

Article

RGB-Derived Haralick Edge-Texture Features Discriminate Mung Bean Responses to Mineral and Biofertilizer Regimes

Eder Pereira Neves ^{1,*}, Jorge González Aguilera ² , Werwerth Costa Martins ² , Roseline da Silva Coêlho ² , Fábio Steiner ² , Marco Aparecido Queiroz Duarte ¹ , Alan Mario Zuffo ³ , César Augusto Masgo Soto ⁴ , Carlos Genaro Morales-Aranibar ⁵ , María Paulina Aliaga Martínez ⁴, Nataniel Linares-Gutiérrez ⁶ and Luis Morales-Aranibar ^{7,*} 

¹ Department of Mathematics, State University of Mato Grosso do Sul (UEMS), Cassilândia Campus, Cassilândia 79543-113, MS, Brazil; marco@uems.br

² Department of Agronomy, State University of Mato Grosso do Sul (UEMS), Cassilândia Campus, Cassilândia 79543-113, MS, Brazil; jorge.aguilera@uems.br (J.G.A.); werwerth@gmail.com (W.C.M.); roselinecoelho1@gmail.com (R.d.S.C.); steiner@uems.br (F.S.)

³ Department of Agronomy, State University of Maranhão (UEMA), Balsas Campus, Balsas 65800-000, MA, Brazil; alan.zuffo@gmail.com

⁴ Department of Environmental Engineering, National University of Engineering (UNI), Lima 15333, Peru; cmasgo@uni.edu.pe (C.A.M.S.); maliagam@uni.edu.pe (M.P.A.M.)

⁵ Faculty of Sciences, National University of Engineering, Tupac Amaru Av. 210, Rimac, Lima 15333, Peru; cgmoralesa@unjb.edu.pe

⁶ Faculty of Engineering, Jorge Basadre Grohmann National University, Tacna 23550, Peru; nlinaresg@unjb.edu.pe

⁷ Grupo de Investigación en Sistemas Agroambientales y Sostenibilidad (GISAS), Universidad Nacional Intercultural de Quillabamba, Cusco 08741, Peru

* Correspondence: ederpereira@uems.br (E.P.N.); luis.morales@uniqu.edu.pe (L.M.-A.)

Abstract

Low-cost RGB imaging can accelerate crop phenotyping, but its ability to capture plant responses to fertilizer regimes through edge-based texture descriptors remains insufficiently tested. Mung bean [*Vigna radiata* (L.) R. Wilczek] was grown in a randomized complete block design with six fertilizer regimes and four replicates. Side-view RGB images acquired under controlled conditions were segmented, converted to grayscale, transformed into Canny edge maps, and summarized using six gray-level co-occurrence matrix (GLCM) features. Agronomic variables were evaluated: plant height, stem diameter, nodule weight, fresh weight, pod weight, shoot dry matter, grain yield per plot, the chlorophyll index, root length, and root volume. Contrast, energy, homogeneity, entropy, and variance differed across regimes, whereas the GLCM correlation did not. Mineral fertilization resulted in the highest values of stem diameter, nodule mass, fresh biomass, shoot dry matter, and the chlorophyll index. Baker's Gamma coefficient (0.9369) and the cophenetic correlation (0.9498) showed high similarity between the hierarchical structures, indicating that the texture descriptors preserved a treatment organization highly similar to that observed for the agronomic variables. The Haralick features calculated from controlled RGB-derived edge maps revealed fertilizer-associated differences in the mung bean canopy structure. This method is promising for nondestructive screening, but replicate-level predictive validation, full reporting of image-processing parameters, and external testing are needed before agronomic traits can be estimated from images.

Keywords: *Vigna radiata*; computer vision; gray-level co-occurrence matrix; image-based phenotyping; nutritional management; proximal sensing



Academic Editors: Rubi Quiñones and Francisco Muñoz-Arriola

Received: 25 August 2026

Revised: 6 October 2026

Accepted: 9 October 2026

Published: 13 October 2026

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1. Introduction

Agriculture faces the challenge of increasing crop productivity while reducing the environmental impacts of agricultural production, which requires technologies capable of monitoring plants with greater speed, precision, and efficiency [1,2]. In this scenario, digital agriculture has transformed the way in which phenotypic information is acquired and analyzed by integrating tools such as remote and proximal sensing, computer vision, artificial intelligence, and data analysis to support crop management [3,4]. Among these technologies, high-throughput plant phenotyping stands out for allowing rapid, objective, and nondestructive characterization of the morphological and physiological characteristics of plants [5,6], contributing to genetic improvement programs, precision agriculture, and the development of more sustainable production systems [3,7,8].

Although technological advances have significantly expanded data acquisition capabilities in agriculture, obtaining phenotypic information still represents one of the main challenges in plant research, often described as the “phenotyping bottleneck” [5]. Conventional assessments are predominantly based on manual measurements and visual observations, which are often time-consuming, susceptible to evaluator subjectivity, and, in many cases, destructive [9]. These limitations hinder the continuous monitoring of plant development and restrict large-scale data acquisition [6]. Consequently, automated and nondestructive methods have been widely employed to increase the accuracy, speed, and reproducibility of phenotypic assessments under different growing conditions [6,7].

Among the different approaches to digital phenotyping, computer vision based on RGB images has become one of the main tools for plant phenotyping because of its low cost, operational simplicity, and wide availability of digital cameras [3,10]. In addition to enabling its use in both controlled environments and field conditions [4], this technology allows for the automatic extraction of attributes related to plant architecture, leaf area, color, vegetative vigor, and development through digital image processing algorithms [4,10]. Compared with multispectral and hyperspectral sensors and LiDAR systems, red, green and blue color (RGB) images have lower acquisition and processing costs, indicating that they are favorable for use in research and agricultural monitoring systems [11]. As a result, the use of computer vision has expanded rapidly to treatment discrimination, plant growth monitoring, and early identification of physiological changes in different crops [3,4,10].

In recent years, advances in computer vision have significantly expanded the ability to extract phenotypic information from digital images, allowing the characterization of plant growth, nutritional status, and responses to different growing conditions through image-derived attributes with high interpretive capacity. These advances have strengthened the use of image-based phenotyping as a tool for digital and precision agriculture, expanding its application in the nondestructive monitoring of agronomic traits in different crops [3,7,10,12,13].

Although RGB images allow for the quantification of attributes related to color, leaf area, and plant architecture, many physiological responses induced by nutritional management also modify the spatial organization of plant tissues. These alterations are not always detected by conventional spectral or morphological attributes, making texture analysis a complementary strategy for extracting the phenotypic information contained in images [3,14,15]. In this context, textural descriptors allow for the capture of structural patterns associated with the spatial distribution of pixels, providing additional information about plant responses to different nutritional management practices.

However, physiological changes resulting from nutritional management are not always reflected solely in changes in plant shape or color [4,10]. Among the available approaches to characterize these responses, texture analysis stands out for quantifying the spatial organization of pixel intensity levels, allowing the identification of structural patterns that

are often imperceptible to visual inspection [14]. In this context, the gray-level co-occurrence matrix (GLCM) is among the most widely used techniques for textural characterization, allowing the extraction of descriptors proposed by Haralick, such as contrast, correlation, homogeneity, energy, and entropy [15]. These descriptors have been widely used to characterize responses associated with nutritional status, disease occurrence, biotic and abiotic stresses, and plant development, significantly expanding the potential of image-based phenotyping [3,4].

Among the species with the potential for application of these approaches, mung bean [*Vigna radiata* (L.) R. Wilczek] stands out because it is a legume with high nutritional value, a short cycle, and high biological nitrogen fixation capacity, characteristics that favor its inclusion in more sustainable agricultural systems [16]. In parallel, biofertilizers have received increasing attention because they promote greater nutrient use efficiency, stimulate plant growth, and reduce the dependence on mineral fertilizers [17]. Studies have demonstrated that the association between mineral fertilization and biofertilizers improves the growth, nutrient absorption, and productivity of mung bean [17]; however, these responses are still predominantly evaluated through conventional agronomic variables such as plant height, biomass, and productivity [6]. Despite the growing number of studies using RGB images for plant phenotyping [4,10], the application of textural descriptors derived from GLCM to evaluate responses to nutritional management in mung beans remains practically unexplored. Furthermore, few studies have investigated whether these descriptors are capable of reproducing the patterns observed by conventional agronomic evaluations, which limits their use as substitutes or complementary tools in plant phenotyping.

We hypothesized that fertilizer-associated changes in mung bean canopy structure would alter the Haralick features calculated from standardized RGB-derived edge maps. The objectives were to (i) determine whether six GLCM features discriminate mineral and AFERT-based fertilizer regimes; (ii) compare treatment-level patterns from image features with patterns from conventional agronomic traits; and (iii) define the scope and limitations of these image features as nondestructive phenotyping indicators.

2. Materials and Methods

2.1. Experimental Site and Plant Material

The experiment was conducted under greenhouse conditions at the Agronomic Experimental Station of the State University of Mato Grosso do Sul (UEMS), Cassilândia Campus, Mato Grosso do Sul, Brazil (19°05'20" S, 51°48'24" W; altitude of 510 m), during the period from August to December 2025. The internal air temperature (25 ± 2 °C), internal relative humidity ($70 \pm 5\%$), and internal global radiation (178 ± 2 W m⁻²) were recorded using an automatic weather station (E4000, Irriplus, Viçosa, MG, Brazil) installed inside the center of the greenhouse. Internal global radiation measurements (W m⁻²) were collected from 10:00 to 17:00.

Under greenhouse conditions, pots with a capacity of 5 dm³ were used, filled with a substrate composed of soil collected from the surface layer (0–20 cm) of an Orthic Latoxolic Quartzarenic Neosol (NQo) with a sandy texture (120 g kg⁻¹ of clay, 40 g kg⁻¹ of silt, and 840 g kg⁻¹ of sand). The initial chemical characterization of the soil, performed before lime application, revealed the following composition: pH—5.0; P-resin—5 mg dm⁻³; K—1.2 mmolc dm⁻³; Ca—10 mmolc dm⁻³; Mg—6 mmolc dm⁻³; cation exchange capacity (CEC)—33.2 mmolc dm⁻³; base saturation (V%) 52%; organic matter (OM)—9 g dm⁻³; B—0.08 mg dm⁻³; Cu—0.5 mg dm⁻³; Fe—16 mg dm⁻³ and Zn—0.2 mg dm⁻³. The soil was amended with lime, and 5 g was applied per pot approximately 30 days before sowing. The soil moisture content was maintained close to field capacity with daily manual irrigation.

Pest and disease control during the experiment was carried out according to the needs and technical recommendations for green mung cultivation.

2.2. Experimental Design

The experimental design used was a randomized block design with four replications. Five treatments based on the AFERT biofertilizer were employed (100, 80, 60, 40, and 20%, representing 2, 1.6, 1.2, 0.8, and 0.4 t ha⁻¹, and BIO100, BIO80, BIO60, BIO40 and BIO20, respectively), and the control (MIN) was based on complete mineral fertilizer with the formula 04-14-08 (rate of 2 t ha⁻¹) and 133 kg ha⁻¹ of KCl. A 100% dose of AFERT is equivalent to the applied dose of mineral fertilizer. AFERT is the commercial name of a pelleted biofertilizer containing a mixture of organic and biological materials encapsulated in a polymer that retains water and allows for the gradual release of nutrients, minimizing leaching and volatilization [18,19]. Its composition includes bacteria (genera *Bacillus*, *Azospirillum*, *Rhizobium*, *Pseudomonas*, and *Bradyrhizobium*) and fungi (genera *Trichoderma*, *Beauveria*, and *Metarhizium*), which complement the response to biofertilizer. The fertilizer AFERT was formulated as 04-14-12 and contains all necessary macro- and micronutrients in sufficient quantities for soil health, optimal performance, and crop production [18]. At 30 days after emergence, top-dressing fertilizer was applied at rates of 200, 160, 120, 80, and 40 kg ha⁻¹ of AFERT (02-02-30), whereas in the control treatment (mineral fertilizer), 10 kg ha⁻¹ of urea (45% N) and 100 kg ha⁻¹ of KCl (60% K₂O) were applied. Each experimental unit consisted of a pot containing three green mung bean seeds. After emergence, the plants were thinned, and two plants were left per pot.

2.3. Agronomic Measurements

At the end of the experiment, the following agronomic variables were evaluated: plant height (PH, cm), stem diameter (SD, mm), nodule weight (NW, g), fresh weight (FW), pod weight (PW), shoot dry matter (SDM, g), grain yield per plot (GY, g), the chlorophyll index (CI), root length (RL, cm) and root volume (RV, cm³). The shoot and root lengths were measured in centimeters using a millimeter ruler with 1 mm precision. The stem diameter was measured using a digital electronic caliper (Neiko 01407A Electronic Digital Caliper, Zhejiang Kangle Group, Wenzhou, China) with 0.1 mm accuracy. The fresh weights of the root system, nodules and shoots of each plant were individually measured on a precision balance with an accuracy of 0.001 kg. The collected samples were dried in a forced-air oven at 60 °C for 72 h, after which the dry weights of the roots, shoots, pods and nodules were determined using an analytical balance with an accuracy of 0.001 g. The plants of individual plots were harvested and threshed via a manual thresher, and the grains were weighed and extrapolated to grain yield in g plot⁻¹ at 13% humidity (wet basis). The chlorophyll index (CI) was also measured using a digital meter. Roots were removed from the containers and washed with water to remove soil adhering to the roots. The RV was determined by water displacement using a calibrated cylinder of 100 mL.

2.4. RGB Image Acquisition

The methodology employed in this study comprises four sequential steps: acquisition of RGB images, preprocessing, digital processing, and extraction of textural descriptors, as illustrated in Figure 1. The images were captured in a studio setup within the greenhouse itself and subjected to segmentation procedures to isolate only the region of interest corresponding to the mung bean plants. At the time of image acquisition, the plants were 60 days post-planting. The segmented images were subsequently converted to grayscale and processed using the Canny edge detection algorithm. Finally, edge and texture map descriptors were extracted using the GLCM, which served to differentiate the phenotypic characteristics of the evaluated treatments. The flowchart of the steps performed is illustrated in Figure 1.

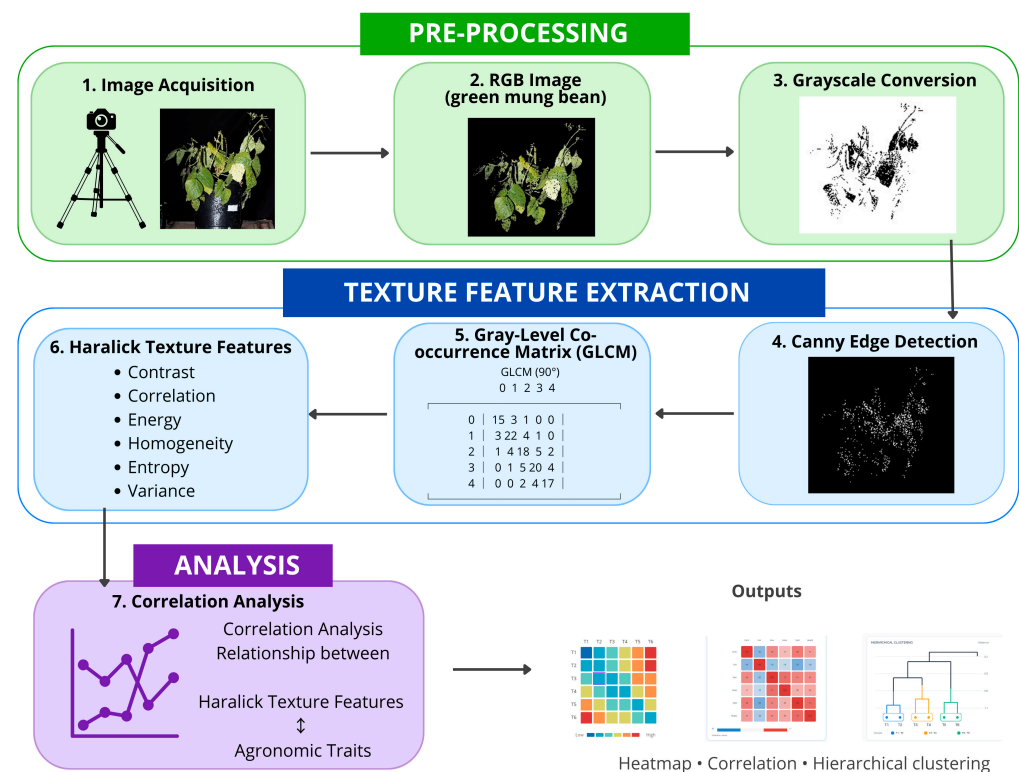


Figure 1. Flowchart of the image acquisition, preprocessing, digital image processing, and textural descriptor extraction workflow used for the analysis of RGB images of mung bean (*Vigna radiata* L.) plants.

The images were acquired using a Canon EOS R6 Mark II digital camera (Melville, NY, USA) equipped with a Canon EF 70–200 mm f/2.8 L USM lens, set to manual mode with an ISO 100 [20], an aperture of f/8, and a shutter speed of 1/125 s; these parameters remained constant throughout the image acquisition process to ensure uniform capture conditions. The photographs were recorded in RGB format at a maximum resolution of 6000 × 4000 pixels (24.2 megapixels) using a 35.9 × 23.9 mm full-frame CMOS sensor. During acquisition, the camera was mounted on a tripod at a height of approximately 1.0 m above the ground, maintaining a distance of approximately 2.0 m between the camera and the plants. The images were collected at night under controlled artificial lighting—conditions that remained constant throughout the experiment—thereby ensuring the standardization of the images used for digital processing and feature extraction. Afterward, the segmented images were converted to grayscale to provide a single-channel intensity representation suitable for subsequent edge detection using the Canny algorithm. The grayscale images were then processed using Canny’s edge detection algorithm. Finally, GLCM-based texture descriptors were extracted from the resulting edge maps and used to characterize the phenotypic responses of the evaluated treatments. Representative examples of the original images are shown in Figure 2. After acquisition, the images were organized into specific directories for the processing and texture descriptor extraction steps.

2.5. RGB Image Preprocessing

In the preprocessing stage, a segmentation algorithm was developed to identify only the region corresponding to the mung bean plants, eliminating the pots and other objects present in the images (Figure 2c). This procedure preserved only the region of interest (ROI), reducing interference during subsequent digital processing stages.

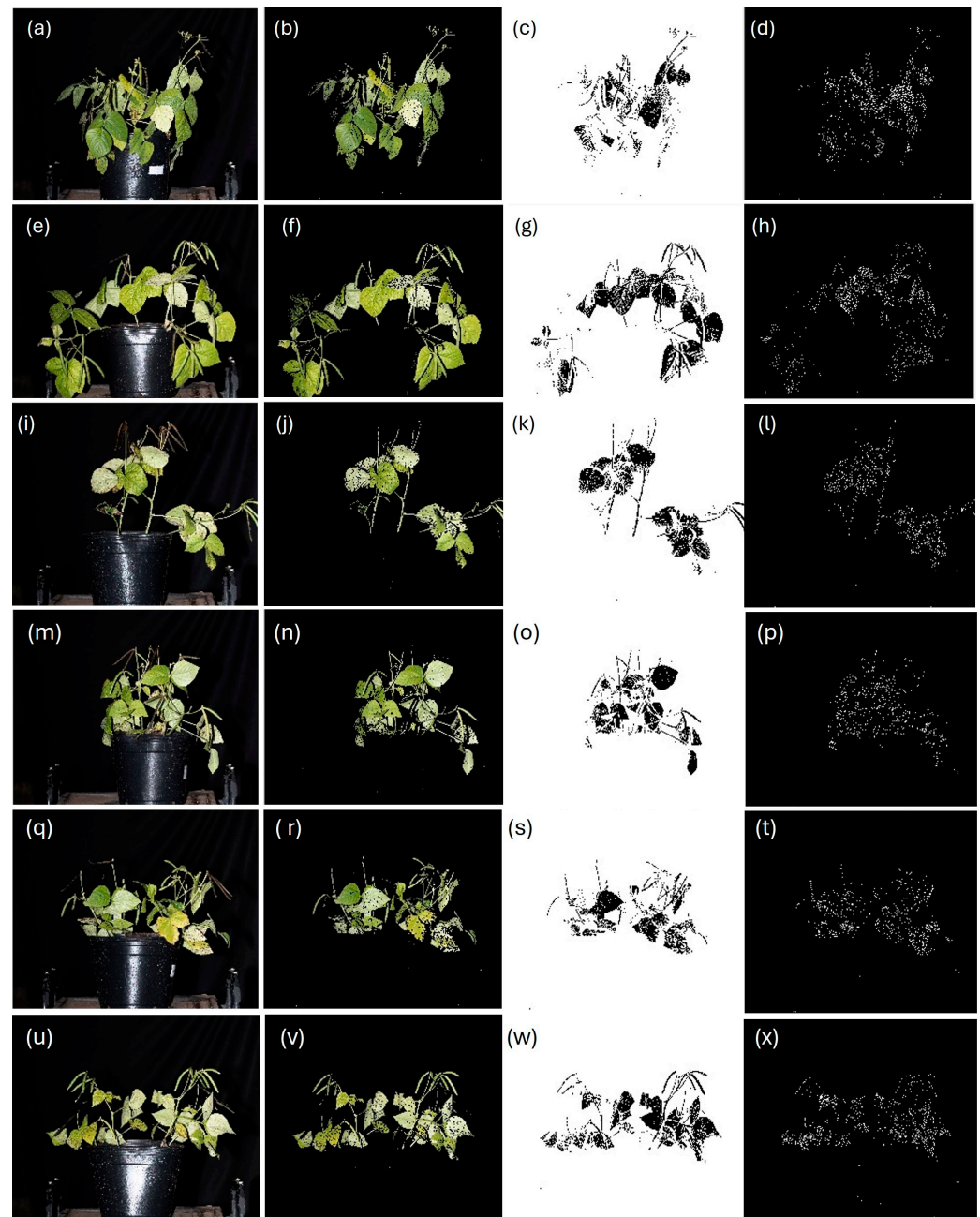


Figure 2. Processing of the original RGB image (a,e,i,m,q,u), only green parts (b,f,j,n,r,v), grayscale (c,g,k,o,s,w), and detection of Canny edges (d,h,l,p,t,x) obtained when evaluating mung bean subjected to mineral fertilization (a–d) and different doses of the biofertilizer (AFERT [100% (e–h), 80% (i–l), 60% (m–p), 40% (q–t) and 20% (u–x)]).

The algorithm involves creating a segmentation mask in the HSV color space (H: Hue; S: Saturation; V: Value/Intensity/Brightness). The H parameter represents the specific color type to be highlighted—in this study, green-colored areas—and its adjustment range is typically [0, 1]. Saturation (S) represents color intensity, also defined within the [0, 1] range; values close to zero (0) indicate a grayscale appearance, while values close to one (1) indicate more intense colors. The Value/Intensity/Brightness settings allow for the distinction between dark and light regions based on lighting conditions and are likewise defined within the [0, 1] range. For this study, the H, S, and V parameters were computationally implemented and tuned to isolate the Region of Interest (ROI); the specific settings used are detailed in a dedicated section.

After segmentation, the RGB images were converted to grayscale, reducing the chromatic information to a single light-intensity channel, which is a requirement for applying the Canny algorithm. The images converted to grayscale are shown in Figure 2c,g,k,o,s,w.

In the digital processing stage, the Canny edge detection operator [21], which is widely used to identify regions with abrupt intensity transitions and highlight structures present in the image, was employed. During the digital processing stage, the Canny edge detection operator [22] was employed; this operator is widely used to identify regions with abrupt intensity transitions and to highlight structures present in the image. Applying this algorithm enhanced the plant outlines, facilitating the generation of edge maps. In these maps, pixels corresponding to detected edges were represented by the value 1, while all other pixels were represented by the value 0. Consequently, background pixels and pixels within objects where no edges were detected contributed equally with a value of zero to the GLCM analysis. The results of this stage are illustrated in Figure 2d,h,l,p,t,x.

Thus, the Canny operator was applied following four processing stages: image smoothing using a Gaussian filter for noise reduction; calculation of the intensity gradient; non-maximum suppression to obtain thinner edges; and hysteresis thresholding, which defines the final edges of the image.

In the smoothing stage, the image $I(x,y)$ was filtered using a Gaussian function $G(x,y,\sigma)$, described by Equation (1)

$$I_G(x,y) = G(x,y,\sigma) * I(x,y) \quad (1)$$

where $G(x,y,\sigma) = \frac{1}{2\pi\sigma^2} \exp\left(-\frac{x^2+y^2}{2\sigma^2}\right)$ is the Gaussian function, $*$ represents the convolution operation, and σ is the standard deviation that determines the extent of the smoothing of image I_G .

Next, the partial derivatives in the horizontal and vertical directions (x and y) were calculated to obtain the image gradient [Equation (2)].

$$G_x = \frac{\partial I_G}{\partial x}, \quad G_y = \frac{\partial I_G}{\partial y} \quad (2)$$

The magnitude and orientation of the gradient are computed using Equation (3), which converts rectangular coordinates to polar coordinates

$$M(x,y) = \sqrt{G_x^2 + G_y^2} \quad (3)$$

The direction of the gradient was determined according to Equation (4).

$$\theta(x,y) = \arctan\left(\frac{G_y}{G_x}\right) \quad (4)$$

where the arctangent function takes two components in x and y and generates the angle of the gradient direction.

Noting that edge points correspond to maxima in the filtering result $M(x,y)$, a non-maximum suppression step was subsequently performed, preserving only the local maxima along the gradient direction, which resulted in thinner and well-defined contours. Finally, hysteresis thresholding was applied using two thresholds ($T_{\{inf\}}$ $T_{\{sup\}}$), defined by Equations (5) and (6).

$$M(x,y) \geq T_{\{sup\}} \Rightarrow \text{strong edge} \quad (5)$$

$$T_{\{inf\}} \leq M(x,y) < T_{\{sup\}} \Rightarrow \text{weak edge (Retained if connected to a strong edge)} \quad (6)$$

This process ensures edge continuity and reduces the influence of noise on the final detection.

2.6. Haralick Texture Feature Extraction

Following Canny edge detection, an image texture characterization technique based on the GLCM was applied; this method allows for the quantification of the spatial distribution of gray levels in digital images. The GLCM describes the frequency of occurrence of pixel pairs separated by a specific distance and spatial orientation, enabling the characterization of various structural patterns present in the images.

In this study, co-occurrence matrices were calculated considering four orientations (0° , 45° , 90° , and 135°), making it possible to evaluate the spatial dependence of gray levels in these directions.

The co-occurrence matrix is represented by Equation (7), where $P(i, j, d, \theta)$ represents the frequency with which two pixels with intensities i and j occur separated by a distance d and direction θ , formally defined as follows:

$$P(i, j, d, \theta) = T \{ [(x, y), (x + Dx, y + Dy) | f(x, y) = i, f(x + Dx, y + Dy) = j] \} \quad (7)$$

where T represents the total number of pixel pairs, $i, j = 0, 1, 2, \dots, N - 1$ are the gray levels, (x, y) are the coordinates of the pixel with gray level i , $(x + \Delta x, y + \Delta y)$ are the coordinates with gray level j , Δx and Δy are the horizontal and vertical displacements respectively, and $d = \sqrt{\Delta x^2 + \Delta y^2}$ is the distance along the angle θ [14].

Subsequently, the matrix must be normalized to obtain the probability distribution, presented by Equation (8).

$$P(i, j, d, \theta) = \frac{P(i, j, d, \theta)}{\sum_i \sum_j P(i, j, d, \theta)} \quad (8)$$

Applying Equation (8) allows the matrix values to fall within the $[0, 1]$ range, facilitating the consistent extraction of textural descriptors based on the spatial distribution of gray levels.

From the GLCM normalized by Equation (9), six textural descriptors proposed by Haralick et al. [15], widely used in the characterization of textural patterns in agricultural images, were extracted. The descriptors used in this study were Contrast, Correlation, Energy, Homogeneity, Entropy and Variance, whose mathematical expressions are presented in Table 1. Haralick descriptors extracted from the GLCM quantify spatial pixel distribution patterns; when calculated on binary edge maps, these descriptors primarily characterize the spatial distribution of the detected edges.

Table 1. Haralick textural descriptors used in this study.

Descriptors	Mathematical Expressions	Description
Contrast (CON)	$\sum_{i=1}^{N_g} \sum_{j=1}^{N_g} i - j ^2 \cdot P(i, j)$	Measures the local variation in gray levels.
Correlation (COR)	$\sum_{i=1}^{N_g} \sum_{j=1}^{N_g} \frac{\{i \cdot j\} \cdot P(i, j) - \{\mu_x \cdot \mu_y\}}{\sigma_x \cdot \sigma_y}$	Evaluates the linear dependence between neighboring pixels.
Energy (ENG)	$\sum_{i=0}^{N_g-1} \sum_{j=0}^{N_g-1} P^2(i, j)$	Measures the uniformity of the texture.
Homogeneity (HOM)	$\sum_{i=0}^{N_g-1} \sum_{j=0}^{N_g-1} \frac{1}{1 + (i - j)^2} \cdot P(i, j)$	Quantifies how closely the distribution is aligned with the diagonal of the GLCM.
Entropy (ENT)	$-\sum_{i=0}^{N_g-1} \sum_{j=0}^{N_g-1} P(i, j) \cdot \log(P(i, j))$	Represents the randomness of the texture.

Table 1. Cont.

Descriptors	Mathematical Expressions	Description
Variance (VAR)	$\sum_{i=0}^{N_g-1} \sum_{j=0}^{N_g-1} (1 - \mu)^2 \cdot P(i, j)$	Measures the dispersion of gray levels.

where $P(i, j)$ represents the joint probability of occurrence of gray levels i and j ; N_g is the number of gray levels; and μ and σ correspond to the mean and standard deviation of the GLCM, respectively.

2.7. Computational Implementation

Computational implementations were carried out to execute the proposed methodological procedures. During the phase of obtaining the image of interest corresponding to the segmentation mask in the HSV (H: Hue; S: Saturation; V: Value/Intensity/Brightness)—these parameters aimed to separate plant tissue from background elements. Computationally, the parameters were adjusted, and pixels were classified as belonging to the plant region when their values fell within the following ranges: $(0.15 < H < 0.40)$, $(S > 0.40)$, and $(V > 0.60)$. This process yielded the images shown in Figure 2b,f,j,n,r,v. The images segmented via the HSV process were converted to grayscale and smoothed using Gaussian filters with a kernel 5×5 and $\sigma = 1$. To complete the process, the Canny detection thresholds were set at 0.10 (low) and 0.30 (high) to obtain contour maps, resulting in binary images. From these images, Gray-Level Co-occurrence Matrices (GLCMs) were calculated using a pixel distance of $d = 1$ and four principal directions (0° , 45° , 90° , and 135°) to generate a symmetric matrix.

2.8. Statistical Analysis

The texture descriptors obtained from RGB image processing were initially treated as quantitative variables and subjected to statistical analysis to evaluate their ability to discriminate between treatments and represent the phenotypic responses of mung bean plants.

Initially, the Haralick descriptor data were subjected to analysis of variance (ANOVA), considering the combination of descriptors (contrast, correlation, energy, homogeneity, entropy, and variance) and GLCM extraction angles (0° , 45° , 90° , and 135°) as variables; this generated a total of 24 variables while maintaining the same experimental design used for the agronomic variables. When significant differences between treatments were detected, means were grouped using the Scott-Knott test at the 5% probability level.

Based on the ANOVA results, the combination (texture descriptor and extraction angle) demonstrating the greatest discrimination capacity among the evaluated treatments was selected. This combination was used in subsequent analyses to investigate the relationships between attributes derived from RGB images and the agronomic variables traditionally used to characterize plant growth and development.

The agronomic variables and Haralick texture descriptors were standardized using Z-scores prior to heatmap construction to eliminate scale differences between variables. Two independent heatmaps were generated: one containing the agronomic variables and the other containing the Haralick descriptors associated with the 90° GLCM extraction angle. Within each dataset, treatments were independently clustered using Euclidean distance and Ward's hierarchical method (Ward.D2), allowing for the identification of natural similarity patterns in each set of variables without imposing a common ordering across the panels. All statistical analyses were performed in the R environment (The R Project for Statistical Computing 4.6.1).

ANOVA and the Scott-Knott mean comparison test were conducted using RBio software, version 245 [23]. Multivariate analyses—including data standardization (Z-score), heatmap construction, hierarchical clustering (Euclidean distance and Ward's method—

Ward.D2), dendrogram comparisons (Baker’s Gamma coefficient and cophenetic correlation), and the Pearson correlation matrix—were performed using specific packages within the R environment. The agreement between the dendrograms obtained for the agronomic and Haralick datasets was assessed using Baker’s Gamma coefficient and cophenetic correlation, considering the six treatment means ($n = 6$). For Baker’s Gamma, the 95% confidence interval was estimated using a paired-label bootstrap procedure with 10,000 resamples, in which the same resampled treatment labels were applied to both dendrograms.

3. Results

3.1. Selection of Haralick Texture Descriptors Derived from RGB Images

Analysis of variance demonstrated that five of the six textural descriptors, regardless of the angle, derived from the transformation of RGB images, were able to discriminate the fertilization treatments applied to green mung beans. Only the correlation descriptor did not significantly affect the treatments ($p > 0.05$), whereas contrast, energy, homogeneity, entropy, and variance significantly differentiated the treatments evaluated (Table 2).

The coefficients of variation ranged from 0.49% for Homogeneity and 0° angle to 36.76% for Contrast and 0° angle, reflecting the intrinsic variability of each textural descriptor. However, high variability may have reduced the detection power of the tests, without necessarily compromising the validity of the effects that were statistically detected (Table 2).

Table 2. Analysis of variance and mean comparison of Haralick texture descriptors extracted from RGB images of mung bean plants under mineral fertilization and different biofertilizer doses.

Treatment	0° Angle					
	Contrast *	Correlation	Energy	Homogeneity	Entropy	Variance
MIN	1.446 a	0.377 a	0.925 b	0.974 b	0.205 a	1.143 a
BIO100	0.559 b	0.370 a	0.970 a	0.990 a	0.091 b	0.451 b
BIO80	0.687 b	0.392 a	0.963 a	0.988 a	0.112 b	0.563 b
BIO60	0.709 b	0.366 a	0.963 a	0.987 a	0.113 b	0.563 b
BIO40	0.663 b	0.385 a	0.965 a	0.988 a	0.108 b	0.536 b
BIO20	0.355 b	0.380 a	0.981 a	0.994 a	0.064 b	0.288 b
Average	0.7364 ± 0.42	0.3783 ± 0.02	0.9612 ± 0.02	0.9869 ± 0.01	0.1154 ± 0.06	0.5908 ± 0.33
ANOVA (<i>p</i> value)	0.010	0.310	0.009	0.010	0.013	0.008
CV (%)	36.76	3.79	1.43	0.49	31.3	34.99

Treatment	45° Angle					
	Contrast	Correlation	Energy	Homogeneity	Entropy	Variance
MIN	1.656 a	0.277 a	0.921 b	0.970 b	0.212 a	1.144 a
BIO100	0.645 b	0.283 a	0.969 a	0.988 a	0.094 b	0.451 b
BIO80	0.804 b	0.287 a	0.961 a	0.986 a	0.117 b	0.564 b
BIO60	0.818 b	0.276 a	0.961 a	0.985 a	0.117 b	0.563 b
BIO40	0.797 b	0.259 a	0.962 a	0.986 a	0.113 b	0.536 b
BIO20	0.413 b	0.289 a	0.980 a	0.993 a	0.067 b	0.288 b
Average	0.8557 ± 0.48	0.2785 ± 0.02	0.9588 ± 0.02	0.9847 ± 0.01	0.1202 ± 0.06	0.5910 ± 0.33
ANOVA (<i>p</i> value)	0.010	0.422	0.009	0.010	0.013	0.008
CV (%)	36.12	6.45	1.51	0.56	31.08	34.99

Table 2. Cont.

Treatment	90° Angle					
	Contrast	Correlation	Energy	Homogeneity	Entropy	Variance
MIN	1.288 a	0.436 a	0.928 b	0.977 b	0.199 a	1.144 a
BIO100	0.506 b	0.443 a	0.971 a	0.991 a	0.088 b	0.451 b
BIO80	0.642 b	0.430 a	0.964 a	0.989 a	0.110 b	0.563 b
BIO60	0.622 b	0.454 a	0.965 a	0.989 a	0.108 b	0.563 b
BIO40	0.606 b	0.433 a	0.966 a	0.989 a	0.105 b	0.536 b
BIO20	0.325 b	0.438 a	0.982 a	0.994 a	0.062 b	0.288 b
Average	0.6648 ± 0.37	0.4388 ± 0.02	0.9626 ± 0.02	0.9881 ± 0.01	0.1122 ± 0.05	0.5909 ± 0.33
ANOVA (<i>p</i> value)	0.007	0.266	0.008	0.007	0.012	0.008
CV (%)	33.71	2.73	1.34	0.4	30.63	34.99

Treatment	135° Angle					
	Contrast	Correlation	Energy	Homogeneity	Entropy	Variance
MIN	1.762 a	0.230 a	0.919 b	0.969 b	0.216 a	1.144 a
BIO100	0.673 b	0.265 a	0.968 a	0.988 a	0.095 b	0.451 b
BIO80	0.848 b	0.250 a	0.960 a	0.985 a	0.119 b	0.564 b
BIO60	0.833 b	0.260 a	0.960 a	0.985 a	0.118 b	0.563 b
BIO40	0.773 b	0.282 a	0.963 a	0.986 a	0.113 b	0.536 b
BIO20	0.417 b	0.275 a	0.980 a	0.993 a	0.067 b	0.288 b
Average	0.8842 ± 0.51	0.2603 ± 0.02	0.9583 ± 0.02	0.9842 ± 0.01	0.1212 ± 0.06	0.5910 ± 0.33
ANOVA (<i>p</i> value)	0.006	0.292	0.008	0.006	0.011	0.008
CV (%)	35.20	6.14	1.52	0.56	30.88	34.99

* Means followed by different lowercase letters within each column differ significantly according to the Scott–Knott test ($p \leq 0.05$). Overall mean of the data ± standard deviation of the data ($n = 24$).

Among the treatments, contrast, entropy, and variance showed similar behaviors, with the highest values observed in the mineral fertilization (MIN) treatment and the lowest values in the BIO20 treatment. In contrast, the energy and homogeneity descriptors showed inverse behavior, with the highest values in the BIO20 treatment and the lowest values in the control treatment (Table 2).

The variables analyzed included combinations of descriptors and the four angles proposed for information extraction following image transformation. The results indicate that, regardless of the angle employed, there was no variation in the results regarding the descriptors. The angular orientation had only a minor influence on the evaluated descriptors. Thus, the 90° orientation was adopted as the standard for subsequent analyses, simplifying result interpretation without compromising the discriminatory capacity of the textural descriptors. This selection is based on previous experience showing that this 90° orientation was the best angle associated with the same descriptors employed in this study. Only the contrast, energy, homogeneity, entropy, and variance descriptors obtained in this orientation were used in cluster and correlation analyses to investigate their association with agronomic variables and their potential as non-destructive phenotypic indicators. The correlation descriptor was not used in subsequent analyses because it did not show variation among the evaluated treatments (Table 2).

3.2. Agronomic Responses of Mung Bean Plants to Mineral Fertilization and Biofertilizer Application

The application of different fertilization strategies promoted distinct responses in the growth and development of mung bean plants. Analysis of variance revealed a significant effect of the treatments for most variables related to vegetative growth and plant vigor,

including PH, SD, NW, FW, SDM and CI. In contrast, the PW, GY, RL and RV did not differ significantly among treatments (Table 3).

Table 3. Summary of the analysis of variance (ANOVA) and mean comparison for the agronomic traits of mung bean plants under different fertilization treatments.

Fertilization Treatment	PH * (cm)	SD (mm)	NW (g)	FW (g)	PW (g)
MIN	31.5600 a	4.0850 a	0.104675 a	10.360825 a	3.020600 a
BIO100	32.7775 a	3.5625 b	0.034625 b	2.861475 b	3.142175 a
BIO80	33.5925 a	3.5900 b	0.038350 b	3.763700 b	3.254525 a
BIO60	32.3925 a	3.4875 b	0.035525 b	3.898250 b	3.621150 a
BIO40	29.4550 b	3.2975 b	0.050325 b	4.132150 b	3.628650 a
BIO20	26.4050 c	3.4075 b	0.050750 b	2.557350 b	3.056425 a
Average	31.0304 ± 3.01	3.5717 ± 0.37	0.0524 ± 0.03	4.5956 ± 2.88	3.2873 ± 0.63
ANOVA (<i>p</i> value)	0.000	0.030	0.004	0.000	0.6298
CV (%)	6.16	8.52	13.98	24.82	19.89
Fertilization Treatment	SDM (g)	GY (g)	CI	RL (cm)	RV (cm ³)
MIN	13.381425 a	5.009150 a	65.150 a	33.315 a	5.625 a
BIO100	6.003650 b	7.770525 a	18.700 b	31.190 a	7.000 a
BIO80	7.018225 b	7.659550 a	12.500 b	31.690 a	8.875 a
BIO60	7.519400 b	8.912075 a	20.225 b	31.940 a	6.000 a
BIO40	7.760800 b	7.720700 a	24.950 b	28.125 a	6.000 a
BIO20	5.613775 b	5.664725 a	24.750 b	32.875 a	6.750 a
Average	7.8828 ± 2.82	7.1228 ± 1.47	27.7125 ± 21.57	31.5225 ± 4.54	6.7083 ± 1.33
ANOVA (<i>p</i> value)	0.000	0.062	0.001	0.946	0.111
CV (%)	20.22	25.74	15.72	17.97	14.51

* PH, plant height; SD, stem diameter; NW, nodule weight; FW, fresh weight; PW, pod weight; SDM, shoot dry matter; GY, grain yield; CI, chlorophyll index; RL, root length; RV, root volume. Means followed by different lowercase letters within a column differ significantly according to the Scott–Knott test ($p \leq 0.05$). Overall mean of the data ± standard deviation of the data ($n = 24$).

The greatest values for stem diameter, nodule weight, fresh weight, shoot dry matter, and the chlorophyll index were observed in the mineral fertilization (MIN) treatment. With respect to these variables, all the treatments involving AFERT had statistically similar effects, regardless of the dose applied (Table 3).

The response of plant height differed from that of the other vegetative variables. Although the MIN, BIO100, BIO80, and BIO60 treatments resulted in the formation of the same statistical group, a significant reduction in height was observed at the lowest dose of biofertilizer, especially at BIO20 (Table 3).

On the other hand, no statistically significant difference was detected in pod weight, grain yield, or root length and volume; this indicates that, under the experimental conditions evaluated, using four replicates in a greenhouse, the partial substitution of mineral fertilizer with biofertilizer did not affect these productive characteristics or the root system. The limited number of replicates ($n = 4$) may have reduced the statistical power to detect treatment differences in grain yield. This behavior suggests that some of the physiological responses promoted by the treatments were sufficient to maintain important components of production, even in the face of the reductions observed in vegetative growth variables (Table 3).

3.3. Multivariate Relationships Between RGB Texture Descriptors and Agronomic Traits

Heatmap cluster analysis revealed consistent patterns of association between treatments, both when considering agronomic variables and textural descriptors obtained from

RGB images. In both datasets, hierarchical cluster analysis revealed very similar organizational patterns among the treatments (Figure 3). Since the dendrograms were constructed independently for each dataset, small differences in the order of treatments and the internal composition of the groups were expected. Even so, a high degree of agreement was observed between the hierarchical structures obtained for the agronomic variables and the Haralick descriptors.

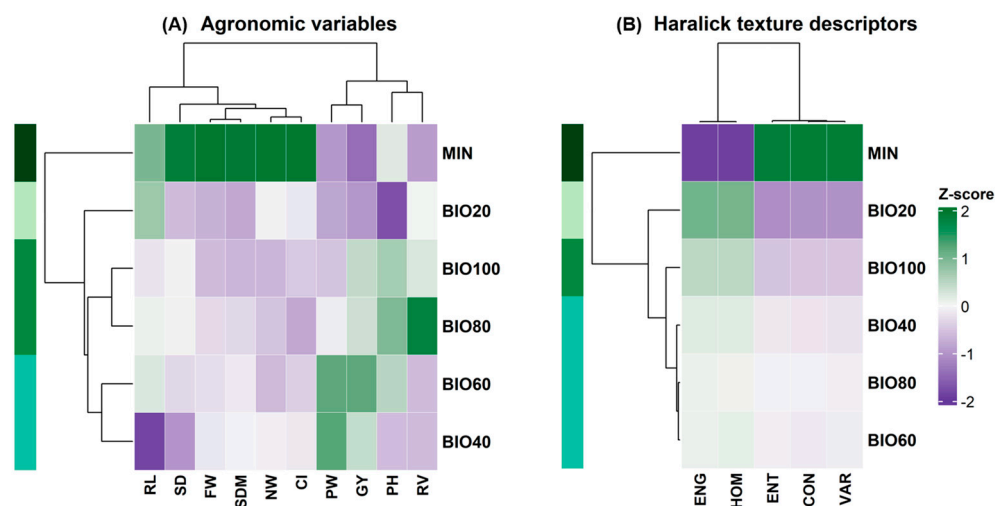


Figure 3. Heatmaps of standardized agronomic variables (A) and Haralick texture descriptors (B) of mung bean plants under mineral fertilization and biofertilizer treatments. Treatments were independently clustered in each panel using Euclidean distance and Ward's hierarchical clustering method (Ward.D2). The colored side bars represent the clusters identified within each dataset. High agreement between dendrograms was confirmed by Baker's Gamma (0.9369) and cophenetic correlation (0.9498). PH, plant height; SD, stem diameter; NW, nodule weight; FW, fresh weight; PW, pod weight; SDM, shoot dry matter; GY, grain yield; CI, chlorophyll index; RL, root length; RV, root volume; CON, contrast; ENG, energy; HOM, homogeneity; ENT, entropy and VAR, variance.

With respect to the agronomic variables (Figure 3A), the MIN treatment group remained isolated in terms of stem diameter, nodule weight, chlorophyll index, shoot dry matter, and fresh weight. The other treatments were distributed into groups characterized mainly by variables related to yield and root development, reflecting differences in the physiological response of the plants to the evaluated nutritional management practices.

When the textural descriptors derived from the RGB images were used (Figure 3B), a clustering pattern similar to that obtained for the agronomic variables was observed. The MIN treatment remained isolated, whereas the treatments containing biofertilizer showed clustering that was compatible with that observed in conventional evaluations, although with slight alterations in the composition of the groups. Furthermore, the contrast, entropy, and variance descriptors had opposite effects on energy and homogeneity, indicating complementary responses of the image texture to the different nutritional treatments. These results demonstrate that the descriptors extracted from the RGB images were able to discriminate the treatments in a manner similar to the agronomic variables traditionally used in characterizing plant development (Figure 3). To quantify this agreement, the dendrograms obtained independently for the two datasets were compared using the six treatment means ($n = 6$). Baker's Gamma coefficient (0.9369; 95% bootstrap CI: 0.9237–1.0000) and the cophenetic correlation (0.9498) showed high similarity between the hierarchical structures, indicating that the texture descriptors preserved a treatment organization highly similar to that observed for the agronomic variables.

To quantitatively validate these associations, Pearson correlations were estimated between textural descriptors and agronomic variables (Figure 4). Initially, high redundancy was observed among some textural descriptors, with positive correlations close to 1.0 between energy and homogeneity, contrast and variance, entropy and contrast, and entropy and variance, in addition to high-magnitude negative correlations between these two sets of descriptors. These results indicate that different textural metrics captured similar information about the spatial organization of pixels in the images, although distinct mathematical measures were used. Positive correlations ($SD \times ENT$, $r = 0.87$; $SD \times CON$, $r = 0.89$; $SD \times VAR$, $r = 0.89$; $SD \times FW$, $r = 0.88$; $SD \times SDM$, $r = 0.87$; $CL \times ENT$, $r = 0.87$; $CL \times CON$, $r = 0.86$; $CL \times VAR$, $r = 0.86$; $NW \times ENT$, $r = 0.84$; $NW \times CON$, $r = 0.85$; $NW \times VAR$, $r = 0.85$; $NW \times ENG$, $r = -0.85$. significant correlations ($p < 0.05$ and $NW \times HOM$, $r = -0.85$) were obtained at $p < 0.05$ (Figure 4). Positive and significant correlations at $p < 0.01$ were obtained between $CL \times FW$ ($r = 0.94$), $CL \times SDM$ ($r = 0.92$) and $NW \times FW$ ($r = 0.94$). Strongly significant correlations ($p < 0.001$) were obtained, both positive ($FW \times SDM$, $r = 1.00$ and $NW \times CL$, $r = 1.00$) and negative ($SDM \times ENG$, $r = -0.98$; $SDM \times HOM$, $r = -0.98$; $FW \times ENG$, $r = -0.98$ and $FW \times HOM$, $r = -0.98$) (Figure 4).

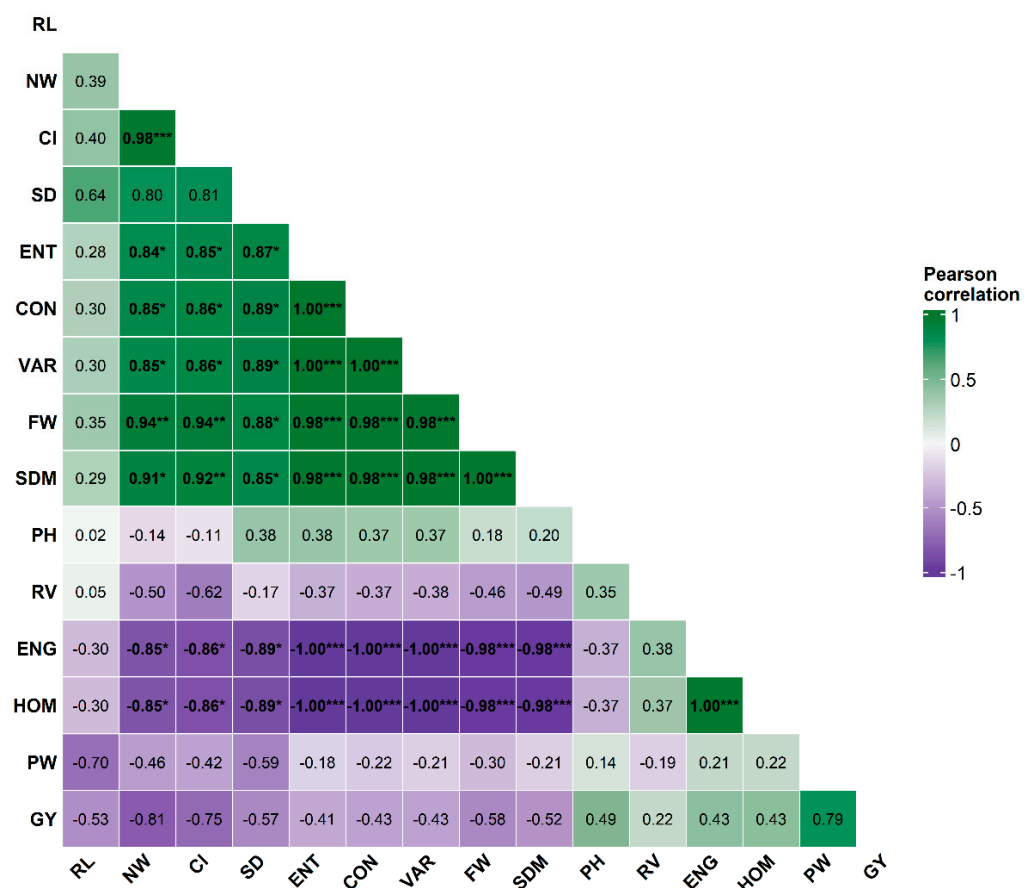


Figure 4. Pearson correlation matrix showing the relationships between RGB-derived Haralick texture descriptors and the agronomic variables of mung bean plants under mineral fertilization and different biofertilizer doses. Variables were ordered by hierarchical clustering using Euclidean distance and Ward's method (Ward.D2) to facilitate visualization of correlation patterns. The color scale represents the direction and magnitude of the correlation coefficients, which range from negative to positive. Asterisks (*, ** and ***) indicate statistically significant correlations ($p < 0.05$; $p < 0.01$; and $p < 0.001$, respectively). PH, plant height; SD, stem diameter; NW, nodule weight; FW, fresh weight; PW, pod weight; SDM, shoot dry matter; GY, grain yield; CI, chlorophyll index; RL, root length; RV, root volume; CON, contrast; ENG, energy; HOM, homogeneity; ENT, entropy; and VAR, variance.

The Pearson correlation matrix (Figure 4), organized by hierarchical grouping of variables, showed consistent patterns of association between textural descriptors derived from RGB images and agronomic variables. The strongest associations between image descriptors and agronomic variables were observed for stem diameter, chlorophyll index, nodule weight, fresh weight, and shoot dry matter. The descriptors contrast, entropy, and variance showed strong positive correlations with these variables, whereas energy and homogeneity showed negative correlations of similar magnitude. Furthermore, strong positive correlations were detected between agronomic variables related to vegetative growth, especially between fresh weight and shoot dry matter, between nodule weight and the chlorophyll index, and between the chlorophyll index and fresh weight (Figure 4).

Taken together, the results obtained by hierarchical clustering and Pearson correlation analysis demonstrate that the textural descriptors derived from the RGB images adequately reflect the phenotypic changes promoted by different nutritional management practices, reinforcing the potential of this approach as a nondestructive tool for characterizing plant responses to nutritional management.

4. Discussion

Image-based plant phenotyping has significantly expanded the capacity for nondestructive plant monitoring, allowing for rapid, objective, and large-scale assessments of characteristics related to growth, vigor, and plant architecture. In this context, RGB images remain among the most accessible tools for applications in digital agriculture because of their low cost, ease of acquisition, simplicity of processing, and characteristics that favor their use in agronomic experiments, plant breeding programs, and high-efficiency phenotyping systems [4–6,8,10]. The results of this study demonstrate that when associated with textural analysis using Haralick descriptors, RGB images are capable of representing phenotypic changes induced by different nutritional management strategies in mung bean, indicating that structural information of the canopy can be obtained quickly and nondestructively. This capacity was also evidenced by the high agreement observed between the hierarchical groupings obtained from the agronomic variables and Haralick's descriptors. Although the dendrograms were constructed independently for each dataset, both presented highly consistent hierarchical organization, as demonstrated by the high values of Baker's Gamma coefficient (0.9369) and the cophenetic correlation coefficient (0.9498). These results indicate that the textural descriptors preserved the similarity structure between treatments, reinforcing their potential as nondestructive indicators of phenotypic responses to nutritional management. Furbank and Tester [5] directly discuss the role of high-efficiency phenotyping technologies in reducing the so-called phenotypic bottleneck, whereas Tardieu et al. [8] emphasize the challenges involved in converting information obtained by sensors and imaging techniques into biologically relevant knowledge.

Regarding the importance of phenotyping for analyzing mung bean production quality, Boddepalli et al. [24] present a study analyzing the morphological characteristics of mung bean pods and identifying genomic regions associated with these traits. The methodology employed deep learning-based image analysis integrated with genome-wide association studies. Results showed high agreement between automated and manual measurements, alongside the identification of genetic markers and candidate genes related to pod development. The study concluded that integrating digital phenotyping with genomic tools can help improve and accelerate mung bean breeding programs. Van Haefen et al. [25] conducted a study aimed at evaluating the potential of unmanned aerial vehicles (UAVs) for phenotyping agronomic and physiological traits in mung beans. The methodology utilized drone-acquired imagery from various field trials, applying linear regression, stepwise regression, and partial least squares regression models. Results demonstrated that canopy

cover allows for the assessment of early vigor, while predictive models estimate biomass and stomatal conductance with greater accuracy during the early and intermediate stages of development. It was concluded that drone-based phenotyping can enhance the efficiency of mung bean breeding programs, particularly when utilizing real-time calibration.

In their study, Shahid et al. [26] present a method to distinguish four varieties of mung bean based on quantitative parameters regarding color, shape, and size; using a classification approach, 10 parameters were extracted via GLCM in radial directions at a distance of 5 pixels. The data classification and clustering capability was verified through two simultaneous approaches using an Artificial Neural Network for the training and testing stages. The method yielded good results in both the training and testing phases for the data derived from the 10 features selected from 64×64 ROIs (regions of interest).

The ability of textural descriptors to discriminate between treatments indicates that nutritional management promoted detectable modifications in the spatial organization of the canopy. Among the descriptors evaluated, only the correlations did not differ significantly among treatments, whereas contrast, entropy, variance, energy, and homogeneity responded consistently to the changes promoted by mineral fertilization and different doses of biofertilizer. These results suggest that nutritional management mainly modified the spatial heterogeneity of the images, altering the distribution and relative frequency of gray levels without significantly modifying the statistical dependence between neighboring pixels. A study that developed a labeling method combining the timing of GLCM and Haralick image acquisition with land-use types revealed that changes in crop appearance over time affect image characteristics and treatment classification [27], confirming observations made in our own work. This behavior is consistent with the mathematical nature of the co-occurrence matrix descriptors, since contrast, entropy, energy, and homogeneity respond to changes in the uniformity and spatial distribution of gray levels, whereas correlation describes the statistical dependence between the values of neighboring pixels and may present less predictable behavior in certain applications [14,15].

The opposite response observed between contrast, entropy, and variance in relation to energy and homogeneity reinforces this interpretation. In general terms, the first three descriptors tend to increase as variability or disorder in the distribution of gray levels increases, whereas energy and homogeneity assume higher values in images with more uniform patterns or with a greater concentration of occurrences near the main diagonal of the GLCM [14,15]. Thus, the differences observed between treatments indicate that nutritional management altered the structural characteristics of the plants, possibly related to the distribution of leaf biomass, leaf overlap, and canopy space occupation. These alterations were reflected in the texture of the images, demonstrating that relatively simple mathematical descriptors can capture integrated phenotypic responses related to plant development.

Another relevant aspect was the stability of the descriptor responses in relation to the orientation of the co-occurrence matrix. The descriptor responses and angles demonstrate that the differences between nutritional management practices were consistent across the different directions used to construct the GLCM. Although the 90° orientation was selected for the subsequent analyses, a choice based on prior experience showing this orientation to be superior [10], the minor influence of the angle factor on most descriptors indicates that the structural patterns associated with the treatments were detected across different analysis directions. This stability contributes to the internal consistency of the methodology under the evaluated conditions, although the influence of orientation should continue to be investigated in images obtained under different camera positions, plant architectures, and phenological stages.

The results of the agronomic evaluations corroborate the differences detected by the textural analysis. Mineral fertilization promoted greater vegetative development, reflected

by greater values of stem diameter, fresh weight, shoot dry matter, chlorophyll index, and nodule weight. This performance may be related to the greater initial availability of nutrients supplied by mineral fertilization under the experimental conditions, which favor processes associated with leaf expansion, biomass formation, and photosynthetic activity. However, the treatments containing biofertilizer resulted in less vegetative growth without a significant reduction in pod weight or grain yield. These results indicate that the differences observed in shoot growth were not accompanied by statistically detectable changes in the productive components during the evaluated period.

The maintenance of productive components, even in the face of differences in vegetative growth, may be related to the lack of a direct correlation between biomass production and the allocation of assimilates to reproductive structures. In grain-producing crops, yield results from the interaction between the capacity of source tissues to produce and remobilize photoassimilates and the capacity of sink organs to utilize them during seed formation and filling [28]. Therefore, greater shoot growth does not necessarily imply a proportional increase in yield, especially when the availability of assimilates is not the main limiting factor for grain formation.

The response observed in treatments containing biofertilizer should be interpreted considering the mechanisms and limitations inherent in the action of beneficial microorganisms. Unlike mineral fertilizers, microbial biofertilizers act primarily through processes such as biological nitrogen fixation, nutrient solubilization and mobilization, the production or modulation of phytohormones, the stimulation of root growth, and alterations in the interactions between plants and soil microbial communities [29,30]. The expression of these effects depends on the survival, establishment, and activity of the introduced microorganisms, as well as their compatibility with the host plant, the native microbiota, and the physical and chemical conditions of the environment. Consequently, responses to biofertilizers can be gradual and vary among crops, formulations, soils, and growing conditions [29–31].

For this reason, the lower vegetative growth observed in the AFERT treatments should not be automatically interpreted as evidence of inefficiency of the microorganisms present in the formulation. However, it is also not possible to attribute these results solely to the gradual nature of microbial action, since the study did not evaluate the survival of microorganisms, root colonization, soil microbiological activity, or the temporal availability of nutrients. Thus, the results demonstrate that under the evaluated conditions, the vegetative growth promoted by mineral fertilization did not match that promoted by the biofertilizer treatments, although the values for the productive and root components did not respond significantly to the treatments [19].

Regardless of the differences observed between treatments, the most relevant aspect of this study was the high agreement between the agronomic responses and those obtained through digital image processing. If nutritional management modified plant architecture, it was expected that these changes would be reflected in canopy texture, since the spatial distribution of leaves constitutes the main source of information used by Haralick's descriptors. This hypothesis was confirmed by multivariate analyses, which demonstrated high consistency between the patterns identified by the images and those obtained by conventional agronomic evaluations. Similar results have been reported in plant phenotyping studies, in which attributes derived from images show a high capacity to represent morphological and physiological differences between treatments, allowing the replacement or complementation of conventional evaluations [3,4,6].

The high concordance between the heatmaps obtained from the textural descriptors and the agronomic variables confirms this interpretation. Although they represent distinct datasets, both produced similar patterns of treatment clustering, consistently sepa-

rating mineral fertilization from biofertilizer treatments. These results demonstrate that the structural changes captured by the images mirrored the behavior observed in agronomic evaluations, indicating that canopy texture is an indicator that yielded consistent results regarding phenotypic responses induced by nutritional management, and that Haralick descriptors consistently reproduced the multivariate structure observed in the agronomic evaluations.

This agreement has important implications for plant phenotyping. Variables such as shoot dry matter, leaf biomass, and dry matter accumulation depend on destructive assessments, preventing continuous monitoring of the same plant throughout the growing cycle. In contrast, RGB images can be obtained repeatedly without interfering with plant development, allowing the monitoring of growth dynamics and responses to treatments at different phenological stages. Thus, the high similarity between the patterns obtained by images and conventional assessments highlights the potential of digital image processing as a complementary tool to reduce the number of destructive analyses and increase the efficiency of experiments involving nutritional management, bioinputs, and plant breeding programs [3,6,32].

Pearson correlations reinforced this capacity for phenotypic representation. The descriptors contrast, entropy, and variance were strongly positively associated with stem diameter, shoot dry matter, the chlorophyll index, fresh weight, and nodule weight, whereas energy and homogeneity were inversely correlated. These relationships indicate that increased vegetative vigor promotes consistent changes in the spatial organization of the canopy, modifying the distribution of gray levels and, consequently, the textural attributes extracted from the images. In other words, as plants accumulated biomass and developed a more complex architecture, the texture of the images also changed, demonstrating that Haralick's descriptors can act as phenotypic proxies for plant development.

Among the variables evaluated, stem diameter, shoot dry matter, and the chlorophyll index showed the strongest associations with textural descriptors. These variables are directly related to vegetative growth and influence canopy density, leaf expansion, and leaf overlap, which are the factors that determine the spatial heterogeneity of the image. In contrast, plant height was less significantly correlated, suggesting that compared with changes related to biomass accumulation and leaf architecture, linear changes in growth exerted less influence on canopy texture. These results reinforce that textural descriptors capture integrated structural responses of the plant and not just isolated morphological characteristics [4].

Another aspect observed was the strong association between some of Haralick's descriptors. The strong correlations between contrast, entropy, and variance, as well as between energy and homogeneity, indicate that these metrics describe different dimensions of the same structural response of the image. Although they are calculated using distinct mathematical formulations, all these methods reflect changes in the spatial organization of pixels resulting from modifications in plant architecture. This association between descriptors is expected, since different metrics of the co-occurrence matrix may present partially redundant or complementary information, depending on the characteristics of the image and the objective of the analysis [15]. This behavior suggests that future studies could use variable selection techniques to identify a reduced set of descriptors capable of maintaining high discriminatory capacity, simplifying analyses without compromising the quality of interpretations.

The strong association observed between textural descriptors and agronomic variables expands the potential for using this approach in predictive models based on machine learning. Currently, descriptors derived from RGB images are being used as input variables to estimate the biomass, vegetative vigor, nutritional status, and productivity of different crops

and are frequently associated with supervised learning algorithms and deep neural networks [33–35]. Although deep learning-based models exhibit high predictive performance, Haralick descriptors offer an important advantage related to biological interpretability, allowing us to understand which structural changes in the canopy are associated with the observed phenotypic responses. This characteristic makes this approach particularly interesting in agronomic research, where the biological interpretation of the results is as important as the predictive capacity of the models.

Despite the promising results, several limitations should be considered. The images were obtained under controlled lighting and uniform background conditions, reducing the influence of external factors on the extraction of textural descriptors. Although this strategy increased the consistency of the analyses, studies conducted under field conditions should consider additional challenges, such as variations in luminosity, shading, background complexity, and overlapping plants, which can influence the performance of segmentation algorithms and the stability of attributes derived from the images [3,4]. Furthermore, validation in other genotypes, environments, and management systems contributes to expanding the robustness and generalizability of the proposed approach.

From a future perspective, integrating Haralick's descriptors with spectral indices, morphological attributes, and machine learning algorithms could enhance the predictive capacity of the methodology, allowing for the estimation of agronomic variables directly from RGB images. Sequential image acquisition throughout the phenological cycle will also allow monitoring of the temporal dynamics of responses to nutritional management and identification of early changes in plant development [10]. These approaches represent a natural advancement of the presented methodology and expand its potential for applications in high-efficiency phenotyping and precision agriculture.

The results obtained demonstrate that textural analysis based on Haralick descriptors is a promising tool to complement conventional agronomic evaluation, allowing for the rapid, objective, and nondestructive detection of phenotypic changes induced by nutritional management. Beyond its application in controlled environment experiments, this approach shows potential for integration with automated image acquisition platforms, including ground-based phenotyping systems and unmanned aerial vehicles (UAVs), expanding its application in genetic improvement programs, precision agriculture, and large-scale crop monitoring [3,36–38]. The combination of textural descriptors, machine learning, and automated imaging platforms represents a promising perspective for the development of systems capable of estimating agronomic attributes and monitoring crop performance in real time.

5. Conclusions

Haralick textural descriptors extracted from RGB images were able to detect phenotypic changes associated with different nutritional management strategies in mung bean plants, demonstrating the potential to complement agronomic evaluations quickly, objectively, and nondestructively. Thus, the integration of RGB images and Haralick descriptors represents a promising approach for applications in plant phenotyping and digital agriculture under controlled conditions.

Author Contributions: Conceptualization, E.P.N., J.G.A. and L.M.-A.; methodology, E.P.N., J.G.A., F.S. and L.M.-A.; software, E.P.N.; validation, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; formal analysis, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; investigation, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; resources, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; data curation, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z. and

L.M.-A.; writing—original draft preparation, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; writing—review and editing, E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; visualization, E.E.P.N., J.G.A., W.C.M., R.d.S.C., F.S., M.A.Q.D., A.M.Z., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A.; supervision, E.P.N., J.G.A. and L.M.-A.; project administration, E.P.N., J.G.A., A.M.Z. and L.M.-A.; funding acquisition, E.P.N., J.G.A., C.A.M.S., C.G.M.-A., M.P.A.M., N.L.-G. and L.M.-A. All authors have read and agreed to the published version of the manuscript.

Funding: This research was funded by the Universidad Nacional Intercultural de Quillabamba (UNIQ).

Data Availability Statement: The data presented in this study are available upon request from the corresponding authors.

Acknowledgments: The State University of Mato Grosso do Sul (UEMS) for providing the facilities where the experiments were conducted and the Intercultural University of Quillabamba (UNIQ) for financial support.

Conflicts of Interest: The authors declare that they have no conflicts of interest.

Abbreviations

The following abbreviations are used in this manuscript:

RGB	Red, Green and Blue colors
GLCM	Gray-level co-occurrence matrix
AFERT	Biofertilizer
NQo	Orthic Latexolic Quartzarenic Neosol
CEC	Cation exchange capacity
V	Base saturation
OM	Organic matter
PH	Plant height
SD	Stem diameter
NW	Nodule weight
FW	Fresh weight
PW	Pod weight
SDM	Shoot dry matter
GY	Grain yield per plot
CI	Chlorophyll index
CR	Root length
RV	Root volume
ROI	Region of interest
ANOVA	Analysis of variance
MIN	Treatments mineral fertilization
BIO	Treatments biofertilizer
CON	Contrast
COR	Correlation
ENG	Energy
HOM	Homogeneity
ENT	Entropy
VAR	Variance

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