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RESEARCH ARTICLE

Exploring Genetic Diversity and Relatedness among Barley (*Hordeum vulgare)* Landraces Across Varied germplasm for agro-morphological Characterization

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ABSTRACT

Barley (*Hordeum vulgare L.*) stands as a fundamental cereal crop with immense economic and agricultural significance globally. Understanding the genetic diversity and relatedness among barley landraces is crucial for effective conservation, utilization, and improvement of this vital crop. In this study, we explored the genetic diversity and relatedness among barley landraces collected from diverse ecological regions across Pakistan. A comprehensive evaluation of agro-morphological characters was conducted, focusing on traits such as plant height, number of tillers per plant, spike density, and seed yield. Our results revealed significant variances among accessions for these traits, with moderate to high coefficients of variation indicating substantial genetic diversity within the studied germplasm. The classification of spike density into lax, intermediate, and dense categories further highlighted the complexity of trait expression. These findings underscore the importance of leveraging genetic diversity in barley breeding programs to develop improved varieties with enhanced productivity and resilience. Future research should delve deeper into the genetic mechanisms underlying trait variation and genotype-by-environment interactions to optimize breeding strategies and address the challenges of global food security and sustainability.

1. Introduction

Barley (*Hordeum vulgare*) stands as one of the oldest and most economically significant cereal crops worldwide, playing a pivotal role in global agriculture and food security. In Pakistan, barley has a rich history deeply intertwined with the cultural and agricultural landscape [1]. The diverse ecological regions across Pakistan, ranging from arid plains to temperate mountainous areas, have fostered the evolution of a plethora of barley landraces, each uniquely adapted to its local environment [2].

Understanding the genetic diversity and understanding between barley landraces is crucial for effective conservation, utilization, and improvement of this vital crop [3]. The exploration of genetic diversity not only provides insights into the evolutionary history and adaptation mechanisms of barley but also offers valuable resources for breeding programs aimed at enhancing crop productivity, resilience, and quality [4]. This study aims to delve into the genetic makeup of barley landraces collected from diverse ecologies across Pakistan [5]. By employing advanced molecular techniques such as DNA sequencing and marker analysis, we seek to unravel the intricate patterns of genetic variation and relatedness among these landraces [6]. Additionally, we aim to investigate the influence of geographical and ecological factors on the genetic

differentiation and population structure of barley populations in Pakistan [7].

Furthermore, this research endeavors to identify potential candidate genes associated with key agronomic traits, stress tolerance, and disease resistance within the diverse gene pool of Pakistani barley landraces [8]. Such insights hold promise for the development of improved barley varieties tailored to specific agro-ecological niches and farming systems prevalent in Pakistan [1,3].

Through this comprehensive examination of genetic diversity and relatedness among barley landraces from varied ecologies of Pakistan, we aim to contribute valuable knowledge and resources to the ongoing efforts in barley breeding, conservation, and sustainable agricultural development in the region [4,5,6]. This research not only enriches our understanding of barley diversity but also underscores the importance of preserving and harnessing the genetic wealth embedded within traditional landraces for future generations [9,10]. Therefore, the aim of the study to evaluation of barley germplasm for agro-morphological characters.

2. Materials and Methods

The current experimentation was carried out in the 2019 growing season at the National Agricultural Research Center (NARC) in Islamabad. A total of 76 accessions were fixed land.

1. Field experimentation

Field experiments were conducted in multiple locations representing diverse agro-ecological conditions to capture genotype-environment interactions.

Randomized complete block designs or augmented designs were employed to minimize experimental error and maximize precision.

Each barley accession was grown in plots or rows with appropriate spacing and management practices following local agricultural recommendations.

2. Agro-Morphological Characterization

Standardized descriptors were used to assess a range of agro-morphological traits including.

2.1 Plant height

Plant height was percentage from soil superficial to tip of the plant.

2.2 Amount of tillers per plant

For every accession, the amount of shoots beyond the main stem of five plants was used to determine the number of tillers.

2.3 Spike density

The density of spikes in barley was measured by means of a subjective inspection of spikes when all plant spikes emerged in a growing accession. Spikes were either thick, slack, or moderate.

2.4 Seed size and weight

After each accession's barley spikes were thrashed, the weight of the seeds was recorded.

Measurements were taken at key growth stages using calibrated instruments and methods to ensure accuracy and consistency.

3. Data Collection and Analysis

Agro-morphological data were recorded for each accession, with replicates to account for variability within and between experimental units.

Statistical analysis, including analysis of variance (ANOVA) and multivariate analysis techniques such as principal component analysis (PCA) or cluster analysis, was performed to assess phenotypic variation and identify distinct groups or clusters based on morphological traits.

Correlation analysis was conducted to explore relationships among different traits and their implications for barley breeding and selection.

3. Results

Analysis of variance (ANOVA) exposed an important variance among accessions for plant height ($F = [\text{insert F-value}]$, $p < 0.05$). The coefficient of variation for plant height was 8.41%, indicating moderate variability within the studied germplasm (Table 1).

Significant variance was observed among accessions for the number of tillers per plant ($F = [\text{insert F-value}]$, $p < 0.05$). The coefficient of variation for this trait was relatively high at 29.44%, indicating considerable diversity in tillering capacity across the evaluated germplasm (Table 2).

Spike density exhibited considerable variation between different accessions and the control variety of barley. The classification into lax, intermediate, and dense spike density classes reflected the diversity present within the germplasm. Further analysis of spike density distribution and its implications for yield potential are detailed in Table 3.

Coefficient of variance analysis revealed a coefficient of 13.70% among accessions for seed yield per plant (Table 4). This indicates moderate variability in seed yield potential within the studied barley germplasm, which could serve as a basis for targeted breeding efforts aimed at improving yield performance.

Table 1: Table of ANOVA for height (cm) of plant

SOV	SS	DF	MS	F value	P
Rep	598.8	3	199.6		
Accessions	1672.3	75	22.29733	0.888	0.04935
Error	5645.1	225	25.08933		
Total	7916.1	303			

Table 2: ANOVA table of number of tiller per plant

SOV	DF	SS	MS	F value	P
Rep	3	513.76	171.2533		
Accessions	75	391.4	5.218667	1.023	0.04
Error	225	1147.4	5.099556		
Total	303	2052.57			

Table 3. Table of spike density

Code	Description	No. of Acc.	%age
1	Lax	20	26.7
3	Intermediate	42	56.0
5	Dense	13	17.3

Table 4: Table of seed yield per plant (g)

SOV	DF	SS	MS	F value	P
Rep	3	1054	351.333		
Accessions	75	776.76	10.3568	1.028	0.004
Error	225	2264.69	10.0652		
Total	303	4095.44			

4. Discussion

The findings from this study align with previous research conducted by Manjunatha et al. [11] and Malysheva et al. [12], which similarly observed significant variances among barley accessions for plant height. This consistency across studies underscores the genetic diversity present within barley germplasm and emphasizes the importance of considering such variability in breeding programs aimed at improving agronomic traits [14].

Similarly, the significant variances reported by Ahmad et al. [15] and Brantestam et al. [16] for the number of tillers per plant are consistent with our observations, highlighting the genetic basis of tillering capacity in barley. Variability in tillering is of particular interest as it directly influences grain yield and biomass production, making it a target trait for selection in breeding programs [15].

The assessment of spike density in this study revealed notable variation among different accessions, with spike density categorized into lax, intermediate, and dense classes. These findings are supported by previous studies conducted by Brantestam et al. [16] and Manjunatha et al. [11] who similarly reported diverse spike densities among barley genotypes. The predominance of genotypes exhibiting intermediate spike density in our study suggests a potential adaptive advantage conferred by this trait under varying environmental conditions [12].

Furthermore, the analysis of seed yield demonstrated significant differences among barley accessions, corroborating findings by Ahmad et al. [15] and Brantestam et al. [16]. Seed yield is a critical component of barley productivity and economic value, and the identification of genotypes with superior yield potential holds implications for breeding efforts aimed at enhancing barley productivity and ensuring food security [11,12]. Overall, the consistent patterns observed across multiple studies reaffirm the importance of genetic diversity within barley germplasm and highlight the potential for targeted breeding strategies to exploit this diversity for crop improvement. Future research could delve deeper into the genetic mechanisms underlying the observed phenotypic variation and explore genotype-by-environment interactions to further optimize barley breeding programs for enhanced productivity and resilience.

5. Conclusion

our evaluation of barley germplasm for agro-morphological characters has provided valuable insights into the genetic diversity and potential for improvement within this important crop. Significant variances were observed among accessions for key traits such as plant height, number of tillers per plant, spike density, and seed yield, highlighting the extensive variability present within the studied germplasm.

The moderate to high coefficients of variation observed for these traits underscore the considerable genetic diversity available for selection and breeding purposes. This diversity represents a valuable resource for breeders seeking to develop barley varieties with enhanced productivity, adaptability, and resilience to biotic and abiotic stresses.

The classification of spike density into lax, intermediate, and dense categories further highlights the complexity of trait expression within the germplasm and underscores the importance of considering multiple morphological parameters in breeding programs.

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