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Phenotypic Variability of Cucumber (*Cucumis sativus* L.) Accessions From Cameroon and Implications for Breeding and Genetic Resource Conservation

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ABSTRACT

Cucumber (*Cucumis sativus* L.) improvement in sub-Saharan Africa remains constrained by the limited characterization of locally available germplasm. This study aimed to assess under uniform field conditions the phenotypic variability of seven *C. sativus* accessions collected from different localities in Cameroon to identify traits of potential interest for breeding. The experiment was conducted at a single site during one growing season, and 31 vegetative, phenological, and yield-related traits were analyzed. Data were analyzed using descriptive statistics, analysis of variance (ANOVA), multivariate analysis of variance (MANOVA), principal component analysis (PCA), and hierarchical clustering. Significant differences ($p < 0.05$) were observed among accessions for most traits, indicating substantial phenotypic variability. Traits such as fruit weight, yield, and flowering duration exhibited high broad-sense heritability and genetic advance, indicating strong genetic control and potential for selection. The first three principal components explained 81.9% of the total variation, with male flower number, branch number, and fruit weight traits contributing most to diversity. Hierarchical clustering on principal components (HCPC) grouped accessions into three distinct phenotypic clusters, suggesting distinct trait combinations and genetic profiles. The Shannon–Weaver diversity index indicated moderate diversity among accessions, with EBEBDA showing the highest diversity index (2.82) and MONATÉLÉ the lowest (2.67). This preliminary phenotypic characterization highlights the value of local cucumber accessions as genetic resources for breeding programs and provides a foundation for future multienvironment and molecular studies.

1 | Introduction

Cucumber (*Cucumis sativus* L., $2n = 2x = 14$), a member of the Cucurbitaceae family, is a widely cultivated vegetable crop known for its nutritional, medicinal, and economic importance [1]. Globally, cucumbers contribute significantly to agricultural trade, with production reaching a record of 97.8 million tons in 2023, cultivated across 2.19 million hectares [2]. Cucumber is becoming an increasingly important crop in many African countries, including Cameroon, where its production reached over 264,437 tons, contributing to food security and income generation for smallholder farmers [2]. Its fruits are rich in

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nutrients such as glucose and fructose, making them a valuable dietary component for promoting human health [3]. Beyond its nutritional value, cucumber serves as a key export commodity, generating foreign exchange for several countries [4].

Despite its global significance, the potential of cucumber remains underutilized in many regions, particularly in sub-Saharan Africa, where low yields are often reported. In Cameroon, cucumber production is limited by the lack of high-yielding varieties and suboptimal cultivation practices. Recent studies in the region have highlighted significant variability in cucumber genotypes, with flowering time, fruit weight, and yield per plant showing significant differences among accessions [5]. For instance, in Cameroon, cucumbers grown in diverse agroecological zones show varying levels of adaptation to local conditions, such as heat and disease resistance [6, 7]. These findings underline the need to explore the genetic diversity of local cucumber accessions to enhance productivity and adaptability.

Genetic variability is a cornerstone of plant breeding, offering opportunities to improve yield, quality, and resistance traits. High phenotypic and genotypic variability for key traits, such as fruit weight and yield per plant, has been reported in cucumber studies across Asia and Africa, emphasizing the potential of the species for genetic improvement [8, 9]. Research on cucumber accessions has revealed high heritability and genetic advancement for traits related to yield, suggesting strong genetic control and a high response to selection [10]. For example, in Iranian cucumber accessions, traits like fruit length and weight exhibited significant variability, demonstrating their utility for breeding programs targeting both productivity and quality [11].

Cucumbers also show considerable adaptability to diverse environments, with genotype-by-environment interactions influencing trait expression. Studies have shown that environmental factors, such as soil fertility and climatic conditions, significantly affect the growth and yield of cucumbers [12]. In Cameroon, traditional farming practices and local environmental conditions have shaped the genetic diversity of cucumber landraces, making them an invaluable resource for breeding programs. However, the genetic potential of these landraces remains largely unexplored, with limited studies assessing their morphological and genetic diversity.

In this study, seven cucumber accessions were selected to capture a representative range of morphological traits observed in local germplasm. Rather than focusing on a larger collection of accessions, which can often limit the depth of trait assessment due to logistical constraints, this study prioritizes a more profound characterization of key morphological traits. By working with a focused set of accessions, it becomes possible to evaluate a wide array of growth, flowering, and yield-related traits in greater detail, providing robust insights into the phenotypic variation present within the species. This approach allows for a comprehensive understanding of the genetic potential of these accessions, which can inform targeted breeding programs for both productivity and adaptability in diverse environments [13, 14].

Comprehensive characterization of genetic resources is essential for effective conservation and utilization. Recent advances in agromorphological and molecular marker-based approaches have facilitated the evaluation of genetic diversity in cucumbers. For instance, clustering and principal component (PC) analyses have been employed to identify traits contributing to diversity and to classify accessions based on morphology. These methodologies help quantify phenotypic variability and provide understanding of trait correlations and groupings among genotypes within a given environment, which is a necessary first step for breeding programs prior to more advanced multienvironment and genotype × environment interaction analyses. Such analyses not only reveal the extent of variability but also help in the identification of promising accessions for breeding program profiles [15, 16].

To address the knowledge gap in Cameroonian cucumber resources, this study aims to assess under uniform field conditions the phenotypic variability of seven *C. sativus* accessions using 31 morphological traits.

By identifying key traits contributing to phenotypic variation, this study seeks to provide valuable understanding for breeding programs and contribute to the conservation and sustainable use of cucumber genetic resources.

2 | Materials and Methods

2.1 | Study Area and Plant Material

The study was conducted in Obala, located in the Lékié Division of the Centre Region, Cameroon (3°57′0″–4°14′0″ N, 11°21′0″–11°38′0″ E). Covering an area of 475 km^2, Obala experiences a transitional equatorial climate with an annual average rainfall of 1476 mm and a mean temperature of 25.5 °C. The region features four distinct seasons: a long dry season (mid-November–mid-March), a short rainy season (mid-March–late June), a short dry season (July–mid-August), and a long rainy season (mid-August–mid-November). Soils in the area are predominantly ferrallitic, sandy-loam, and hydromorphic, with a slightly undulating plateau averaging 550 m above sea level.

The plant material used in this study consisted of cucumber (*Cucumis sativus* L.) accessions collected from seven distinct locations: OBALA, NTUI, EBEBDA, BATCHENGA, MONATÉLÉ, YAOUNDÉ, and SAA. One accession was sourced from each location, ensuring variability in genetic and morphological traits. These accessions were either obtained directly from local farmers or sourced from phytosanitary stores.

2.2 | Experimental Design

A randomized complete block design (RCBD) was used for the experiment, with three replications, each representing a block. The blocks were subdivided into seven experimental units, each measuring 4 m^2 (2 × 2 m), corresponding to the seven cucumber (*Cucumis sativus* L.) accessions. The spacing between experimental units and between blocks was 1 m to minimize edge effects. Within each experimental unit, nine planting hills were established, spaced 80 cm apart in both directions (80 × 80 cm). Each hill was filled with chicken manure before sowing. Five seeds were sown per hill, and thinning was performed 15 days after sowing to retain three plants per hill, ensuring uniform plant density.

2.3 | Data Collection

In each experimental unit, five plants were randomly selected per experimental unit at the early vegetative stage and monitored

throughout the growing season. Vegetative, phenological, and fruit and yield traits were measured at predefined developmental stages to ensure consistent trait assessment across accessions.

2.3.1 | Vegetative Traits

Vegetative traits were evaluated at 50% flowering or 30 days after sowing when plants had reached stable vegetative development.

Plant height (cm) was measured from the base of the plant to the tip of the main stem using a measuring tape. Root collar diameter (cm) was recorded with a caliper at the base of the plant to assess root growth. Leaf length (cm) and leaf width (cm) were measured on fully expanded leaves with a ruler, while petiole length (cm) was recorded from the base of the leaf blade to its attachment point on the stem. These leaf traits serve as indicators of overall plant health and vigor. Internode length (cm) was measured from the base of one node to the base of the next along the main stem. Node number and branch number were recorded at the same stage to characterize plant architecture. In addition, male peduncle length (cm) and female peduncle length (cm) were measured at first flowering as the length of the stalk supporting male and female flowers, respectively.

2.3.2 | Phenological Traits

Phenological traits were recorded to describe the flowering behavior and reproductive development of the cucumber accessions. Observations were initiated at the onset of flowering and continued until the end of the fruiting period.

Germination time (days) was recorded as the number of days from sowing to the emergence of the first seedlings. The vegetative growth period (days) was noted as the time taken for the plant to reach 50% of its final size, marking the end of the vegetative stage. The flowering date was recorded as the date on which the first flowers became visible, and days to 50% flowering (days) were recorded to gauge the uniformity in flowering time across accessions. Nodes to the first flower were noted to measure the number of nodes between the base of the plant and the first flower. Flowering duration (days) was calculated as the period from the appearance of the first flower to the fading of the last flower, reflecting the plant's reproductive timeline. The node formation rate and node formation period were calculated to track how quickly nodes and flowers developed along the stem. Additionally, male and female flower emergence frequencies were recorded to assess the reproductive capacity of each accession, which is essential for breeding purposes. Fruiting start and end dates were also noted to monitor the period of fruit development in each accession.

2.3.3 | Fruit and Yield Traits

Fruit and yield traits were recorded from the onset of fruiting until the end of harvest. Five plants were randomly selected per experimental unit and used consistently for yield assessments. For fruit size measurements, five fruits per plant were randomly sampled, resulting in 25 fruits per experimental unit. Fruit length (cm) and diameter (cm) were measured on the same fruits using a caliper. Average fruit weight (kg) was determined from these same fruits using an electronic balance. The number of fruits harvested per month was recorded to track the timing and frequency of fruiting throughout the season. Yield was measured in terms of total fruit weight per unit area (kg/m^2) to evaluate the productivity of each accession. Finally, the fruit-to-flower ratio (%) was calculated to understand the efficiency of the fruit set in relation to the number of flowers produced, a crucial factor for breeding high-yielding varieties.

2.4 | Statistical Analyses

2.4.1 | Descriptive Statistics and Post Hoc Analysis

Descriptive statistics were calculated for all traits, including mean, standard deviation, and range. The coefficient of variation (CV) was also computed to assess the relative variability of each trait. Post hoc analysis was conducted using the *agricolae* package in R statistical software [17] to identify significant differences between accessions for each trait. Significant differences were indicated by letters, with traits sharing the same letter not differing significantly at a 5% significance level.

2.4.2 | Genetic Parameters for Trait Improvement

Genetic and phenotypic variances [18] were estimated for each trait using a mixed linear model. The model is specified as

$$\mathbf{Y} = \mathbf{X}\boldsymbol{\beta} + \mathbf{Z_g g} + \mathbf{Z_b b} + \varepsilon, \tag{1}$$

where $\mathbf{Y}$ is a $\boldsymbol{n} \times 1$ vector of observed trait values for $\boldsymbol{n}$ experimental units (accessions), $\mathbf{X}$ is $\mathbf{n} \times \mathbf{p}$ matrix of fixed effects, which includes the overall mean, β is $p \times 1$ vector of fixed effect parameters, $\mathbf{Z_g}$ is a design matrix for the random effects due to accessions, $\mathbf{u}$ is a vector of random effects for the accessions, assumed to follow a normal distribution $\mathbf{g} \sim N(0, \mathbf{I}\sigma_g^2)$, $\mathbf{Z_b}$ is a design matrix for the random effects due to blocks, $\mathbf{b}$ is a vector of random effects for the blocks, assumed to follow a normal distribution $\boldsymbol{b} \sim N(0, \mathbf{I}\sigma_b^2)$, ε is a vector of residual errors, assumed to follow a normal distribution $\varepsilon \sim N(0, \mathbf{I}\sigma_\varepsilon^2)$, and $\mathbf{I}$ is the identity matrix.

The variance components [18] can be derived from the model as

$$\sigma_P^2 = \sigma_g^2 + \sigma_b^2 + \sigma_\varepsilon^2, \tag{2}$$

where σ_P^2 is the total phenotypic variance, σ_g^2 is the genetic variance (variance due to accessions), σ_b^2 is the block variance, and σ_ε^2 is the residual variance (environmental variance).

Broad-sense heritability H^2 is calculated as the ratio of genetic variance to the total phenotypic variance:

$$H^2 = \frac{\sigma_g^2}{\sigma_P^2}. \tag{3}$$

This model assumes that the variance for each random effect follows a normal distribution, and the residuals are independent and normally distributed. The model was fitted using the lme4 package [19]. Broad-sense heritability was classified into three categories: low (0–0.3), medium (0.31–0.6), and high (> 0.6) [18].

2.4.3 | Genetic Advance (GA) and Genetic Advance as a Percent of Mean (GAM)

GA [18] was calculated using the following formula:

$$\mathrm{GA} = k \times H^2 \times \sigma_P, \tag{4}$$

where k is the selection intensity ($k = 2.06$ at 5% of selection intensity), and σ_P is the phenotypic standard deviation.

GAM was calculated using the following formula [20]:

$$\text{GAM} = \frac{\text{GA}}{\overline{X}} \times 100, \quad (5)$$

where $\overline{X}$ denotes the mean of the trait.

2.4.4 | Phenotypic Coefficient of Variation (PCV) and Genotypic Coefficient of Variation (GCV)

The PCV and GCV were calculated for each trait to assess the relative contribution of genetic and environmental factors to the trait variability [21]:

$$\text{PCV} = \frac{\sigma_P}{\overline{X}} \times 100 \,\text{and}\, \text{GCV} = \frac{\sigma_g}{\overline{X}} \times 100. \quad (6)$$

where σ_P, σ_g, and $\overline{X}$ represent the phenotypic standard deviation, the genotypic standard deviation, and the mean of the trait.

PCV and GCV were divided into three categories: low (less than 10%), moderate (10%–20%), and high (more than 20%) [21].

2.4.5 | Principal Component Analysis (PCA)

PCA was performed to reduce the dimensionality of the dataset and identify the key components that explain most of the variance in the morphological traits. The analysis was carried out using the *FactoMineR* [22] and *factoextra* [23] packages in R statistical software. A scree plot was used to determine the number of PCs to retain. A biplot was generated to visualize the relationship between traits and accessions based on the first two PCs. Traits that strongly contribute to the components in the biplot were identified as the most influential in explaining the morphological variation across the accessions.

2.4.6 | Hierarchical Clustering of Accessions

Hierarchical clustering was performed on the PCs to group the accessions based on their morphological similarity. The clustering was done using the *FactoMineR* package [22]. A dendrogram was generated, which grouped the accessions into distinct clusters. This clustering helps identify genetic similarities between accessions and is used for selecting accessions based on trait diversity.

2.4.7 | Multivariate Analysis of Variance (MANOVA)

A MANOVA was performed to assess the genetic differentiation among the accessions by considering multiple morphological traits simultaneously. Accession was included as the fixed factor, and standardized vegetative, phenological, and fruit and yield traits were used as response variables. Statistical significance of multivariate differences among accessions was assessed using Wilks' Lambda. The analysis was performed using the *MVN* package [24].

3 | Results

3.1 | Comprehensive Assessment of Morphological Traits Across Accessions

A total of 31 traits of *Cucumis sativus* accessions, including vegetative, phenological, and fruit and yield traits, were assessed to understand the extent of variation and identify potential candidates for breeding programs. The descriptive statistics and the analysis of variance (ANOVA) revealed substantial variability across the seven accessions for those traits, most of them showing significant differences ($p < 0.05$, Table 1).

Significant differences ($p < 0.05$) were observed for all the vegetative traits. Among these, SAA (139.13 ± 39.19), OBALA (136.53 ± 17.1), and MONATÉLÉ (130.13 ± 31.09) accessions had significantly higher plant height than the other accessions while the highest leaf length (19.85 ± 2.98) and width (26.05 ± 3.87) were observed only for SAA accession (Table 1).

For vegetative traits, the ANOVA showed significant differences ($p < 0.05$) for 7 traits out of 12. The diverse flowering date is useful as it indicates the potential for selection in different environments. Among the traits, SAA (24.8 ± 0.86) and NTUI (24.4 ± 1.06) accessions showed the shortest flowering date, i.e., a high flowering precocity. However, only NTUI in these accessions showed the earliest fruiting, with the fruiting start date of 27.67 ± 0.49, significantly smaller than the other accessions. Five traits, i.e., germination time, vegetative growth period, days to 50% flowering, nodes to first flower, and node formation period, exhibited negligible variation, therefore less relevant for breeding purposes (Table 1).

Regarding fruit and yield traits, the ANOVA reveals significant differences ($p < 0.05$) for the traits. Between these, SAA accession showed both the highest average fruit weight and yield, respectively. In addition, SAA accession showed the second highest number of fruits per plant (3.53 ± 1.19), suggesting that it has a quite large number of heavy fruits, useful for breeding. The significant variation in fruit number and weight across accessions indicates potential candidates for yield improvement in future breeding efforts (Table 1).

To further describe trait dispersion among accessions within the experimental environment, coefficients of variation (CV) were calculated for each trait (Table 2). Traits such as germination time, vegetative growth period, and days to 50% flowering exhibited relatively low CV values, indicating limited variation among accessions under the experimental conditions. In contrast, higher CV values were observed for traits including nodes to first flower, plant height, and fruit number per plant, reflecting greater phenotypic variability. High CVs for several yield-related traits suggest the presence of substantial exploitable variation among accessions, which is relevant for selection within a single environment.

3.2 | Analysis of Genetic Variability and Genetic Parameters for Trait Improvement

3.2.1 | Heritability

Broad-sense heritability (H^2) was calculated to determine the proportion of phenotypic variance attributed to genetic factors (Table 3). High heritability values (> 0.7) were observed for traits such as flowering duration (0.95), fruiting end date (0.93), fruiting start date (0.92), male flower emergence frequency (0.87), and female flower emergence frequency (0.73), which suggests these traits are primarily influenced by genetic factors and can be effectively improved through selection. Traits with moderate heritability (0.40–0.60), such as yield (0.59), average fruit weight (0.55) branch number (0.53), and node formation rate (0.45), indicate that both genetic and environmental factors influence their expression. Low heritability (< 0.40) was found for traits like root collar diameter (0.05), suggesting a limited response to selection.

TABLE 1 | Descriptive statistics of agromorphological traits across accessions.

Traits	BATCHENGA (min–max)	EBEBDA (min–max)	MONATÉLÉ (min–max)	NTUI (min–max)	OBALA (min–max)	SAA (min–max)	YAOUNDE (min–max)
Plant height (cm)	84.93 ± 39.07^{c} (42–170)	83.53 ± 27.27^{c} (53–150)	130.13 ± 31.09^{a} (59–185)	122.13 ± 41.87^{ab} (50–190)	136.53 ± 17.1^{a} (110–170)	139.13 ± 39.19^{a} (45–200)	102.13 ± 48.51^{bc} (11–189)
Root collar diameter (cm)	1.04 ± 0.14^{ab} (0.81–1.25)	1.12 ± 0.19^{ab} (0.92–1.65)	1.1 ± 0.16^{a} (0.8–1.27)	0.94 ± 0.31^{ab} (0.07–1.34)	1.1 ± 0.18^{ab} (0.75–1.39)	1.1 ± 0.18^{ab} (0.7–1.45)	0.97 ± 0.18^{b} (0.62–1.22)
Petiole length (cm)	14.54 ± 3.72^{de} (9–21)	14.07 ± 2.17^{e} (11.5–19.5)	17.59 ± 2.31^{abc} (13–21)	15.83 ± 3.4^{cde} (7.5–20)	19.15 ± 2.85^{ab} (14.6–23.5)	19.95 ± 3.69^{a} (10.5–25.5)	16.81 ± 3.58^{bcd} (9.8–22.3)
Leaf length (cm)	16.89 ± 1.82^{b} (13.2–20.9)	17.74 ± 2.1^{b} (14.6–21.5)	17.81 ± 1.9^{b} (13.5–21)	17.18 ± 2.04^{b} (12–19.5)	18.03 ± 1.49^{b} (15.6–20.5)	19.85 ± 2.98^{a} (12–23.7)	17.31 ± 2^{b} (12.5–20.6)
Leaf width (cm)	22.64 ± 2.41^{bc} (18–27)	24.03 ± 3.34^{ab} (17–29.3)	23.85 ± 2.2^{b} (18–26.7)	21.63 ± 2.83^{c} (15.9–25.4)	24.42 ± 2.4^{ab} (20–30)	26.05 ± 3.87^{a} (15.6–32)	22.93 ± 3.34^{bc} (15.3–28)
Internode length (cm)	6.37 ± 1.54^{e} (4–8)	6.93 ± 1.52^{de} (4–10)	7.9 ± 1.23^{cd} (6–11.5)	9.27 ± 1.7^{a} (8–15)	7.89 ± 1.24^{cd} (6.5–11.5)	8.9 ± 1.24^{ab} (6–11)	8.09 ± 1.36^{bc} (5.5–10)
Node number	14.33 ± 3.27^{cd} (9–20)	13 ± 2.04^{d} (10–16)	17.4 ± 3.4^{b} (10–23)	14.87 ± 3.36^{c} (8–20)	19.67 ± 1.8^{a} (17–22)	17.53 ± 2.95^{b} (9–21)	14 ± 3.21^{cd} (7–20)
Branch number	4.67 ± 2.38^{c} (2–10)	5.07 ± 2.19^{c} (1–8)	11.73 ± 3.79^{a} (2–16)	2.2 ± 2.14^{d} (0–6)	12.4 ± 5.11^{a} (4–17)	8.33 ± 3.64^{b} (0–14)	8 ± 3.74^{b} (0–14)
Male peduncle length (cm)	0.98 ± 0.2^{b} (0.5–1.4)	1.01 ± 0.18^{b} (0.7–1.5)	1.23 ± 0.42^{ab} (0.7–2.2)	1.06 ± 0.49^{ab} (0.05–1.9)	1.88 ± 2.27^{a} (0.7–10)	0.99 ± 0.31^{b} (0.5–1.5)	1.17 ± 0.35^{ab} (0.5–2)
Female peduncle length (cm)	1.14 ± 0.56^{c} (0.5–2.5)	1.27 ± 0.5^{bc} (0.8–2.5)	1.14 ± 0.31^{c} (0.6–1.9)	1.93 ± 0.55^{a} (1.2–2.9)	1.54 ± 0.5^{ab} (0.8–2.5)	1.27 ± 0.61^{bc} (0.5–2.5)	1.31 ± 0.42^{bc} (0.5–2)
Flowering date	25.67 ± 0.72^{b} (25–27)	25.73 ± 0.8^{b} (25–27)	26.07 ± 0.96^{b} (25–28)	24.4 ± 1.06^{c} (23–26)	27.8 ± 0.77^{a} (27–29)	24.8 ± 0.86^{c} (24–26)	27.93 ± 0.88^{a} (27–29)
Flowering duration (days)	31 ± 1^{d} (30–33)	30.47 ± 0.74^{d} (30–32)	39 ± 0.85^{a} (38–40)	30.8 ± 1.15^{d} (29–33)	38.73 ± 1.03^{a} (37–40)	35 ± 0.85^{c} (34–36)	36.87 ± 1.06^{b} (36–39)
Node formation rate (%)	4.33 ± 2.02^{b} (1–9)	4.07 ± 1.58^{b} (2–7)	3.27 ± 1.71^{b} (1–6)	8.8 ± 3.14^{a} (4–14)	3.73 ± 1.87^{b} (1–8)	3.67 ± 0.98^{b} (2–6)	4.2 ± 1.97^{b} (1–8)
Male flower number	50.93 ± 19.53^{c} (15–86)	48.07 ± 13.97^{c} (27–74)	68.47 ± 17.63^{b} (37–94)	18.13 ± 8.11^{d} (6–31)	90.13 ± 13.53^{a} (62–106)	71.93 ± 23.56^{b} (17–101)	52.2 ± 24.67^{c} (11–91)
Female flower number	5.27 ± 2.37^{b} (1–11)	4.69 ± 3.5^{b} (1–12)	3.83 ± 2.86^{b} (1–10)	9.93 ± 3.13^{a} (4–15)	5.07 ± 1.87^{b} (3–9)	4.43 ± 1.79^{b} (2–9)	5.08 ± 2.56^{b} (2–12)
Male flower emergence frequency (%)	1.2 ± 0.41^{cd} (1–2)	1.27 ± 0.46^{c} (1–2)	2.87 ± 0.64^{b} (2–4)	6.93 ± 1.67^{a} (4–9)	1 ± 0^{d} (1-1)	2.4 ± 0.51^{b} (2–3)	1.4 ± 0.74^{c} (1–3)
Female flower emergence frequency (%)	7.47 ± 0.64^{ab} (7–9)	5.8 ± 0.68^{c} (5–7)	6.07 ± 0.8^{c} (5–8)	3.8 ± 0.68^{d} (3–5)	7.27 ± 0.88^{b} (6–8)	6.27 ± 1.33^{c} (5–8)	7.87 ± 0.52^{a} (7–9)
Fruiting start date (days)	29.2 ± 0.94^{de} (28–31)	29.33 ± 0.82^{d} (28–30)	28.8 ± 0.77^{e} (28–30)	27.67 ± 0.49^{f} (27–28)	33.07 ± 0.8^{b} (32–34)	29.93 ± 0.88^{c} (28–31)	35 ± 0.76^{a} (34–36)
Fruit number/plant	3 ± 1.2^{bc} (1–5)	3.07 ± 0.96^{bc} (2–4)	1.87 ± 1.25^{d} (0–5)	5.6 ± 2.82^{a} (3–12)	2.33 ± 1.45^{cd} (0–5)	3.53 ± 1.19^{b} (2–7)	3.8 ± 1.57^{b} (1–8)
Fruit length (cm)	24.03 ± 2.84^{cd} (19.5–30)	25.4 ± 2.53^{c} (20–30)	25.27 ± 2.84^{c} (20–30)	33.93 ± 3.8^{a} (26–40)	25.67 ± 2.13^{c} (21–29)	30.73 ± 4.16^{b} (24–38.5)	22.93 ± 1.44^{d} (20–25)
Fruit diameter (cm)	6.05 ± 0.63^{ab} (4.8–6.99)	6.2 ± 0.62^{a} (4.69–7.22)	5.45 ± 0.57^{c} (4.43–6.37)	4.05 ± 0.39^{d} (3.25–4.63)	5.76 ± 0.48^{bc} (5.05–6.89)	6.37 ± 0.7^{a} (4.78–7.5)	5.5 ± 0.55^{c} (4.62–6.65)
Average fruit weight (kg)	0.56 ± 0.16^{bc} (0.31–0.85)	0.6 ± 0.14^{b} (0.28–0.89)	0.5 ± 0.13^{cd} (0.26–0.74)	0.4 ± 0.08^{e} (0.27–0.57)	0.53 ± 0.11^{bc} (0.36–0.73)	0.94 ± 0.28^{a} (0.53–1.5)	0.44 ± 0.09^{de} (0.3–0.63)
Number of fruits harvested/month	2.93 ± 1.28^{bc} (1–5)	2.93 ± 1.1^{bc} (2–5)	1.67 ± 0.9^{d} (0–3)	5.13 ± 2.53^{a} (3–10)	2.33 ± 1.45^{cd} (0–5)	3.53 ± 1.13^{ab} (2–7)	3.2 ± 1.32^{bc} (1–6)
Yield (kg/m^2)	1.89 ± 0.47^{bc} (1.3–2.9)	2.27 ± 0.37^{b} (1.8–2.9)	1.58 ± 0.51^{c} (1–2.5)	2.28 ± 0.95^{b} (1–3.9)	1.86 ± 0.56^{bc} (1.1–3)	3.76 ± 0.89^{a} (2.7–5.5)	1.31 ± 0.46^{c} (0.75–2.1)
Fruiting end date (days)	57.07 ± 0.8^{d} (56–58)	52.93 ± 1.91^{f} (50–55)	64.47 ± 3^{b} (61–69)	51.27 ± 1.33^{g} (50–54)	68.73 ± 1.28^{a} (65–70)	55 ± 1.46^{e} (53–59)	59.67 ± 1.23^{c} (58–62)
Fruit-to-flower ratio	0.44 ± 0.2^{bc} (0.14–0.74)	0.57 ± 0.17^{ab} (0.28–0.83)	0.31 ± 0.22^{c} (0–0.83)	0.58 ± 0.29^{ab} (0.21–1)	0.5 ± 0.35^{abc} (0–1)	0.54 ± 0.29^{ab} (0–1.4)	0.68 ± 0.34^{a} (0–1)
Germination time (days)	5 ± 0 (5-5)	4 ± 0 (4-4)	4 ± 0 (4-4)	4 ± 0 (4-4)	4 ± 0 (4-4)	5 ± 0 (5-5)	5 ± 0 (5-5)
Vegetative growth period (days)	25 ± 0 (25-25)	25 ± 0 (25-25)	25 ± 0 (25-25)	23 ± 0 (23-23)	27 ± 0 (27-27)	24 ± 0 (24-24)	27 ± 0 (27-27)
Days to 50% flowering (days)	26 ± 0 (26-26)	26 ± 0 (26-26)	26 ± 0 (26-26)	25 ± 0 (25-25)	28 ± 0 (28-28)	25 ± 0 (25-25)	28 ± 0 (28-28)
Nodes to the first flower	0.53 ± 0.52 (0–1)	0.27 ± 0.46 (0–1)	1.6 ± 0.51 (1–2)	0.93 ± 0.7 (0–2)	1.07 ± 0.26 (1–2)	1 ± 0.53 (0–2)	1.27 ± 0.59 (0–2)
Node formation period (days)	4.2 ± 0.56 (3–5)	3.87 ± 0.35 (3–4)	4 ± 0 (4-4)	3.47 ± 0.52 (3–4)	4.73 ± 0.46 (4–5)	3.53 ± 0.52 (3–4)	5.4 ± 0.51 (5–6)

Note: For each column, values followed by the same letters are not statistically significant at the 5% level.

TABLE 2 | Coefficient of variation of the traits across accessions.

Traits	BATCHENGA	EBEBDA	MONATÉLÉ	NTUI	OBALA	SAA	YAOUNDE
Plant height	46.00	32.65	23.89	34.28	12.53	28.17	47.50
Root collar diameter	13.51	16.95	14.45	33.10	16.71	16.85	18.07
Petiole length	25.58	15.40	13.12	21.50	14.88	18.48	21.29
Leaf length	10.78	11.84	10.66	11.89	8.25	15.04	11.52
Leaf width	10.65	13.89	9.22	13.08	9.83	14.85	14.55
Internode length	24.18	21.95	15.54	18.34	15.75	13.96	16.78
Node number	22.79	15.66	19.53	22.58	9.15	16.82	22.91
Branch number	51.01	43.16	32.29	97.49	41.21	43.66	46.77
Germination time	0	0	0	0	0	0	0
Vegetative growth period	0	0	0	0	0	0	0
Male peduncle length	20.11	17.44	34.08	46.18	120.65	31.32	29.78
Female peduncle length	49.15	39.55	27.50	28.44	32.36	47.72	32.27
Flowering duration	2.82	3.10	3.69	4.33	2.79	3.48	3.16
Date of 50% flowering	0	0	0	0	0	0	0
Nodes to first flower	96.82	171.65	31.69	75.40	24.21	53.45	46.86
Flowering date	3.23	2.44	2.17	3.72	2.67	2.41	2.88
Node formation rate	46.70	38.84	52.34	35.73	50.08	26.62	46.93
Node formation period	13.35	9.10	0.00	14.90	9.67	14.62	9.39
Male flower number	38.34	29.06	25.74	44.70	15.01	32.75	47.25
Male flower emergence frequency	34.50	36.14	22.32	24.05	0.00	21.13	52.63
Female flower emergence frequency	8.57	11.66	13.17	17.79	12.16	21.30	6.56
Fruiting start date	3.22	2.78	2.69	1.76	2.42	2.95	2.16
Fruit number/plant	39.84	31.34	66.75	50.42	62.04	33.60	41.25
Fruit length	11.81	9.96	11.24	11.19	8.29	13.53	6.27
Fruit diameter	10.36	9.94	10.51	9.67	8.37	11.03	10.08
Average fruit weight	28.91	23.71	25.45	21.25	20.63	29.97	21.56
Number of fruits harvested/month	43.63	37.49	53.98	49.32	62.04	31.85	41.26
Fruiting end date	1.40	3.60	4.65	2.60	1.86	2.66	2.07
Fruit-to-flower ratio	44.30	30.08	69.50	50.41	70.32	53.19	50.22
Female flower number	45.08	74.53	74.48	31.48	36.90	40.31	50.51
Yield	24.75	16.21	32.59	41.69	30.02	23.60	35.36

3.2.2 | GCV and PCV

The GCV and PCV were computed to assess the extent of variability at both the genetic and phenotypic levels (Table 3). The PCV values were always higher than or equal to the GCV values, indicating that environmental factors contributed to the total variation for most traits. For instance, traits like fruit length (PCV = 0.18, GCV = 0.15) and fruit diameter (PCV = 0.17, GCV = 0.14) showed relatively small differences between GCV and PCV, suggesting strong genetic control. However, traits such as male peduncle length (PCV = 0.79, GCV = 0.18) or root collar diameter (PCV = 0.19, GCV = 0.05) showed a larger difference between PCV and GCV, reflecting more environmental influence.

3.2.3 | GA and GAM

The GAM was used to evaluate the expected gain from selection (Table 3). High GAM values, particularly male flower emergence (165.06%), branch number (73.28%), male flower number (62.22%), node to first flower (57.18%), and yield (57.02%), indicate these traits have strong potential for genetic improvement. Traits with moderate GAM values, such as flowering duration (22.4%) and leaf length (18.9%), can still be improved, though the progress may be slower compared to traits with higher GAM. Conversely, traits with low GAM values, like days to 50% flowering (10.7%), may require more intensive selection efforts to achieve meaningful gains.

3.3 | PCA and Trait Correlation

PCA was conducted to summarize the variation across the 31 morphological traits in the seven *Cucumis sativus* accessions, to facilitate the identification of patterns and the most influential traits contributing to overall diversity. This analysis also aimed to understand the interrelationships among traits for potential selection in breeding programs.

TABLE 3 | Genetic parameters across traits.

Traits	Genetic variance	Phenotypic variance	Environmental variance	Broad-sense heritability	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Genetic advance (GA)	Genetic advance as a percent of mean (GAM)
Plant height	477.71	1798.56	1283.71	0.27	0.37	0.19	23.2	20.34
Root collar diameter	0	0.04	0.04	0.05	0.19	0.05	0.02	2.18
Petiole length	4.26	14.26	10	0.3	0.22	0.12	2.33	13.8
Leaf length	0.66	5.09	4.25	0.13	0.13	0.05	0.61	3.4
Leaf width	1.45	10.38	8.51	0.14	0.14	0.05	0.93	3.93
Internode length	0.9	2.94	1.93	0.31	0.22	0.12	1.09	13.74
Node number	5.2	13.75	8.55	0.38	0.23	0.14	2.89	18.25
Branch number	13.36	25.19	11.82	0.53	0.67	0.49	5.49	73.28
Germination time	0.02	0.02	0	1	0.03	0.03	0.27	5.99
Vegetative growth period	0.12	0.12	0	1	0.01	0.01	0.72	2.88
Male peduncle length	0.05	0.89	0.83	0.05	0.79	0.18	0.1	8.58
Female peduncle length	0.06	0.32	0.25	0.2	0.41	0.18	0.23	16.8
Flowering date	1.81	2.57	0.76	0.7	0.06	0.05	2.32	8.91
Days to 50% flowering	0.09	0.09	0	1	0.01	0.01	0.62	2.36
Nodes to the first flower	0.18	0.45	0.28	0.39	0.71	0.44	0.54	57.18
Flowering duration	14.31	15.23	0.93	0.94	0.11	0.11	7.55	21.85
Node formation rate	3.35	7.41	3.7	0.45	0.59	0.4	2.53	55.26
Node formation period	0.46	0.68	0.19	0.69	0.2	0.16	1.16	27.81
Male flower number	495.18	823.66	328.47	0.6	0.5	0.39	35.54	62.22
Female flower number	3.66	10.56	6.9	0.35	0.58	0.34	2.32	41.71
Male flower emergence frequency	4.37	4.99	0.61	0.87	0.92	0.86	4.02	165.06
Female flower emergence frequency	1.84	2.52	0.67	0.73	0.25	0.21	2.38	37.4
Fruiting start date	6.81	7.43	0.63	0.92	0.09	0.09	5.14	16.9

(Continues)

TABLE 3 | (Continued)

Traits	Genetic variance	Phenotypic variance	Environmental variance	Broad-sense heritability	Phenotypic coefficient of variation (PCV)	Genotypic coefficient of variation (GCV)	Genetic advance (GA)	Genetic advance as a percent of mean (GAM)
Fruit number/plant	1.28	3.83	2.55	0.34	0.59	0.34	1.35	40.79
Fruit length	15.2	24	8.4	0.63	0.18	0.15	6.39	23.8
Fruit diameter	0.58	0.91	0.33	0.64	0.17	0.14	1.26	22.33
Average fruit weight	0.03	0.05	0.02	0.55	0.41	0.3	0.26	46.25
Number of fruits harvested/month	1.03	3.19	2.17	0.32	0.58	0.33	1.18	38.13
Yield (kg/m^2)	0.59	1	0.39	0.59	0.47	0.36	1.22	57.02
Fruiting end date	39.68	42.59	2.91	0.93	0.11	0.11	12.53	21.43
Fruit-to-flower ratio	0.01	0.08	0.08	0.11	0.56	0.18	0.06	12.13

Note: σ_G^2: genetic variance, σ_P^2: phenotypic (total) variance, σ_E^2: environmental variance, H^2: broad-sense heritability, PCV: phenotypic coefficient of variation, GCV: genetic coefficient of variation, GAM: genetic advance as percent of mean. GA and GAM are computed for $k = 2.06$, i.e., at 5% of selection intensity.
Abbreviation: GA, genetic advance.

The PCA showed that the first three PCs accounted for 81.9% of the total variance (PC1 = 42%, PC2 = 22%, and PC3 = 27.9%), indicating that a limited number of trait combinations are responsible for most of the morphological diversity observed in the accessions (Figure 1).

PC1 was heavily weighted by traits such as male flower number, branch number, node formation rate, and number of fruits harvested (Figure 2, Table 4). PC2 was influenced by traits like average fruit weight, yield, and leaf length, which are a combination of yield-related and vegetative traits (Table 4). PC3 captured variation in plant height and nodes to first flower and petiole length traits, which are phenological (Table 4).

These components suggest that vegetative, phenological, and reproductive traits contribute to diversity in *Cucumis sativus*, with yield and growth-related traits playing the most important roles. The PCA results showed key traits that could be prioritized for breeding efforts.

3.4 | Clustering and Genetic Diversity Analysis

3.4.1 | Clustering of Accessions

Hierarchical clustering analysis was performed to classify the seven *Cucumis sativus* accessions based on their morphological trait profiles. The resulting dendrogram grouped the accessions into three principal clusters, indicating varying degrees of morphological similarity and diversity among them (Figure 3). Cluster 1 contained only NTUI accessions, which may indicate that it has unique genetic characteristics distinct from the other accessions. NTUI accessions predominantly had larger phenological and vegetative traits, such as male flower emergence frequency, node formation rate, and female peduncle length. Cluster 2, constituted of EBEBDA, BATCHENGA, and SAA, with moderate growth and reproductive trait values, suggesting they represent an intermediate profile in terms of both growth vigor and yield potential. Cluster 3 comprised accessions with higher phenological traits, such as YAOUNDE, MONATÉLÉ, and OBALA, which may indicate a reduced yield potential but probably unique adaptation traits relevant to specific breeding goals (Figure 3).

This clustering pattern implies that the accessions exhibited considerable diversity, with each cluster representing a different combination of growth, phenological, and fruit traits.

3.5 | MANOVA

MANOVA revealed highly significant differences among the seven *Cucumis sativus* accessions (*Wilks' Lambda* $= 5.82 \times 10^{-7}$, $F = 12.06$, $p = 2.2e - 16$), indicating substantial multivariate phenotypic variation among the accessions (Table 5). These results confirm that the accessions differ significantly when multiple morphological traits are considered simultaneously. The observed interaccession variation reflects contrasting phenotypic profiles, which may be associated with differences in origin, farmer selection, and local adaptation, and highlights their potential value for breeding programs.

4 | Discussion

The present study provided a comprehensive assessment of the phenotypic variability in seven *Cucumis sativus* accessions. Significant variability was observed across 31 traits, with high heritability and GA estimates for key traits, indicating their

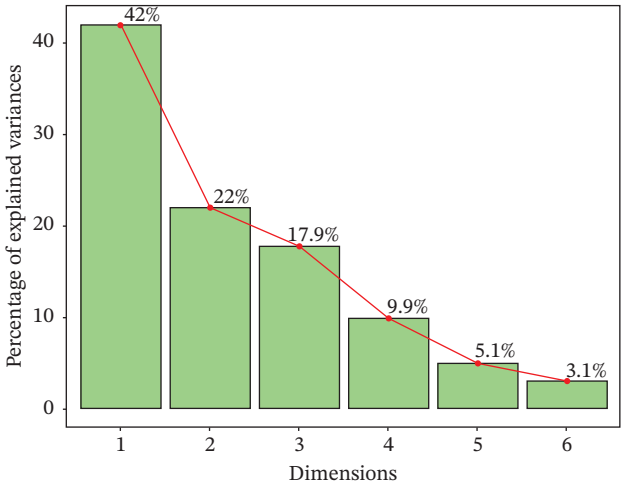


FIGURE 1 | Scree plot showing explained variance according to the first five components.

potential for selection in breeding programs. The results from PCA and hierarchical clustering revealed considerable morphological diversity among the accessions, demonstrating their value as genetic resources for improving critical traits like yield, fruit size, and flowering time.

4.1 | Genetic Diversity and Morphological Variation

Genetic diversity observed among *C. sativus* accessions highlights the rich phenotypic variability inherent in the species, which is crucial for breeding and genetic improvement programs. Moderate to high variability was observed for most traits, particularly those related to fruit and yield, such as fruit weight, fruit number per plant, and plant height. These findings align with recent reports on cucumber landraces in Bangladesh, where significant morphological diversity was observed for traits related to yield, underlining their selection potential [25, 26].

Significant variability in vegetative traits, such as plant height and branch number, underscores the genetic variability present within *C. sativus* accessions. These traits exhibited high CVs in this study, consistent with findings in cucumber landraces, where vegetative traits displayed substantial variability, making them valuable for breeding programs targeting plant architecture and yield improvement. For instance, studies on tropical cucumber accessions revealed considerable variability in vegetative traits like plant height, which is crucial for optimizing canopy structure and improving yield potential [5, 27].

The ANOVA further validates the genetic basis of key traits. Traits like fruit weight and number per plant exhibited the most pronounced differences among accessions, indicating strong potential for genetic improvement. Studies on cucumber landraces have reported similar results, where traits related to yield showed significant variability across accessions, underlining their breeding importance. For instance, a study on the phenotypic variation of 103 cucumber accessions observed broad phenotypic variation for traits such as yield per plant and fruits per plant, highlighting the potential for selection in breeding programs [26].

Moderate diversity observed for traits like flowering time and fruiting duration suggests more consistent expression under

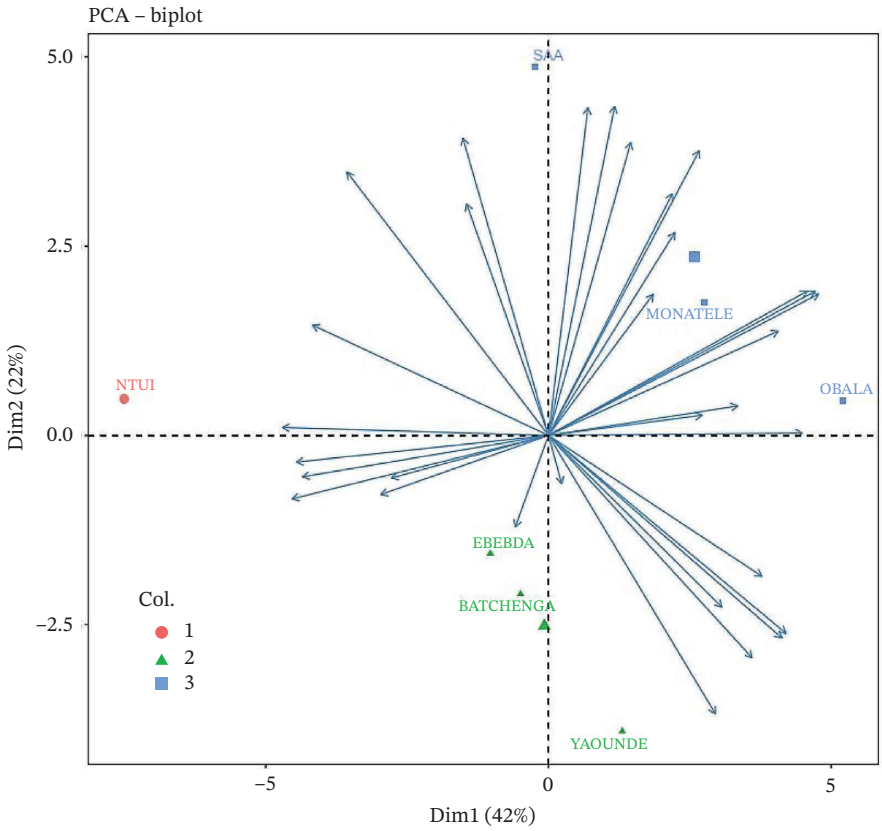


FIGURE 2 | Biplot of the traits across accessions.

TABLE 4 | Contribution of traits to the first five principal components.

Traits	Dim.1	Dim.2	Dim.3	Dim.4	Dim.5
Plant height	0.59	3.43	11.92	0.49	1.2
Root collar diameter	2.4	5.24	2.52	1.25	8.47
Petiole length	0.88	1.95	11.12	2.76	0.83
Leaf length	0.43	11.56	0.07	4.31	1.08
Leaf width	2.47	7.09	1.26	1.92	1.05
Internode length	0.31	1.08	10.34	7.67	0.66
Node number	2.44	2.19	6.7	2.47	0.12
Branch number	6.36	0.32	2.11	0.53	1.22
Germination time	0.06	0.56	1.15	15.95	7.39
Vegetative growth period	5.4	3.53	0.04	1.48	1.46
Male peduncle length	2.74	0.22	2.51	1.8	28.1
Female peduncle length	2.09	4.44	5.87	0	7.75
Flowering date	5.37	4.4	0.02	0.35	0.7
Days to 50% flowering	3.98	5.85	0.13	1.55	3.06
Nodes to first flower	0.94	0.24	11.87	0.03	13.87
Flowering duration	4.82	0.03	6.2	0.02	1.91
Node formation rate	6.21	1.31	1.16	0.22	0.82
Node formation period	2.65	7.46	0	4.44	0.02
Male flower number	7.21	0.87	0.28	0.09	0.29
Female flower number	5.5	1.89	0.19	0.5	6.04
Male flower emergence frequency	5.29	0.01	5.19	0.49	0.4
Female flower emergence frequency	4.52	0.26	1.81	5.14	0.44
Fruiting start date	3.15	2.38	0.38	9.67	3.04
Fruit number/plant	5.05	0.07	0.71	7.8	0.43
Fruit length	3.94	3.4	3.84	0.67	2.37
Fruit diameter	2.2	2.8	9.26	0.03	0
Average fruit weight	0.07	13.77	0.64	1.21	0.48
Number of fruits harvested/month	6.16	0.19	0.02	5.03	0.13
Yield	0.64	12.24	0.02	0.43	6.52
Fruiting end date	5.6	0.86	2.61	1.58	0.05
Fruit-to-flower ratio	0.53	0.33	0.07	20.1	0.13

the tested environmental conditions. Traits such as fruit number and plant height exhibited higher variability, making them primary targets for breeding programs. This pattern is consistent with findings in *C. sativus* landraces from diverse agroecological zones, where environmental adaptation played a crucial role in trait variability. For instance, a study on the phenotypic variation of 103 cucumber accessions observed broad phenotypic variation for traits such as yield per plant and fruits per plant, highlighting the potential for selection in breeding programs [26, 28].

Although this study was limited by the small number of accessions, the observed diversity demonstrates significant potential for improving agronomic traits through targeted selection. Expanding future studies to include molecular markers, such as SNP or SSR, could complement morphological assessments and refine the genetic characterization of cucumber accessions [5].

4.2 | Heritability and GA

The estimation of heritability and genetic advance provides crucial insights into the genetic control of key traits in *C. sativus* and their potential for genetic improvement. High broad-sense heritability (H^2) for traits like flowering duration (0.95), fruiting start date (0.92), and fruit weight (0.90) highlight their genetic determinism, suggesting they are ideal for reliable phenotypic selection. Similar trends were reported in *C. sativus* and Bangladeshi cucumber landraces, where traits related to yield consistently exhibited high heritability [26, 29].

High GAM for traits like male flower emergence frequency (165.06%), branch number (73.28%), and male flower number (62.22%) underlines their response to selection. These results align with findings from Indian cucumber genotypes, where high heritability coupled with high GA highlighted their potential for rapid improvement [30].

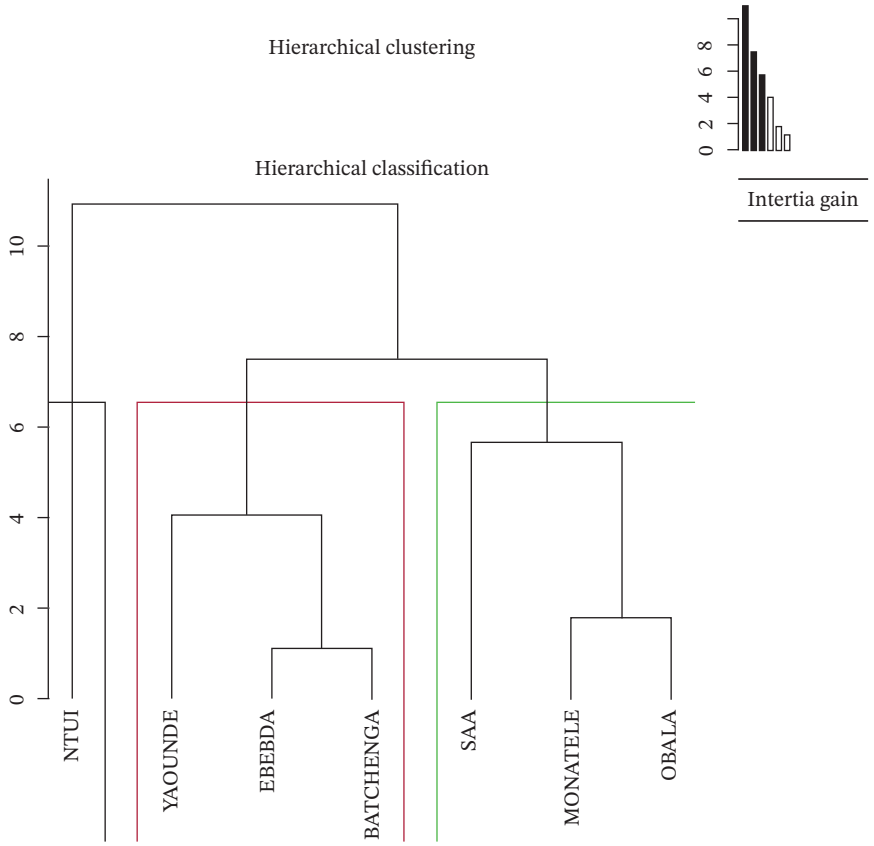


FIGURE 3 | Hierarchical clustering on principal components of the accessions.

TABLE 5 | Multivariate analysis of variance.

Variation sources	df	Wilks	Approx F	Num Df	Den Df	Pr (> F)
Accessions	6	$5.82e-07$	12.058	156	178.19	$< 2.2e-16^{***}$
Residuals	54					

Note: Significance codes. $^{***}p \leq 0.001$, df: degree of freedom, Wilks: Wilks lambda statistics.

Moderate heritability observed for traits such as branch number (0.53) and yield (0.59) indicates nonnegligible influence of environmental factors. This underlines the importance of multienvironment trials to fully capture genetic potential and improve selection accuracy. Recent studies on cucumber diversity have similarly emphasized the need for environmental standardization when targeting traits with moderate heritability [31].

GCV and PCV provided additional comprehension of trait variability. Traits like fruit weight and fruit length, which exhibited small differences between GCV and PCV values, suggest a stronger genetic contribution relative to environmental effects under the conditions of this study. Conversely, larger differences for traits like male peduncle length reflected greater environmental influence, consistent with observations in *C. sativus,* but for mean fruit weight and number of branches, including melons and pumpkins [32]. This pattern is consistent with observations in other *Cucurbitaceae* species, including pumpkins, where traits like fruit weight and length show high genetic variability, while traits such as vine length are more environmentally influenced [33].

4.3 | PCA and Trait Clustering

PCA and hierarchical clustering on principal component (HCPC) provided critical insights into the morphological diversity and genetic relationships among accessions. The first three PAs explained 81.9% of the total variation, with traits such as male flower number, branch number, and node formation rate highly contributing to PC1. Similar trends were observed in studies on *C. sativus* landraces from Bangladesh, where PCA highlighted the dominance of reproductive traits in explaining genetic diversity [26, 34]. In agreement with previous findings always in *C. sativus*, the findings of [32, 34], this study also demonstrated that vegetative traits exhibited a high influence on the PAs.

HCPC grouped the accessions into three distinct clusters, reflecting their morphological similarity and divergence. Cluster 1, containing NTUI, was characterized by traits such as higher male flower emergence frequency, suggesting unique genetic traits. Clusters 2 and 3 grouped accessions with varying combinations of yield, phenological, and vegetative traits, emphasizing their potential for targeted breeding programs. These results align with clustering analyses reported in *C. sativus*,

where distinct genetic groups were identified based on morphological data [26, 32, 35].

The PCA and clustering results complement each other, offering a framework for crossbreeding strategies. Crossing accessions from distinct clusters could combine complementary traits, such as early flowering from NTUI with high fruit yield from SAA, to develop high-performing cucumber varieties.

5 | Conclusion

This study assessed the morphological diversity of seven *Cucumis sativus* accessions from Cameroon using agromorphological traits. Significant variation was observed among accessions for several vegetative, phenological, and yield-related traits, indicating substantial phenotypic diversity within the local germplasm. Traits such as fruit weight, yield, and flowering duration showed strong potential for selection and could be prioritized in cucumber breeding programs. Multivariate analyses (PCA and clustering) clearly discriminated the accessions, highlighting distinct phenotypic profiles that may be exploited for targeted improvement. Overall, the results demonstrate the value of local cucumber accessions as genetic resources for breeding and conservation and provide a foundation for future studies involving a wider range of accessions and complementary molecular approaches.

Funding

This study was not funded by any external sources.

Ethics Statement

This study was conducted in accordance with standard ethical research practices. No human or animal subjects were involved in this research.

Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

The data that support the findings of this study are available on request from the corresponding author. The data are not publicly available due to privacy or ethical restrictions.

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