of genetic diversity that can be exploited in breeding programs to improve agronomic and yield-related traits. Broad phenotypic variation provides a strong basis for identifying superior genotypes (Fajriani et al., 2012; Suaib et al., 2000; Priyanto et al., 2023). Moreover, local clones have already adapted to specific biotic and abiotic stresses, making them valuable parental material in the development of high-yielding and stress-tolerant varieties (Julianto et al., 2021; Fellahi et al., 2024; Getahun et al., 2019).

However, information on genetic parameters, heritability, and interrelationships among agronomic traits in local sweet potato genotypes remains limited, resulting in less efficient selection strategies (Teklu et al., 2021; Faysal et al., 2022). Traits such as tuber weight and tuber diameter have generally been reported to possess high heritability and play a major role in yield improvement (Patel et al., 2022). To better understand the relationships among these traits, correlation analysis and path coefficient analysis are widely used to identify both direct and indirect effects on yield (Wright, 1921; Dewey & Lu, 1959; Saroj et al., 2021; (Yadav et al., 2024).

Integrated studies combining analysis of variance, estimation of genetic parameters, correlation analysis, and path analysis on local sweet potato germplasm in Southeast Sulawesi are still very limited, despite the region’s considerable genetic resources. Therefore, this study aims to (1) evaluate genetic variability and heritability of various agronomic traits in 20 local sweet potato clones from Southeast Sulawesi, (2) analyze the correlation between agronomic traits and total tuber yield per plant, and (3) determine the direct and indirect effects of these traits on yield using path coefficient analysis. The novelty of this study lies in the integrated application of multiple quantitative genetic approaches to comprehensively assess local Indonesian sweet potato germplasm.

MATERIALS AND METHODS

Plant Materials and Experimental Site

This study is a continuation of research conducted in 2018, which analyzed 20 sweet potato (*Ipomoea batatas* (L.) Lam.) clones using cluster analysis based on morphological characters. Although the previous study successfully grouped the clones according to phenotypic similarities, the functional relationships among traits influencing tuber yield were not fully elucidated. Therefore, the 2025 study applied path analysis to quantify the direct and indirect effects of key morphological and agronomic traits on tuber yield per plant, aiming to deepen the understanding of yield-determining characteristics in superior local sweet potato clones from Southeast Sulawesi, Indonesia.

Twenty sweet potato clones were collected from diverse agroecological zones in Southeast Sulawesi Province to capture broad morphological and physiological variability representative of the regional genetic resources. The field experiment was conducted at the Research Farm of the Faculty of Agriculture, Halu Oleo University, Kendari. The site represents a lowland tropical environment with average daily temperatures of 26–32°C and relative humidity of 70–85%, and is characterized by Inceptisol soil with sandy loam to loam texture and moderate organic matter content. Fertilization consisted of Urea (75 kg ha^{-1}), SP-36 (75 kg ha^{-1}), and KCl (100 kg ha^{-1}), applied in two stages: one-third of the urea along with the full doses of SP-36 and KCl at one week after planting, and the remaining urea at six weeks after planting. Crop management was uniformly applied across all plots, including vine training, weeding, irrigation, replanting of missing plants, and disease control using the fungicide Ditane. Harvesting was conducted at four months after planting.

Experimental Design

The trial was arranged in a Randomized Complete Block Design (RCBD) with three replications. Each clone represented one treatment and was randomized within each block to minimize environmental bias. The experimental unit consisted of a 2.4 × 2.4 m plot, with plants spaced at 60 × 30 cm, resulting in uniform plant density across treatments.

Trait Measurement

Fourteen agronomic and physiological traits were recorded to assess genetic variability: leaf length (X01), petiole length (X02), stem length (X03), stem diameter (X04), internode length of vine (X05), vine length (X06), number of vines (X07), internode diameter (X08), internode length (X09), tuber diameter (X10), tuber length (X11), weight per tuber (X12), number of tubers per plant (X13), and total tuber weight per plant (Y). Observations were conducted on eight randomly selected plants per plot. These traits were chosen based on their relevance to yield potential and tuber quality, and are commonly employed in sweet potato breeding programs.

Data Collection and Statistical Analysis

Data processing and statistical analyses were performed using R software (Team, 2023). The packages openxlsx, tidyr, and dplyr facilitated data handling, cleaning, and organization, ensuring transparency and reproducibility (Boer et al., 2024). Analysis of variance (ANOVA) was carried out using the agricolae package (de Mendiburu, 2020) based on the additive linear model for RCBD (Karyawati & Puspitaningrum, 2021):

$$Y_{ij} = \mu + \beta_j + \tau_i + \varepsilon_{ij}$$

where μ is the overall mean, β_j is the block effect, τ_i is the treatment effect, and ε_{ij} is the experimental error. From the ANOVA results, genetic variance (σ^2g), environmental variance (σ^2e), and phenotypic variance (σ^2p) were derived to estimate broad-sense heritability ($H^2 = \sigma^2g/\sigma^2p$) and the genotypic coefficient of variation (GCV) (Priyanto et al., 2023). Correlation analysis was performed using the Hmisc package (Harrell, 2021) to calculate Pearson's correlation coefficients and evaluate linear associations between yield and its component traits.

Path analysis was employed to partition the direct and indirect effects of morphological and agronomic traits on yield per plant using the *lavaan* package (Rosseel, 2012), following the theoretical framework of Wright (1921) and Dewey & Lu (1959). An initial conceptual diagram was developed to represent the hypothesized causal relationships among traits, with total tuber yield per plant (Y) as the endogenous variable and the following morphological/agronomic traits as exogenous variables: leaf length (X01), petiole length (X02), stem length (X03), stem diameter (X04), vine internode length (X05), vine length (X06), number of vines (X07), internode diameter (X08), internode length (X09), tuber diameter (X10), tuber length (X11), tuber weight (X12), and tuber number per plant (X13).

Mathematically, the path model can be expressed in the following structural equation form:

$$Y = p_{YX01}X_{01} + p_{YX02}X_{02} + p_{YX03}X_{03} + \cdots + p_{YX13}X_{13} + \varepsilon$$

where p_{YXi}represents the path coefficient (direct effect) of the i^{th} variable on total tuber yield per plant (Y), and εdenotes the residual error accounting for unexplained variation. The indirect effect of each trait on Y was calculated as the product of path coefficients along the relevant mediating pathways.

Predictor variables were selected using stepwise regression based on the lowest Akaike Information Criterion (AIC), with a significance threshold of $p \leq 0.05$. Structural relationships among variables were visualized using the *semPlot* package (Epskamp, 2015). This analytical framework facilitates the identification of key traits that contribute the greatest direct effects on yield, while also explaining indirect effects mediated by correlated traits (Mohanty et al., 2016; Julianto et al., 2021; Saroj et al., 2021; Yadav et al., 2024).

RESULTS AND DISCUSSION

Genetic Diversity and Heritability of Agronomic Traits

Analysis of variance revealed significant genetic variation across all measured agronomic traits among the 20 local sweet potato clones (Table 1). The broad-sense heritability (H^2) values ranged from 58.43% for total tuber yield (Y) to 97.08% for vine internode length (X05), indicating a wide genetic base for most traits. High H^2 values (above 80%) were observed for the majority of morphological and physiological characters such as: leaf length (X01), stem diameter (X04), and vine length (X06), suggesting that these traits are largely under genetic rather than environmental control.

Table 1. Mean values, variance components, and broad-sense heritability of agronomic traits in local sweet potato clones from Southeast Sulawesi.

Traits	Min	Max	Mean	Genotipic variance (σ^2g)	Environ-mental variance (σ^2e)	Phenotypic variance (σ^2p)	Broad-sense heritability H^2 (%),	Coefficient of variation CV (%)	Criteria
Leaf length	6.58	14.69	10.31	2.148	0.132	2.280	94.20	6.11	High
Petiole length	8.93	19.88	14.14	6.736	0.759	7.495	89.87	10.67	High
Stem length	37.00	290.50	123.81	2691.673	268.506	2960.178	90.93	22.92	High
Stem diameter	0.33	0.72	0.57	0.005	0.001	0.006	89.15	7.49	High
Vine internode length	1.00	6.18	3.43	1.731	0.052	1.783	97.08	11.51	High
Vine length	22.00	259.63	102.16	1427.142	215.518	1642.660	86.88	24.89	High
Number of vines	1.67	25.38	7.54	19.382	2.117	21.500	90.15	33.43	High
Internode diameter	0.30	0.63	0.50	0.003	0.000	0.004	88.65	6.97	High
Internode length	1.62	6.57	3.91	1.009	0.120	1.128	89.41	15.31	High
Tuber diameter	2.88	7.38	4.93	0.965	0.137	1.102	87.57	13.00	High
Tuber length	6.83	20.45	12.31	5.751	0.704	6.455	89.10	11.80	High
Tuber weight	49.72	347.60	175.96	2348.396	651.099	2999.495	78.29	25.12	High
Tuber number per plant	1.86	5.88	3.45	0.225	0.128	0.353	63.74	17.94	Low
Total tuber yield per plant	104.29	1103.75	572.91	15344.743	10915.529	26260.272	58.43	31.59	Low

Notes: Leaf length (X01), petiole length (X02), stem length (X03), stem diameter (X04), vine internode length (X05), vine length (X06), number of vines (X07), internode diameter (X08), internode length (X09), tuber diameter (X10), tuber length (X11), tuber weight (X12), tuber number per plant (X13), and total tuber yield per plant (Y).

These results are in line with previous studies on sweet potato and other root crops, which reported that high heritability in morphological traits reflects stable gene expression and minimal environmental influence (Dash et al., 2015; Mohanty et al., 2016). Similarly, high H^2 values for vine and leaf traits were also observed in sesame (Teklu et al., 2021) and rice (Faysal et al., 2022), reinforcing the idea that such vegetative traits can serve as reliable indicators for genotype selection under field conditions.

Conversely, total tuber yield (Y) and number of tubers per plant (X13) showed relatively low heritability (<70%), suggesting strong environmental influence on these complex yield traits. Yield is an integrative parameter influenced by multiple genetic and non-genetic factors, and its improvement is typically more effective through indirect selection of yield components rather than direct selection (Patel et al., 2022; Getahun et al., 2019).

Therefore, breeding programs should prioritize traits with high heritability and moderate genotypic coefficient of variation, such as vine internode length (X05), stem length (X03), number of vines (X07), and petiole length (X02) as they are more responsive to selection pressure. These findings strengthen earlier observations in tropical sweet potato populations by Julianto et al. (2021), who emphasized that morphological uniformity and stable heritability serve as the foundation for identifying elite genotypes in local germplasm improvement.

Trait Correlations

Pearson correlation analysis showed strong positive associations between total tuber weight per plant (Y) and both weight per tuber (X12; r = 0.827) and tuber diameter (X10; r = 0.819) (Table 2). These results highlight the importance of tuber diameter and weight per tuber as indicators for yield improvement, consistent with findings by Zayed et al. (2023) in rice (Oryza sativa).

In contrast, negative correlations were observed between yield and vine internode length (X05; r = -0.611) as well as internode length (X09; r = -0.512), indicating that excessive vegetative growth may reduce tuber formation. Furthermore, a negative correlation between weight per tuber (X12) and number of tubers per plant (X13; r = -0.313) revealed a trade-off between tuber size and number. Such trade-offs have also been reported in rice, highlighting the importance of balancing productivity with quality (Yadav et al., 2024). These findings suggest that correlation analysis provides valuable insights for designing breeding strategies that enhance yield while maintaining tuber quality and production stability.

Table 2. Pearson’s correlation coefficients among agronomic traits in local sweet potato clones.

	X01	X02	X03	X04	X05	X06	X07	X08	X09	X10	X11	X12	X13	Y
X01	1													
X02	0.48	1												
X03	0.26	0.35	1											
X04	0.53	0.36	-0.02	1										
X05	0.09	0.46	0.76	0.05	1									
X06	0.07	0.39	0.61	0.06	0.72	1								
X07	-0.14	-0.46	-0.71	-0.07	-0.79	-0.78	1							
X08	0.40	0.63	0.09	0.52	0.24	0.35	-0.47	1						
X09	0.03	0.48	0.70	-0.08	0.83	0.89	-0.78	0.28	1					
X10	0.08	-0.32	-0.34	0.45	-0.36	-0.11	0.29	-0.19	-0.35	1				
X11	0.29	0.28	0.06	0.07	-0.15	0.05	0.11	0.35	0.03	-0.33	1			
X12	0.24	-0.19	-0.41	0.46	-0.56	-0.20	0.45	-0.03	-0.41	0.83	0.20	1		
X13	-0.52	-0.16	-0.14	-0.35	-0.06	-0.18	0.10	-0.29	0.01	-0.09	-0.43	-0.31	1	
Y	-0.01	-0.34	-0.45	0.29	-0.61	-0.40	0.50	-0.23	-0.51	0.82	-0.12	0.83	0.17	1

Notes: Leaf length (X01), petiole length (X02), stem length (X03), stem diameter (X04), vine internode length (X05), vine length (X06), number of vines (X07), internode diameter (X08), internode length (X09), tuber diameter (X10), tuber length (X11), tuber weight (X12), tuber number per plant (X13), and total tuber yield per plant (Y).

Selection of Key Traits through Stepwise Regression

Stepwise multiple regression identified five key predictors of yield: stem length (X03), internode length (X09), tuber length (X11), weight per tuber (X12), and number of tubers per plant (X13), that collectively explained 93.75% of yield variation ($R^2 = 0.9375$; adjusted $R^2 = 0.9152$) (Table 3).

Among these, weight per tuber (X12) (B = 2.8687; $p < 0.001$) and number of tubers (X13) (B = 124.4054; $p < 0.001$) had the strongest positive contributions, reinforcing their roles as the principal determinants of yield. Similar findings were reported by Gomathi et al. (2021) in black gram and by Patel et al. (2022) in Indian bean, where yield per plant was primarily driven by a combination of biomass partitioning efficiency and reproductive unit number.

Table 3. Stepwise multiple linear regression analysis of agronomic traits contributing to tuber yield in local sweet potato clones.

Agronomic Trait	Coefficient (B)	Standard Error	t-value	p-value	Remarks
Intercept	-187.79	140.48	-1.337	0.2026	ns
Stem length	0.5868	0.2959	1.983	0.0673	*
Internode length	-39.1673	14.565	-2.689	0.0176	**
Tuber length	-7.5588	4.7525	-1.59	0.134	ns
Tuber weight	2.8687	0.2408	11.915	<0.001	***
Number of tubers per plant	124.4054	21.8908	5.683	<0.001	***

Notes: Stem length (X03), internode length (X09), tuber length (X11), tuber weight (X12), number of tubers per plant (X13); * $p < 0.1$, ** $p < 0.05$, *** $p < 0.001$, ns (not significant); Model statistics: $R^2 = 0.9375$; Adjusted $R^2 = 0.9152$; F = 42.01; $p < 0.001$; residual standard error = 47.19.

In contrast, internode length (X09) exhibited a significant negative effect (B = -39.1673; p = 0.0176), indicating that longer vegetative segments may hinder tuber initiation or assimilate transport to storage organs. These results corroborate the inverse relationship observed by Mohanty et al. (2016) between vine elongation and tuberization efficiency.

Although stem length (X03) showed a marginally positive contribution (p = 0.0673), its effect should be interpreted cautiously, as extreme elongation can lead to competition among vines for light and nutrients. The inclusion of tuber length (X11) in the final model, albeit non-significant, suggests that tuber shape contributes indirectly to marketable yield and post-harvest quality, aligning with consumer preference-driven breeding goals (Saroj et al., 2021).

These findings suggest that the optimal ideotype for local sweet potato genotypes should integrate compact vegetative growth, moderate vine elongation, and efficient tuber biomass allocation, a pattern consistent with adaptive genotypes reported from other tropical regions (Fellahi et al., 2024).

Path Analysis

Path analysis provided a more detailed understanding of causal relationships among traits influencing yield (Table 4;

Figure 1). The analysis confirmed that weight per tuber (X12) exerted the strongest direct positive effect (0.9695) on total tuber yield, followed by number of tubers (X13) with a moderate direct effect (0.4558). Meanwhile, internode length (X09) and tuber length (X11) had negative direct effects (-0.2567 and -0.1185, respectively). The negative direct effect of internode length can be explained biologically: longer internodes are associated with more elongated stems, which may reduce the allocation of assimilates to tuber formation, thereby lowering tuber weight and total yield. Similarly, excessively long tubers may indicate suboptimal partitioning of biomass, limiting the number of storage roots per plant.

Table 4. Direct and indirect effects of agronomic traits on tuber yield based on path analysis in local sweet potato clones.

Standardized Agronomic Traits	**Direct Effect**	**Indirect Effect Through**					**Total Effect**
		Z03	Z09	Z11	Z12	Z13	
Stem length	0.197	-	-0.179	-0.007	-0.396	-0.065	-0.449
Internode length	-0.257	0.137	-	-0.003	-0.395	0.006	-0.512
Tuber length	-0.119	0.011	-0.007	-	0.194	-0.197	-0.118
Tuber weight	0.970	-0.080	0.105	-0.024	-	-0.143	0.827
Number of tubers per plant	0.456	-0.028	-0.003	0.051	-0.304	-	0.172

Notes: Residual effect (unexplained R^2) = 0.0625 (√ = 0.2499); Stem length (Z03), internode length (Z09), tuber length (Z11), tuber weight (Z12), number of tubers per plant (Z13).

The residual effect of 0.2499 indicates that 93.75% of yield variability was accounted for by these five traits, demonstrating the robustness of the model. The findings agree with path analyses in rice (Yadav et al., 2024) and maize (Priyanto et al., 2023), where component traits such as grain weight and ear number showed the most substantial direct effects on yield.

Importantly, the direct influence of weight per tuber underscores its suitability as a primary selection criterion, while the negative path coefficients for internode length reinforce the need to control vegetative growth in breeding programs. Such insights validate the theoretical framework proposed by Wright (1921) and empirically supported by Dewey & Lu (1959), showing that path analysis enhances selection precision by distinguishing between direct and indirect causal relationships. Consistent findings were also reported by Mekonnen et al. (2020) and Magaji & Sodangi (2020), who demonstrated that the number of storage roots per plant and leaf area index exerted significant positive direct effects on total tuber yield, confirming the utility of path analysis in identifying yield-determining traits in *Ipomoea batatas*.

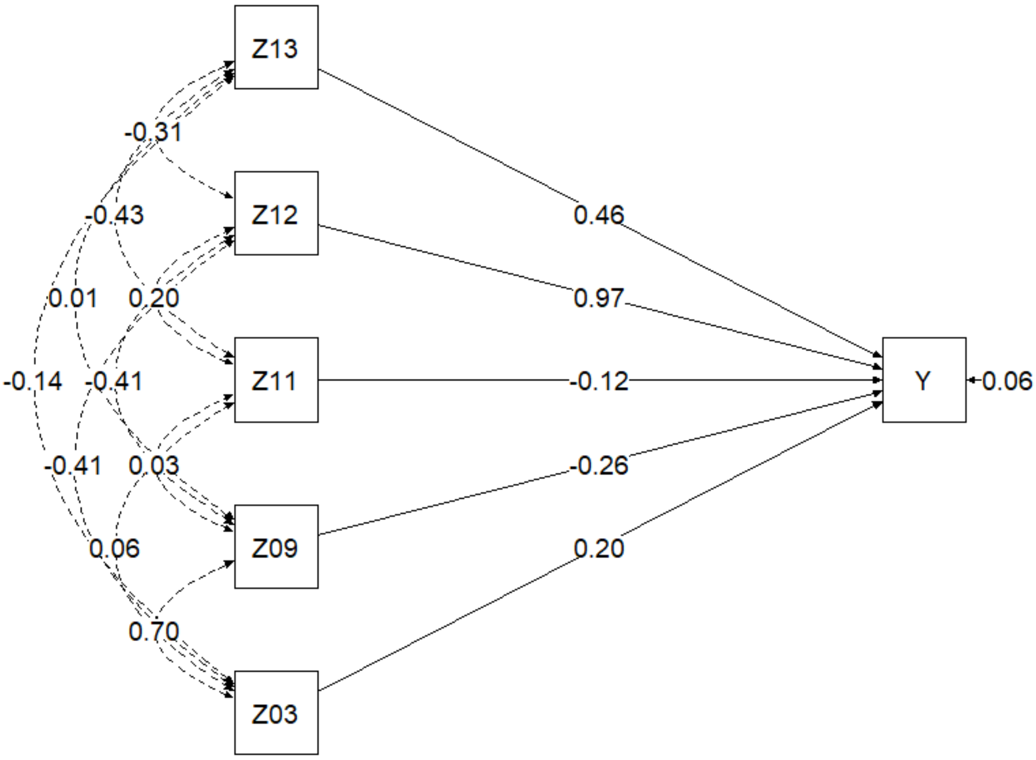

Figure 1. Path diagram illustrating the direct and indirect effects of stem length (Z03), internode length (Z09), tuber length (Z11), tuber weight (Z12), and tuber number per plant (Z13) on total tuber yield per plant (Y) in local sweet potato clones from Southeast Sulawesi.

Integration and Breeding Implications

The integration of ANOVA, correlation analysis, stepwise regression, and path analysis revealed consistent patterns: weight per tuber (X12) and number of tubers per plant (X13) emerged as the most influential predictors of yield, while internode length (X09) had a clear negative effect. Stem length (X03) and tuber length (X11) played supporting roles with more limited impact.

From a practical standpoint, breeding strategies for local sweet potato in Southeast Sulawesi should prioritize improvements in weight per tuber without compromising tuber size, while also controlling internode length to optimize resource allocation. Recognizing the trade-off between tuber number and size is essential to achieving a balance between productivity and quality (Yadav et al., 2024).

Overall, these results advance our understanding of genetic parameters and trait interactions in sweet potato, providing a strong empirical basis for breeding more productive, adaptive, and resilient local varieties that contribute to food security in tropical regions.

Nevertheless, because the present study was based on phenotypic evaluations conducted under a single agroecological condition, the observed relationships primarily reflect phenotypic associations that may be influenced by environmental factors. Future studies should therefore assess the stability of key yield-determining traits across multiple environments to better elucidate genotype × environment interactions and integrate molecular approaches to enhance selection precision and confirm underlying genetic contributions.

CONCLUSION

1. Analysis of variance showed significant phenotypic diversity among 20 local sweet potato clones from Southeast Sulawesi, with moderate to high heritability, indicating that most agronomic traits are genetically influenced and amenable to selection at the phenotypic level, without molecular confirmation.
2. Tuber weight and tuber diameter were strongly and positively correlated with total yield, whereas internode length had a negative association, reflecting a trade-off between vegetative growth and tuber formation.
3. Stepwise regression and path analysis consistently identified tuber weight and number of tubers per plant as the key yield determinants, while internode length negatively affected productivity, emphasizing the need to regulate vegetative growth.

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