Use of Mas Technology Method in Creating High-Yield Varieties of Soft Wheat

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Abstract

This study focuses on the application of marker-assisted selection (MAS) technology to develop high-yielding, protein-rich wheat varieties with enhanced resistance to abiotic stresses, including drought, low temperature, and salinity. The use of molecular markers enables precise identification and selection of desirable genotypes carrying stress-resistance traits, thereby increasing the efficiency of breeding programs.

The results revealed a significant aggregation of resistance-associated marker alleles in the studied lines. In particular, lines L257 and L258 were found to possess all three target marker alleles, while lines L015, L018, L025, L026, L233, and L236 carried two marker alleles each. Such genetic accumulation of favorable alleles contributes to improved adaptability and stability of wheat under adverse environmental conditions.

The introduction of newly developed varieties into agricultural practice has the potential to substantially increase crop productivity and enhance the economic efficiency of farming systems. Furthermore, these findings provide valuable insights for sustainable wheat breeding strategies in the context of ongoing climate change and increasing environmental stresses.

Keywords: Drought, cold, salinity, variety, productivity, abiotic.

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1. Introduction

In recent decades, the combined effects of global climate change and the desiccation of the Aral Sea have led to severe environmental degradation in Uzbekistan, particularly in the Republic of Karakalpakstan. The increasing frequency and intensity of abiotic stresses such as drought, heat stress, and soil salinization have significantly reduced agricultural productivity and threaten the sustainability of crop production systems. These challenges are especially critical for wheat (Triticum aestivum L.), which is one of the most important staple crops and a key component of food security in the region [1].

Wheat production in arid and semi-arid environments is highly sensitive to environmental fluctuations, and yield stability is often compromised under stress conditions. Therefore, the development of high-yielding, protein-rich, and stress-tolerant wheat varieties has become a strategic priority for ensuring stable agricultural output. In this context, improving the adaptive capacity of wheat to multiple abiotic stresses simultaneously represents a major challenge for modern breeding programs [2].

Conventional breeding methods, based primarily on phenotypic selection, have contributed significantly to crop improvement; however, they are often limited by long breeding cycles, environmental variability, and the complex inheritance of quantitative traits such as drought and salinity tolerance. These limitations necessitate the adoption of innovative and more precise approaches in plant breeding. One of the most promising strategies is marker-assisted selection (MAS), which integrates molecular genetics with conventional breeding techniques [3,4].

MAS technology is based on the identification and utilization of molecular markers closely linked to genes or quantitative trait loci (QTLs) controlling economically important traits. This approach enables early and accurate selection of desirable genotypes at the DNA level, independent of environmental influences. As a result, MAS significantly accelerates the breeding process, increases selection efficiency, and reduces the cost and time required for developing new varieties[5].

The successful identification and mapping of QTLs depend on the use of appropriate genetic populations and marker systems. Various types of mapping populations, including F_2 populations, doubled haploids (DH), recombinant inbred lines (RILs), and near-isogenic lines (NILs), are widely used in genetic studies. Each population type has specific advantages and limitations in terms of genetic resolution, homozygosity, and mapping accuracy. In addition, factors such as population size, marker density, and the choice of molecular marker systems (e.g., SSR, SNP) play a crucial role in determining the precision and reliability of QTL detection [6,7].

Recent advances in molecular breeding have demonstrated that the pyramiding of multiple favorable alleles associated with stress tolerance can significantly enhance plant resilience under adverse environmental conditions. In regions affected by soil salinity and water scarcity, such as Karakalpakstan, the integration of MAS with traditional breeding methods provides an effective pathway for developing wheat varieties with improved stress tolerance, yield stability, and grain quality [8].

Therefore, the development of winter wheat varieties adapted to the harsh agro-climatic conditions of Karakalpakstan—characterized by resistance to drought, salinity, and low temperatures—represents an urgent and important scientific and practical objective. The application of MAS-based breeding strategies not only facilitates the rapid development of improved genotypes but also contributes to sustainable agricultural production and long-term food security under changing climatic conditions.

2.Methodology

Genomic DNA was extracted from the studied wheat samples using the commercial kit DNA-Extran-3 (Cat. EX-513, Synthol, Russia), following the manufacturer's protocol with minor modifications to optimize DNA yield and purity. The quality and concentration of the isolated DNA were assessed using standard spectrophotometric and electrophoretic methods to ensure suitability for downstream molecular analysis [9].

Polymerase chain reaction (PCR) analysis was performed for genotyping the selected wheat lines using specific DNA markers associated with target traits. Amplification reactions were carried out using PCR ScreenMix (Cat. PK041L, Eurogen, Russia), which contains all necessary components for efficient DNA amplification, including Taq DNA polymerase, dNTPs, $MgCl_2$, and reaction buffer. PCR conditions were optimized for each primer pair to ensure specificity and reproducibility of amplification [10,11].

The amplified PCR products were separated by agarose gel electrophoresis to determine the presence and size of target amplicons. A 3.0% agarose gel was prepared using Agaroza D1 (Cat. 8024, Conda, Spain), allowing high-resolution separation of DNA fragments. Electrophoresis was carried out under standard conditions, and the gels were visualized under ultraviolet light after appropriate staining.

The molecular size of PCR products was estimated using the DNA ladder AmpliSize Molecular Ruler 50 bp (Cat. 1708200, Bio-Rad Laboratories, USA), which enabled accurate determination of fragment lengths. Based on the presence or absence of specific bands corresponding to marker alleles, genotyping of wheat samples was performed.

The obtained genotypic data were recorded and processed using Microsoft Excel 2021, where allele scoring and data organization were carried out. The results were further analyzed to identify the distribution and aggregation of marker alleles associated with stress resistance traits among the studied wheat lines.

3.Results

The application of molecular marker-based screening enabled the identification of wheat genotypes with enhanced resistance to major abiotic stresses. Based on the analysis of 257 wheat lines, a set of informative DNA markers associated with tolerance to high temperature, drought, and salinity was successfully utilized to evaluate the genetic potential of the studied material.

The screening results revealed substantial variation among the genotypes in terms of stress tolerance. A group of wheat lines demonstrated significant resistance to heat stress, including L015, L018, L010, L013, L021, L022, L023, L025, L026, L233, L236, L257, and L258. Similarly, drought tolerance was observed in a broader set of genotypes, namely L009, L015, L016, L018, L019, L025, L026, L028, L029, L233, L236, L237, L238, L257, L258, and L259. Salinity tolerance, which is particularly critical under the agro-ecological conditions of arid regions, was identified in a more limited number of lines, including L232, L234, L236, L257, and L258. Notably, several genotypes exhibited overlapping resistance to multiple stress factors, indicating their potential as sources of complex adaptability.

PCR-based genotyping confirmed the presence of specific molecular markers linked to abiotic stress tolerance. The marker Xcfa2147 was associated with heat resistance, Xgwm337 with drought tolerance, and Xwmc406 with salinity tolerance. The detection of these markers in the studied lines validates their effectiveness for marker-assisted selection and supports their use in breeding programs targeting stress resilience.

A key outcome of the study was the identification of genotypes with pyramided resistance alleles. In particular, lines L257 and L258 were found to carry all three target marker alleles simultaneously, indicating a high level of combined resistance to heat, drought, and salinity. In contrast, lines L015, L018, L025, L026, L233, and L236 possessed two resistance-associated alleles, suggesting partial but still significant adaptability to multiple stress conditions. The aggregation of favorable alleles in these genotypes highlights the effectiveness of marker-assisted selection in combining multiple traits within a single genetic background.

Importantly, the identified stress-resistant lines also demonstrated high grain and flour quality characteristics, indicating that the incorporation of resistance traits did not negatively affect key agronomic and technological parameters. This balance between stress tolerance and product quality significantly enhances the breeding value of these lines and supports their potential use in both commercial cultivation and advanced breeding programs.

Overall, the results confirm that the integration of molecular markers into wheat breeding programs is an efficient approach for identifying and developing genotypes with комплекс resistance to multiple abiotic stresses, thereby contributing to stable yield performance under adverse environmental conditions.

4.Conclusion

The application of marker-assisted selection (MAS) technology in this study has demonstrated its high efficiency in developing wheat varieties that possess a combination of essential agronomic traits, including high yield potential, elevated protein content, and resilience to major abiotic stresses such as drought, salinity, and low temperature. By utilizing specific molecular markers linked to stress-resistance genes, the study successfully identified wheat lines with pyramided alleles, notably L257 and L258, which simultaneously carry multiple resistance traits. This genetic aggregation not only ensures adaptability under adverse environmental conditions but also maintains superior grain and flour quality, thereby preserving both productivity and end-use value.

These results highlight MAS as a reliable and precise tool for accelerating wheat breeding programs, reducing the time and resources typically required by conventional phenotypic selection methods. Moreover, the development of stress-resilient and high-quality wheat lines has significant implications for improving food security, particularly in arid and semi-arid regions such as Karakalpakstan and other areas affected by climate change, soil salinization, and water scarcity. In conclusion, the integration of molecular marker technologies into breeding strategies provides a sustainable approach to producing wheat varieties that can withstand environmental challenges while meeting the nutritional and economic needs of farmers and consumers alike.

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