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Morphometric Diversity of Rice Bean (*Vigna umbellata*) Landraces from Timor Island, Indonesia: Implications for Conservation and Climate-Resilient Agriculture

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ABSTRACT

Rice bean (*Vigna umbellata*) is an underutilized legume with high nutritional value and considerable potential for dryland agriculture, yet information on its phenotypic diversity in eastern Indonesia remains limited. This study quantified seed morphometric variation among rice bean landraces collected from four dryland localities on Timor Island, Indonesia. Seed samples were obtained through targeted germplasm exploration of farmer-managed seed systems, and variation was assessed based on seed length, width, thickness, and 100-seed weight. Univariate analyses revealed no statistically significant differences among localities for any measured seed traits, indicating the absence of discrete locality-based differentiation. Nevertheless, a wide range of morphometric values was observed among phenotypes within and across localities, reflecting considerable phenotypic variation maintained in farmer-managed populations. Principal component analysis (PCA) explained 96.95% of the total variation, with the first principal component accounting for 84.68% and representing a major axis contrasting seed dimensions (length, width, and thickness) with 100-seed weight. The PCA biplot further demonstrated continuous phenotypic dispersion without clear clustering according to locality. These findings suggest that morphometric diversity in Timor Island rice bean landraces is maintained primarily within farmer-managed populations rather than being structured among geographic localities. Such within-population variation represents an important reservoir of phenotypic diversity and valuable germplasm resources that may support future conservation initiatives and the development of climate-resilient dryland agriculture in eastern Indonesia.

1. INTRODUCTION

Timor Island, located in eastern Indonesia, is characterized by semi-arid conditions marked by prolonged dry seasons, erratic rainfall, and shallow calcareous soils. Agricultural production in this environment relies heavily on drought-tolerant crops and locally adapted landraces that have evolved under long-term moisture limitation [1, 2]. These dryland systems are among the most climate-vulnerable in Indonesia, where increasing moisture deficits threaten crop productivity and local food security [3, 4]. In such environments, the conservation and characterization of adaptive crop diversity are essential for sustaining agricultural systems under ongoing climate change [5, 6].

Rice bean (*Vigna umbellata*) is a drought-tolerant and nutritionally rich legume traditionally cultivated in marginal environments, including Timor Island [7-10]. It is increasingly recognized as a valuable indigenous food resource with potential applications in functional and emergency food products, highlighting its role in strengthening food and nutritional security [11, 12]. In addition, rice bean contributes to soil fertility through biological nitrogen fixation. However, its cultivation has declined due to the expansion of major crops, changing dietary preferences, and the weakening of traditional seed systems, raising concerns about the erosion of locally adapted genetic resources [5, 13]. This decline is particularly critical in dryland regions, where underutilized crops such as rice bean play an important role in maintaining resilience and livelihood stability.

Phenotypic variation, particularly in seed-related traits, is a key component of plant adaptation and performance under environmental stress. Seed size and shape influence germination, seedling vigor, and yield stability, especially under drought and heat stress conditions [14, 15]. In legumes, these traits are shaped by both genetic factors and environmental conditions, including temperature, moisture availability, and agroecological gradients [16-18]. Seed development is particularly sensitive to drought and heat

stress, which influence assimilate partitioning and resource allocation during reproductive stages [19-22]. Previous studies on rice bean have reported substantial variation in yield-related and morphological traits across different environments, reflecting both adaptive responses and farmer selection practices [23-26]. Similar patterns have been observed in other *Vigna* species, where seed traits exhibit continuous variation rather than discrete grouping, indicating complex adaptive strategies in heterogeneous environments.

A more detailed understanding of morphometric seed variation is particularly important for underutilized legumes such as rice bean, where formal breeding efforts remain limited and genetic resources are largely maintained in situ within farmer-managed systems. In such contexts, seed traits serve not only as indicators of phenotypic diversity but also as practical selection criteria used by farmers for adaptation to local environmental conditions. Quantitative characterization of these traits can therefore provide valuable insights into the structure of diversity and the potential for selection and improvement. Previous studies have emphasized that morpho-agronomic traits in rice bean are closely associated with yield stability and adaptation across variable environments, reflecting both genetic variation and farmer-driven selection processes [23-26]. In addition, seed-based variation has been widely used as a proxy for assessing genetic diversity in related legumes under similar agroecological conditions [27], highlighting its relevance for conservation and utilization strategies in dryland agriculture.

Despite its importance, quantitative information on seed morphometric diversity of rice bean in Indonesia remains limited, particularly in relation to dryland agroecological conditions. This knowledge gap constrains efforts to conserve and utilize rice bean genetic resources for breeding and climate-resilient agriculture. Given the rapid decline of traditional landraces and increasing climate pressures, documenting phenotypic variation in farmer-managed populations is both timely and necessary for guiding conservation and selection strategies.

Timor Island exhibits a strongly seasonal monsoonal climate, with rainfall concentrated in a short wet season followed by a prolonged dry period lasting up to seven months. High temperatures and intense solar radiation further constrain crop growth, particularly during reproductive stages [2]. Within this context, farmer-managed seed systems and local knowledge play a crucial role in maintaining adaptive diversity, particularly in upland areas where traditional practices persist [28, 29]. In contrast, cultivation has declined or disappeared in some lowland areas, reflecting spatial variation in crop persistence and management. Recent studies on related legumes in East Nusa Tenggara also highlight the importance of seed traits as indicators of genetic diversity and local adaptation [27].

Based on this context, we hypothesized that rice bean populations maintained under contrasting dryland environments on Timor Island exhibit continuous morphometric variation rather than discrete phenotypic differentiation. Therefore, this study aimed to (1) quantify variation in seed length, width, thickness, and 100-seed weight among rice bean populations from four localities on Timor Island; (2) explore patterns of variation across agroecological gradients through descriptive analysis; and (3) highlight the importance of these landraces as genetic resources for conservation and sustainable dryland agriculture in eastern Indonesia.

2. MATERIAL AND METHODS

2.1 Study area and seed sampling

Rice bean seed samples were collected from four dryland localities on Timor Island, Indonesia, representing contrasting agroecological conditions: Camplong 2, Ekateta, and Sillu in Kupang Regency, and Oinlasi in South Central Timor Regency (Figure 1). These sites span an elevation gradient from 262 m above sea level in Camplong 2 to 699 m in Oinlasi, capturing variation in temperature and rainfall regimes typical of Timor's semi-arid environment. Sampling followed a targeted germplasm exploration approach widely used to document morphometric diversity and capture variation within farmer-managed germplasm populations [27, 29]. Sampling locations within each locality were identified through farmer interviews, local knowledge, and field verification, focusing on areas where rice bean was still cultivated. Seed samples were obtained exclusively from farmer-stored seed lots maintained from previous harvests. This purposive approach ensured that sampling captured the actual distribution of rice bean landraces under farmer management, thereby improving the representativeness of locally maintained genetic diversity compared to purely random selection.

Within each locality, up to ten sampling points were surveyed depending on the presence of rice bean and seed availability. The number of phenotypes identified varied among locations. For instance, Ekateta exhibited higher phenotypic diversity, while Camplong 2 yielded only a single identifiable phenotype. This variation likely reflects actual field conditions, including differences in cultivation intensity, farmer seed management, and possible genetic erosion in certain areas, rather than unequal sampling effort. Sampling intensity across localities was comparable and constrained primarily by crop presence and seed availability, ensuring that differences in observed phenotypic diversity were not driven by unequal sampling.

The number of seeds collected per sampling point ranged from 150 to 500 seeds, obtained from farmer-maintained seed lots. From each locality, a subsample of 100 seeds was randomly selected for morphometric analysis to ensure consistency and comparability across populations. Each sampling point corresponded to an individual farmer or a distinct seed lot, thereby avoiding duplication of the same seed source.

2.2 Seed morphometric measurements

Seed length, width, and thickness were measured using a digital caliper with a precision of 0.01 mm. One hundred–seed weight was determined using an analytical balance. Seed coat color was visually assessed and classified using the Munsell color chart to document qualitative phenotypic variation.

2.3 Climatic data acquisition

Long-term monthly climatic data (1980–2024), including air temperature, precipitation, and relative humidity, were obtained from the ERA5-Land reanalysis dataset via the Google Earth Engine. Temperature data were converted from Kelvin to Celsius, and relative humidity was calculated using standard psychrometric equations. Monthly values were aggregated to derive long-term mean climatic conditions for each sampling site, representing typical dryland climatic patterns of Timor Island.

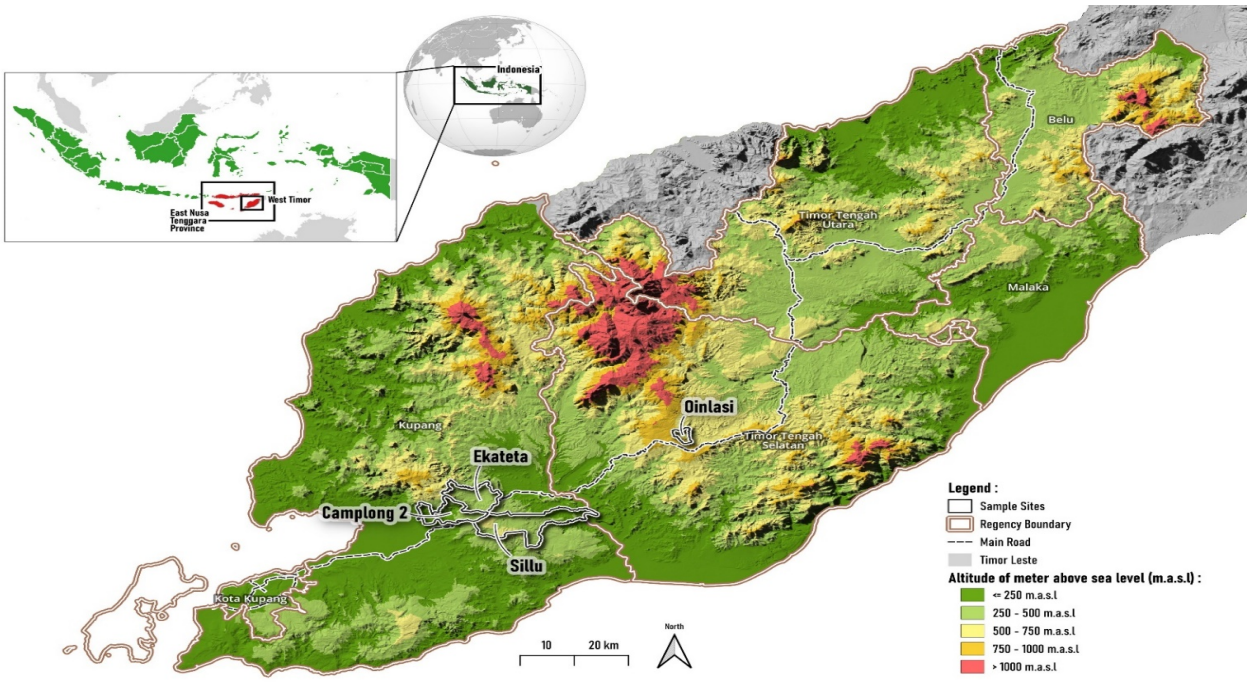

Figure 1. Locations of rice bean (*Vigna umbellata*) seed sampling across four dryland localities on Timor Island, Indonesia

2.4 Statistical and multivariate analysis

Descriptive statistics, including means and standard deviations, were calculated for each seed trait. Data normality and homogeneity of variance were assessed using the Shapiro–Wilk and Levene's tests, respectively. Differences among populations were evaluated using one-way analysis of variance (ANOVA), followed by Tukey's HSD post hoc test.

A stringent significance level ($\alpha < 0.01$) was applied to reduce the likelihood of Type I error associated with multiple comparisons among seed traits and populations. This conservative threshold was selected to ensure robustness of statistical inference, particularly given the relatively small and unbalanced sample sizes among populations, although it may reduce sensitivity to detect subtle differences.

Relationships among seed traits were examined using Pearson's correlation coefficients. Variations across agroecological gradients (e.g., elevation and climatic conditions) were interpreted descriptively rather than through formal regression analysis.

Multivariate patterns of seed morphometric variation were analyzed using principal component analysis (PCA) based on four traits: seed length, seed width, seed thickness, and 100-seed weight. PCA was performed on standardized data (correlation matrix) to account for differences in measurement units. Principal components with eigenvalues greater than one were retained, and biplots of the first two principal components (PC1 and PC2) were used to visualize phenotypic relationships and trait contributions. All statistical analyses were performed using open-source software, including R version 4.3.2, Python version 3.11, PAST version 5, and Google Colab as the computational environment.

3. RESULTS

3.1 Overall morphometric variation

No statistically significant differences were detected among phenotypes or localities for any measured seed traits based on ANOVA followed by Tukey's HSD test at $\alpha < 0.01$, as all means shared the same significance grouping (Tables 1 and 2). Despite the absence of statistical significance, descriptive numerical variation was observed.

Table 1. Morphometric characteristics and 100-seed weight of eleven rice bean (*V. umbellata*) phenotypes collected from four localities on Timor Island

Phenotype Designation	Seed Length (mm)	Seed Width (mm)	Seed Thickness (mm)	100-Seed Weight (g)
Camplong 2 DR	6.9 ± 0.3	5.2 ± 0.2	4.4 ± 0.2	15.18 ± 0.3
Ekateta DR1	8.2 ± 0.1	6.2 ± 0.2	4.5 ± 0.3	11.55 ± 0.3
Ekateta DR2	8.2 ± 0.1	6.4 ± 0.2	4.7 ± 0.1	12.33 ± 0.3
Ekateta MX	8.0 ± 0.1	6.1 ± 0.3	4.3 ± 0.3	18.17 ± 0.2
Ekateta LB	7.9 ± 0.3	6.0 ± 0.3	5.0 ± 0.3	18.38 ± 0.3
Ekateta DM	7.1 ± 0.3	5.5 ± 0.3	4.4 ± 0.3	13.45 ± 0.4
Ekateta MB	7.3 ± 0.3	5.2 ± 0.3	5.4 ± 0.3	20.15 ± 0.1
Oinlasi DR	11.6 ± 0.3	7.2 ± 0.1	5.8 ± 0.3	8.35 ± 0.3
Oinlasi LB	10.5 ± 0.3	6.7 ± 0.2	5.0 ± 0.3	8.08 ± 0.3
Sillu ST	9.5 ± 0.3	6.9 ± 0.3	5.2 ± 0.3	16.38 ± 0.4
Sillu DM	8.0 ± 0.3	6.2 ± 0.3	4.7± 0.3	12.65 ± 0.3

Notes: Values are presented as mean ± standard deviation (SD). One-way ANOVA detected no significant differences among phenotypes for any measured trait (all $p > 0.01$). DR = dark red; DM = deep maroon; LB = light brown; MB = medium brown; MX = mixed; ST = striped.

Table 1 summarizes morphometric characteristics at the phenotype level and reveals substantial numerical variation among the eleven rice bean phenotypes. Seed dimensions

generally tended to be larger in Oinlasi phenotypes, whereas several Ekateta phenotypes were characterized by comparatively higher 100-seed weight. Despite these numerical differences, all phenotypes remained within the same Tukey's HSD significance grouping, indicating the absence of statistically significant differentiation. To facilitate locality-level comparison, phenotype data were subsequently summarized by collection site (Table 2).

Table 2. Descriptive statistics (mean ± SD) for seed traits of rice bean (*V. umbellata*) from four localities on Timor Island

Locality	Seed Length (mm)	Seed Width (mm)	Seed Thickness (mm)	100-Seed Weight (g)
Camplong 2	6.9 ± 0.3	5.2 ± 0.3	4.4 ± 0.2	15.2 ± 1.9
Ekateta	7.8 ± 0.6	5.9 ± 0.6	4.7 ± 0.5	14.4 ± 4.3
Oinlasi	11.1± 0.7	7.0 ± 0.4	5.4 ± 0.6	8.2 ± 0.5
Sillu	8.7 ± 1.4	6.6 ± 0.7	5.0 ± 0.6	14.5 ± 7.7

Within-locality variation differed among sites, reflecting the coexistence of multiple phenotypes with contrasting seed characteristics. In Ekateta, six phenotypes were identified, encompassing variation in seed size, thickness, seed coat color, and 100-seed weight. Among these, the Ekateta MB phenotype was characterized by relatively shorter and narrower but thicker seeds combined with comparatively high 100-seed weight, contributing to the morphometric diversity observed within this locality.

Differences in variability among localities were also influenced by unequal numbers of phenotypes represented at each site. Ekateta contained a greater number of phenotypes than Camplong 2 and Oinlasi, which likely contributed to broader trait dispersion within the locality. Descriptively, accessions from Oinlasi tended to exhibit larger seed dimensions, whereas Camplong 2 generally showed smaller values. However, these patterns represent numerical trends only and do not indicate statistically supported differentiation among localities.

3.2 Seed length

No statistically significant differences in seed length were detected among phenotypes or localities (Table 1 and Table 2). Nevertheless, descriptive numerical variation was observed. Mean seed length tended to be greater in Oinlasi and lower in Camplong 2, with intermediate values recorded in Sillu and Ekateta (Table 2 and Figure 2). These patterns, however, represent descriptive trends only and do not constitute statistically supported differentiation among localities.

At the phenotype level, seed length ranged from 6.9 mm in Camplong 2 DR to 11.6 mm in Oinlasi DR (Table 1), indicating substantial numerical variation despite the absence of significant differences. The uniform Tukey's HSD grouping and the considerable overlap among boxplots (Figure 2) support a pattern of continuous variation rather than discrete size classes. Within Ekateta, phenotypes exhibited diverse combinations of seed dimensions and 100-seed weight, contributing to within-locality variability. The Ekateta MB phenotype was characterized by relatively shorter seeds but comparatively high 100-seed weight, representing a distinct morphometric combination within the locality.

Figure 2. Variation in seed length (mm) among rice bean (*V. umbellata*) populations from four dryland localities on Timor Island, Indonesia

Notes: The boxplot illustrates the median (horizontal line), interquartile range (box), and minimum–maximum values (whiskers); circles represent outliers.

3.3 Seed width

No statistically significant differences in seed width were detected among phenotypes or localities (Table 1 and Table 2). Nevertheless, descriptive numerical variation was observed. Mean seed width tended to be greater in Oinlasi and Sillu and lower in Camplong 2, with Ekateta showing intermediate values (Table 2 and Figure 3). These patterns, however, represent descriptive trends only and do not indicate statistically supported differentiation among localities.

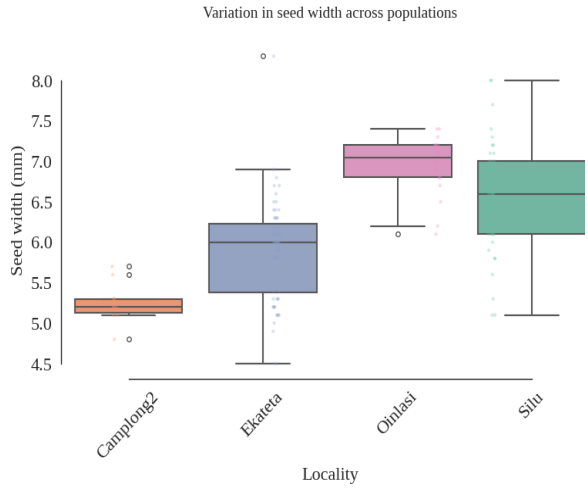

Figure 3. Variation in seed width (mm) among rice bean (*V. umbellata*) populations from Camplong 2, Ekateta, Oinlasi, and Sillu on Timor Island, Indonesia

Notes: The boxplot displays median values (horizontal lines), interquartile ranges (boxes), and whiskers extending to the most extreme observations within 1.5 × the interquartile range (IQR). Open circles represent statistical outliers.

At the phenotype level, seed width ranged from 5.2 mm in Camplong 2 DR and Ekateta MB to 7.2 mm in Oinlasi DR (Table 1), indicating moderate numerical variation despite the absence of significant differences. The substantial overlap among boxplots (Figure 3), together with the uniform Tukey's HSD grouping, supports a pattern of continuous variation rather than discrete population structure.

3.4 Seed thickness

No statistically significant differences in seed thickness were detected among phenotypes or localities (Table 1 and Table 2). Nevertheless, descriptive numerical variation was observed. Mean seed thickness tended to be greater in Oinlasi and Sillu and lower in Camplong 2 and Ekateta (Table 2; Figure 4). These patterns, however, represent descriptive trends only and do not indicate statistically supported differentiation among localities.

At the phenotype level, seed thickness ranged from 4.3 mm in Ekateta MX to 5.8 mm in Oinlasi DR (Table 1), indicating moderate numerical variation despite the absence of significant differences. Ekateta exhibited somewhat broader within-locality variation than Camplong 2 and Oinlasi, reflecting the presence of multiple phenotypes with contrasting seed characteristics. The substantial overlap among boxplots (Figure 4), together with the uniform Tukey's HSD grouping, supports a pattern of continuous variation rather than discrete population structuring.

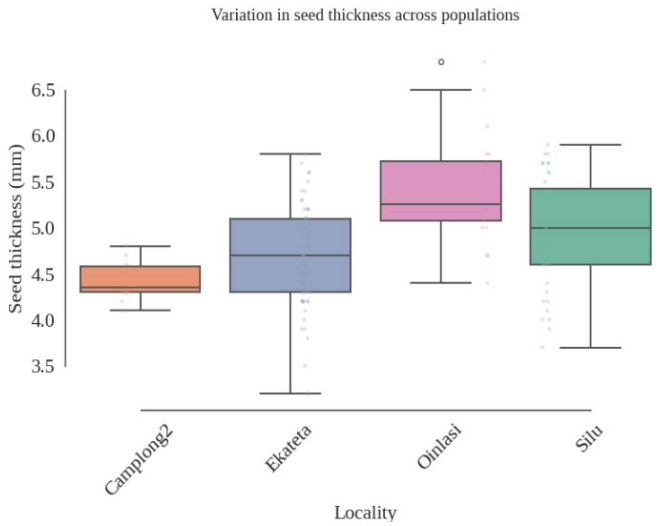

Figure 4. Variation in seed thickness (mm) among rice bean (*V. umbellata*) populations from Camplong 2, Ekateta, Oinlasi, and Sillu on Timor Island, Indonesia
Notes: The boxplot displays median values (horizontal lines), interquartile ranges (boxes), and minimum–maximum values (whiskers); circles represent outliers.

3.5 One hundred–seed weight

No statistically significant differences in 100-seed weight were detected among phenotypes or localities (Table 1 and Table 2). Nevertheless, descriptive numerical variation was observed. Mean values tended to be higher in Camplong 2 and Sillu and lower in Oinlasi, with Ekateta showing intermediate values (Table 2). These patterns, however, represent descriptive trends only and do not indicate statistically supported differentiation among localities.

At the phenotype level, 100-seed weight ranged from 8.080 g in Oinlasi LB to 20.153 g in Ekateta MB (Table 1), indicating substantial numerical variation despite the absence of significant differences. The highest values were observed in several Ekateta phenotypes (MB, LB, and MX), whereas both Oinlasi phenotypes exhibited comparatively low seed weight. Despite these numerical differences, all phenotypes remained within the same Tukey's HSD grouping, indicating extensive overlap among populations.

3.6 Seed coat color diversity

Clear qualitative variation in seed coat color was observed among rice bean phenotypes (Table 1 and Figure 5), although this trait was not subjected to statistical testing. Ekateta exhibited the highest diversity of seed coat colors, whereas Oinlasi and Sillu showed moderate variation, and Camplong 2 was represented by a single-color type. These observations represent descriptive patterns of qualitative variation. The coexistence of multiple seed coat color classes within Ekateta indicates a broader range of phenotypic diversity than observed in the other localities.

Figure 5. Representative rice bean (*V. umbellata*) seeds illustrating seed coat color variation among local populations from Timor Island, Indonesia

3.7 Multivariate structure of seed traits

PCA explained 96.95% of total variation, with PC1 accounting for 84.68% and PC2 for 12.27%, indicating that most variation is captured along a single dominant axis (Figure 6).

PC1 was positively associated with seed length, width, and thickness, and negatively associated with 100-seed weight, representing a gradient contrasting seed dimensions with seed mass. The PCA biplot (Figure 6) shows dispersion of phenotypes along this axis without clear clustering by locality, indicating continuous variation in trait combinations. The Ekateta MB phenotype was positioned toward one end of PC1, reflecting its comparatively high 100-seed weight relative to its seed dimensions. No distinct clustering according to locality was evident, supporting the univariate results that indicated the absence of statistically supported differentiation among populations.

3.8 Climatic context of morphometric variation

All study sites exhibit a unimodal monsoonal climate, with rainfall concentrated in a short wet season followed by a prolonged dry period (Figure 7). Although differences in temperature and rainfall among locations were observed, the present study did not statistically test direct relationships between climatic variables and seed traits. Therefore, any associations should be interpreted cautiously as descriptive context rather than evidence of causal relationships. The climatic data are presented to provide environmental background for the sampled populations and to support future investigations of genotype–environment interactions.

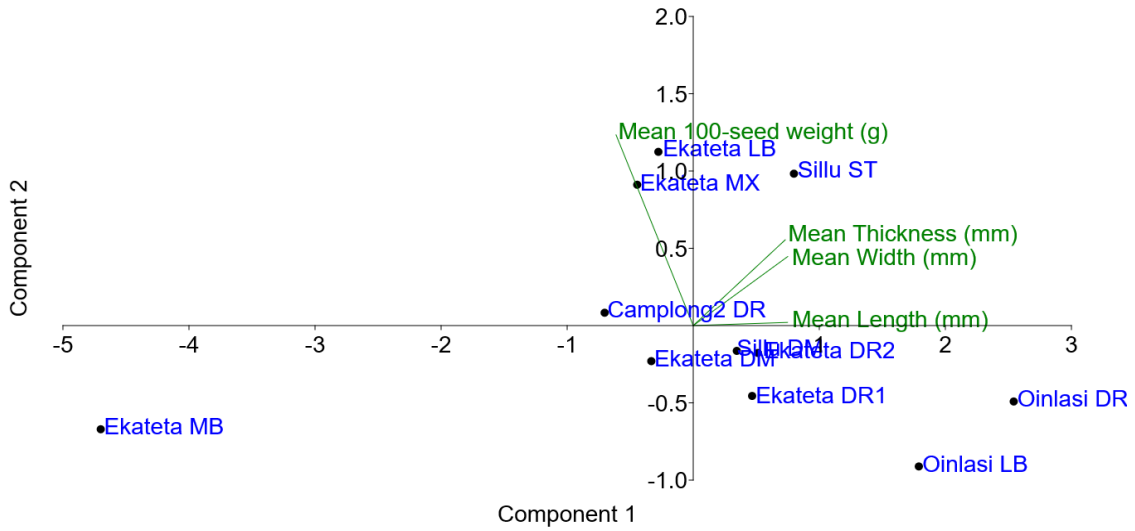

Figure 6. Principal component analysis (PCA) biplot of rice bean seed morphometric traits based on mean values of eleven phenotypes collected from four localities on Timor Island, Indonesia

Notes: The plot shows phenotypic distribution along the first two principal components (PC1 = 84.68% and PC2 = 12.27% of total variance), with arrows indicating trait loadings.

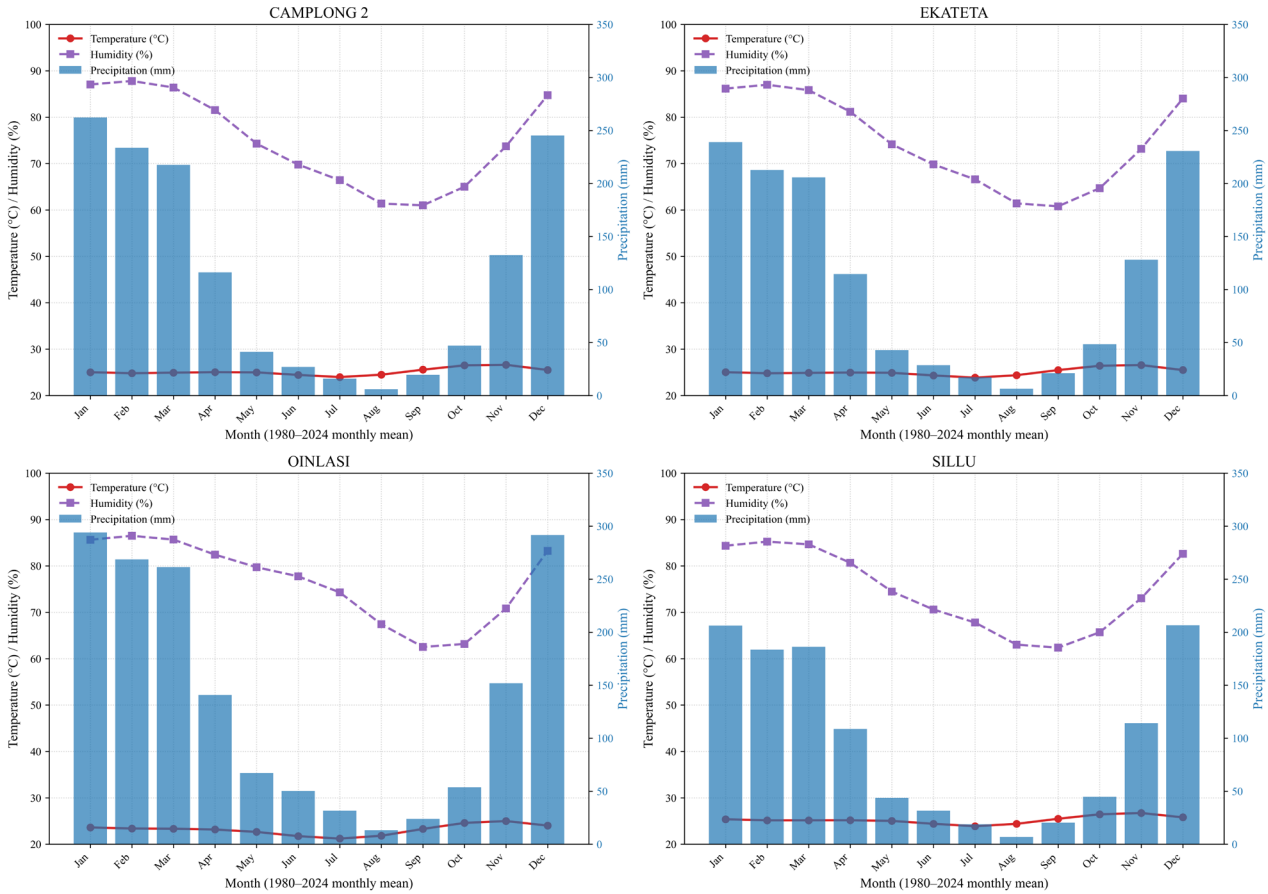

Figure 7. Monthly climatology of temperature, relative humidity, and precipitation for Camplong 2, Ekateta, Oinlasi, and Sillu, Timor Island, Indonesia, based on climate data from 1980–2024

Notes: Values are 1980–2024 monthly means (climatology). Temperature and relative humidity are shown as line graphs, while precipitation is presented as bars.

4. DISCUSSION

The absence of statistically significant differences among populations for all measured seed traits represents the central finding of this study and forms the basis for interpretation. Rather than indicating uniformity, this result reflects a pattern in which morphometric variation is widely distributed and substantially overlapping among populations. The lack of statistical separation suggests that the magnitude of within-population variability exceeds that of between-population differentiation. Comparable patterns have been reported in *Vigna* species and other grain legumes, where morphometric

traits are often continuously distributed across farmer-managed populations [9, 10, 23, 26].

This outcome shifts the analytical perspective away from explaining inter-population differences and toward understanding the structure of variation itself. In systems characterized by high internal variability, statistical comparisons among locations may fail to detect differences even when numerical contrasts are present, particularly when within-population variance exceeds between-population differentiation. Such conditions arise when trait distributions overlap extensively, resulting in continuous rather than discrete phenotypic structuring. In this context, the absence of statistical significance does not indicate a lack of variation, but rather reflects that variation is not partitioned along clear geographic boundaries [30, 31].

The observed pattern is consistent with the dynamics of traditional seed systems in dryland agriculture. In these systems, seeds are typically maintained as heterogeneous mixtures rather than as genetically uniform units. Recurrent processes of seed saving, exchange, and replanting contribute to the maintenance of broad phenotypic ranges within populations. These practices facilitate gene flow and reduce the likelihood of divergence into distinct groups. Conceptual frameworks in agrobiodiversity emphasize that such systems promote population-level variability and adaptive flexibility rather than fixed varietal identity [32, 33].

As a consequence, phenotypic diversity in these populations is more appropriately described as a continuum than as a set of discrete classes. Traits such as seed length, width, and thickness vary gradually across individuals and populations, without forming clear thresholds that separate groups. This continuous organization complicates attempts to categorize populations based on morphometric criteria alone and highlights the limitations of locality-based comparisons when underlying variation is shared across sites. Seed coat color variation, although not subjected to statistical analysis in this study, provides an additional qualitative dimension of diversity within rice bean populations. In grain legumes, seed coat color has been widely associated with underlying genetic variation and population structure, as demonstrated by recent genomic studies linking color polymorphism to genetic differentiation processes [34]. Moreover, variation in seed coat color may also have functional implications, as it has been reported to influence seed quality attributes, including physiological performance and storage-related properties [35]. The coexistence of multiple color types within the same localities observed in this study is therefore consistent with the broader pattern of continuous phenotypic variation maintained in farmer-managed systems, where both quantitative and qualitative traits are preserved as part of dynamic and heterogeneous seed populations.

The observed continuous and overlapping morphometric variation may reflect multiple interacting ecological and management processes operating within farmer-managed populations rather than discrete differentiation among localities. In such systems, intermediate trait values may contribute to the maintenance of phenotypic diversity under variable environmental conditions. Previous studies have shown that legume seed development is highly sensitive to environmental constraints during the reproductive phase, particularly under water-limited conditions, which can influence assimilate partitioning and seed trait expression [14, 17, 18]. Furthermore, the persistence of wide phenotypic ranges within populations suggests that selection pressures are not directional but fluctuate temporally and spatially, thereby maintaining diversity rather than driving uniformity. This dynamic is characteristic of traditional agroecosystems in which environmental unpredictability and farmer-mediated selection interact to preserve multiple adaptive strategies within the same population. Consequently, the lack of distinct morphometric clustering among populations may be consistent with the maintenance of diversity under variable environmental conditions, although the adaptive significance of this pattern remains to be verified.

The multivariate analysis provides additional insight into the structure of this variation. The strong negative association between seed size (length, width, and thickness) and 100-seed weight indicates that these traits do not vary proportionally. Instead, seed mass appears to be partially independent of linear dimensions, suggesting that differences in internal composition contribute to observed variation. Similar decoupling between size and weight has been documented in grain legumes and is often linked to variation in assimilate allocation during seed filling [14, 15, 25].

This relationship can be interpreted as a trade-off in resource allocation during reproductive development. Assimilates may be preferentially invested either in increasing seed volume through cell expansion or in enhancing storage density via the accumulation of reserves such as starch, proteins, and lipids. These alternative allocation pathways result in contrasting combinations of traits, where larger seeds are not necessarily heavier, and smaller seeds may exhibit relatively high mass. The observed pattern indicates that seed traits are governed by multiple interacting physiological and developmental processes rather than by a single scaling relationship [14, 15, 36].

From an ecophysiological perspective, this trade-off may reflect contrasting strategies of assimilate partitioning during seed filling. Greater investment in structural expansion can increase seed dimensions without a proportional increase in mass, whereas greater allocation to reserve accumulation may result in denser seeds despite relatively moderate size. Such variation may influence seed performance under contrasting environmental conditions, although direct evaluation of seed composition, reserve content, and germination performance would be required to verify these functional implications.

The coexistence of these contrasting morphometric configurations within the same populations suggests that no single trait combination is consistently favored. Instead, variability in size–mass relationships may reflect multiple viable outcomes of seed development under varying environmental conditions. This interpretation aligns with the view that phenotypic diversity in traditional cropping systems is maintained through flexible responses rather than fixed optimization [32, 33]. Such diversity may enhance population-level resilience by allowing different trait combinations to perform under fluctuating environmental constraints. However, direct physiological measurements would be required to confirm the specific mechanisms underlying this pattern.

Within the Ekateta population, the MB phenotype exhibited a distinctive combination of morphometric traits characterized by relatively shorter and narrower seeds together with comparatively high 100-seed weight. Although this phenotype occupied a unique position in the PCA ordination, its measurements remained within the overall range observed across the study populations. This result illustrates that alternative combinations of seed dimensions and seed mass

can coexist within the same locality, contributing to the continuous pattern of variation observed among rice bean landraces.

The occurrence of such phenotypes highlights the complexity of morphometric variation in farmer-managed populations. Rather than forming discrete categories, seed traits appear to be expressed through multiple combinations of dimensions and weight that overlap across populations. This finding reinforces the interpretation that variation is structured primarily within populations and supports the broader pattern of continuous phenotypic diversity revealed by both univariate and multivariate analyses.

An additional consideration in interpreting the results is the distinction between phenotypic expression and underlying genetic structure. The present analysis is based on morphological traits, which reflect the combined effects of genetic factors, environmental conditions, and their interaction. Without molecular or genomic data, it is not possible to determine the extent to which observed variation corresponds to genetic differentiation. In legumes, seed traits are known to exhibit both genetic control and environmental responsiveness, particularly during reproductive development [17, 18].

Consequently, the continuous variation documented in this study may represent a composite of genetic diversity and phenotypic plasticity. This limitation does not diminish the relevance of the findings, but it does constrain interpretation regarding the origin of variation. Integrating morphometric analysis with molecular characterization and environmental data would provide a more comprehensive understanding of the processes shaping trait variation in rice bean populations.

Descriptive trends in the data suggest that certain localities tend to be associated with larger or smaller seed dimensions. However, these patterns were not supported by statistical tests and therefore should not be interpreted as evidence of environmental determination. Although previous studies have shown that temperature and moisture conditions can influence seed development in legumes [37, 38], the present study does not provide direct evidence linking specific environmental variables to morphometric traits. Any apparent associations should therefore be regarded as tentative and subject to further investigation.

Farmer management remains a central factor in shaping the observed variation. In dryland agroecosystems, maintaining heterogeneous seed stocks is a common strategy to buffer against environmental uncertainty. This practice supports the persistence of diverse phenotypes within populations and contributes to the continuous structure of variation observed in this study. Such systems are recognized as important reservoirs of agrobiodiversity, where diversity is maintained through ongoing selection and adaptation processes [6, 32, 33]. The morphometric patterns documented here are therefore consistent with a model of dynamic, farmer-mediated diversity rather than discrete population differentiation.

Comparative evidence from other regions further supports the interpretation of rice bean as a highly variable and adaptable legume maintained within farmer-managed systems. Studies in Northeast India have similarly documented substantial phenotypic diversity in rice bean populations, highlighting the role of traditional cultivation practices in maintaining variation across heterogeneous environments [39]. In dryland agricultural contexts such as Timor Island, the persistence of such diversity is particularly relevant for sustaining crop performance under increasing climatic variability. Adaptive management strategies, including improved water management and resource-use efficiency, have been identified as critical for enhancing productivity and resilience in semi-arid systems [4]. Within this broader context, the continuous phenotypic variation observed in this study may represent an important foundation for future efforts aimed at optimizing rice bean cultivation under dryland conditions.

5. CONCLUSION

This study demonstrates that seed morphometric variation in rice bean populations from Timor Island is structured as continuous phenotypic variation rather than discrete differentiation among localities. Both univariate and multivariate analyses consistently showed no statistically significant differences among populations, despite observable numerical variation across traits.

PCA revealed a dominant axis of variation reflecting a trade-off between seed dimensions (length, width, and thickness) and 100-seed weight, indicating that seed size and seed mass are not proportionally related. This pattern suggests variability in seed size–density relationships maintained within farmer-managed populations.

However, several limitations should be acknowledged. The sample size was relatively limited and uneven across localities, which may affect the representation of population-level variability. In addition, no genetic or molecular analyses were conducted; therefore, the relative contributions of genetic factors, environmental influences, and genotype-by-environment interactions cannot be determined. Furthermore, the observed associations between seed traits and environmental conditions are based on descriptive patterns only, as no statistical analyses were performed to test these relationships.

Within these constraints, the findings highlight the presence of substantial within-population variation maintained in traditional rice bean systems. This study provides a valuable morphometric baseline for future research integrating phenotypic, genetic, and environmental data to disentangle the drivers of variation and support evidence-based conservation and utilization of rice bean as a resilient genetic resource for dryland agriculture.

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AUTHOR CONTRIBUTIONS

Conceptualization: AVS and IWM; Methodology: AVS, MVH, PSN, and EYH; Field investigation and data collection: AEN, YRK, MJK, JAL, RP, and WB; Formal analysis and Visualization: AVS and NRK; Writing original draft preparation: AVS; Review and editing: AVS, IWM, NRK, and EYH; Funding acquisition: AVS. All authors have read and agreed to the published version of the manuscript.

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