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Assessing phenotypic variation in a diverse collection of Rice bean [*Vigna umbellata* (Thunb.)]

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Abstract

This study explores the phenotypic diversity within a collection of rice bean (*Vigna umbellata*), a lesser-known legume with potential for enhancing food security in underdeveloped regions. Phenotypic traits such as seed color, plant height, pod length, and resistance to local pests and diseases were systematically analyzed across fifty different genotypes collected from various geographical regions. The objective was to identify distinctive traits and potential candidates for breeding programs aimed at improving crop resilience and nutritional content.

Keywords: Rice bean (*Vigna umbellata*), rice bean cultivation, high protein content, food security

Introduction

Rice bean (*Vigna umbellata*) is a warm-season legume cultivated primarily in East and Southeast Asia. It is valued for its adaptability to poor soil conditions and its high protein content, making it a crucial crop for marginal environments. Despite its benefits, the rice bean remains underutilized and under-researched compared to other legumes. Phenotypic variation among rice bean genotypes has not been extensively documented, which limits the development of improved varieties suited for diverse environmental conditions and agricultural needs.

Understanding the extent of phenotypic diversity within a species is essential for effective plant breeding. This study aims to document and analyze the phenotypic traits of a broad collection of rice bean genotypes, thereby providing a foundational resource for breeding programs focused on enhancing yield, nutritional quality, and environmental resilience.

Objective

The objective of this study is to document and analyze the phenotypic diversity within a collection of rice bean [*Vigna umbellata* (Thunb.)] genotypes to identify traits for targeted improvement through breeding programs.

Materials and Methods

Fifty genotypes of rice bean were collected from various regions known for rice bean cultivation. The study was conducted at the Experimental Farm of the Tropical Crop Research Institute over two growing seasons. Standard agronomic practices were maintained for all genotypes throughout the study period.

Phenotypic data were collected on several traits, including seed color, plant height, pod length, and flowering time. Additionally, genotypes were evaluated for resistance to two major local pests and the common diseases affecting the crop in the region. Statistical analyses, including ANOVA and principal component analysis (PCA), were used to assess the variations and correlations between different phenotypic traits.

Results

Table 1: General Phenotypic Traits of Rice Bean Genotypes

Genotype ID	Plant Height (cm)	Pod Length (cm)	Seed Color	Flowering Time (days)
RB01	45	8	White	55
RB02	60	10	Yellow	50
RB03	30	5	Green	60
RB04	100	12	Brown	45
RB05	85	11	Yellow	48

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Table 2: Resistance to Pests and Diseases in Rice Bean Genotypes

Genotype ID	Pest Resistance (Score)	Disease Resistance (Score)
RB01	High	Moderate
RB02	Moderate	High
RB03	Low	Low
RB04	High	High
RB05	Moderate	Moderate

Discussion and Analysis

The results presented in Tables 1 and 2 highlight significant phenotypic diversity across the rice bean genotypes, illustrating a broad spectrum of traits that could be harnessed for plant breeding and agricultural improvement. The variation in plant height and pod length among the genotypes (from 30 cm to 100 cm and 5 cm to 12 cm, respectively) is indicative of substantial genetic diversity. This diversity is crucial as plant height can influence mechanization suitability and resistance to lodging, while pod length is directly correlated with yield potential. Genotypes with longer pods, such as RB04 and RB05, are promising candidates for enhancing yield efficiency. Conversely, shorter plants, like RB03, may be more suitable for regions with high wind exposure or where plant growth compact is preferred to maximize space efficiency. The variation in seed color, ranging from white to brown, might have implications for market preference and nutritional value, suggesting niche marketing opportunities or breeding for enhanced health benefits. Flowering time, which ranged from 45 to 60 days among the genotypes, is a critical factor for matching crop production cycles to specific climates and for avoiding environmental stresses. Shorter flowering times, as seen in RB04, may be advantageous in regions with shorter growing seasons, enabling farmers to avoid late-season frosts or rainfall that can damage the crop. The scores for pest and disease resistance show a disparity that could be key to developing resilient rice bean varieties. Genotypes such as RB01 and RB04, which exhibit high resistance to pests and diseases, represent excellent breeding stock for developing robust cultivars that require fewer chemical inputs. Such traits are increasingly valuable in sustainable agriculture, where reducing dependency on pesticides is a priority. The observed phenotypic diversity suggests that there is significant untapped potential within the rice bean gene pool. By strategically selecting genotypes with desirable traits, breeders can develop varieties that are tailored to specific climatic conditions, pest challenges, and market demands. Furthermore, the linkage of phenotypic traits with genotypic data could accelerate the breeding process, making it more efficient to select for multiple traits simultaneously. Moreover, the genetic variability observed in this collection can serve as a genetic repository for future breeding programs aimed at improving not only yield and resistance characteristics but also at enhancing nutritional profiles and adaptability to marginal soils. The challenge lies in effectively integrating these diverse traits into commercially viable varieties without compromising the genetic integrity of the native traits that confer natural resilience and adaptability. Overall, the deep phenotypic analysis provided by this study forms a foundational step towards targeted genetic enhancement. Continued research focusing on the genetic basis of these phenotypic traits will be crucial for fully exploiting the potential of rice bean in sustainable agriculture. Future studies should aim to integrate more advanced molecular techniques to map the

phenotypic traits to specific genes or gene clusters, enabling more precise breeding interventions

Conclusion

The study's exploration of phenotypic variation within a collection of rice bean genotypes has elucidated a significant range of traits that hold potential for targeted breeding programs aimed at improving yield, resistance to pests and diseases, and adaptability to diverse agricultural environments. The identified variability in plant height, pod length, seed color, flowering time, and resistance traits underscores the genetic diversity present in rice bean, highlighting its potential as a crop that can be optimized for specific climatic and soil conditions, as well as market preferences. By capitalizing on this genetic diversity, plant breeders can develop rice bean varieties that are not only high-yielding and robust against biotic and abiotic stresses but also tailored to meet the nutritional and economic needs of diverse populations. This study sets the groundwork for future research, suggesting that integrating phenotypic data with genetic analyses could greatly enhance the efficiency and effectiveness of breeding programs. Ultimately, the goal is to unlock the full potential of rice bean to contribute to sustainable agriculture and food security, particularly in regions where agricultural resources are limited and farming conditions are challenging

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