# Exploring genomic selection for accelerated breeding of disease-resistant wheat varieties

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## Introduction

Wheat is one of the most important staple crops worldwide, providing essential nutrients to billions of people. However, wheat production is continually threatened by various biotic stresses, particularly diseases such as wheat rust, Fusarium head blight, and powdery mildew, which can significantly reduce yield and quality. These diseases are often unpredictable and can spread rapidly, causing substantial economic losses. Traditional breeding methods have been the cornerstone of developing disease-resistant wheat varieties, yet the process remains slow and resource-intensive, requiring several generations of crossbreeding and selection [1-3].

Recent advancements in molecular biology and genomics offer new avenues to accelerate wheat breeding and enhance disease resistance more effectively. Genomic selection (GS), which involves the use of genetic markers spread across the entire genome, is a promising tool that can speed up the identification and incorporation of resistance traits in breeding programs. Unlike traditional marker-assisted selection, GS takes into account the overall genetic makeup of a plant to predict its performance for complex traits such as disease resistance, even before phenotypic expression is observed. This approach has the potential to substantially reduce the number of breeding cycles required, making it possible to develop resistant wheat varieties in a shorter timeframe [4].

The application of genomic selection in wheat breeding is particularly important for addressing emerging diseases and adapting to changing environmental conditions, which can influence disease dynamics. Additionally, GS can be combined with other technologies, such as gene editing and high-throughput phenotyping, to further enhance breeding precision and efficiency. However, the successful implementation of genomic selection in disease resistance breeding requires a deep understanding of the genetic architecture of resistance traits and the establishment of large, diverse breeding populations with accurate phenotypic data.

In this study, we explore the potential of genomic selection to accelerate the breeding of disease-resistant wheat varieties. By leveraging genomic data, we aim to identify key genetic markers associated with disease resistance, and integrate this information into breeding strategies. This work seeks to demonstrate the effectiveness of GS in developing wheat varieties that are not only resistant to prevalent diseases but also resilient to future challenges in agriculture. Through this research, we aim to contribute to the improvement of wheat production systems, ensuring greater food security in the face of ongoing environmental and agricultural challenges [5].

#### Description

Exploring genomic selection for accelerated breeding of diseaseresistant wheat varieties aims to revolutionize wheat breeding by incorporating advanced genetic techniques to improve disease resistance more efficiently. Wheat is vulnerable to numerous diseases, which significantly impact global yields and food security. Traditional breeding methods, although effective, often require years or even decades to develop disease-resistant varieties. These conventional approaches are not only slow but also depend heavily on phenotypic expression, making them labor-intensive and subject to environmental variation. Therefore, there is a critical need to speed up the breeding process without compromising on quality or resistance to diseases [6,7].

Genomic selection (GS) offers a promising solution by using genomic data, such as DNA markers, to predict the genetic potential of plants. This allows breeders to select plants with desirable traits earlier in the breeding cycle, even before the traits manifest phenotypically. For disease resistance, GS helps to identify plants that carry specific genetic markers associated with resistance, thereby improving the accuracy of selection. By predicting these genetic traits in a broader, more diverse population of plants, GS reduces the time spent on field trials and accelerates the identification of resistant individuals.

The integration of genomic selection into wheat breeding programs also enables the development of disease-resistant varieties with enhanced genetic diversity. This approach not only speeds up the breeding timeline but also helps address multiple diseases at once, as GS can incorporate markers for various resistance genes simultaneously. Additionally, genomic selection provides an opportunity to adapt wheat breeding to evolving disease pressures, making it more responsive to emerging pathogens or changing climate conditions [8,9].

In this context, the use of genomic tools, including high-density genotyping platforms, molecular markers, and bioinformatics algorithms, is crucial for accurately mapping disease resistance traits. The effectiveness of GS depends on the availability of comprehensive genomic data, large breeding populations, and well-defined phenotypic data that reflect disease resistance under field conditions.

This research will explore the methods and benefits of implementing GS in wheat breeding for disease resistance. The study will evaluate the potential to accelerate the development of disease-resistant varieties, providing insights into how genomic selection can be effectively applied to improve wheat production. The results could significantly enhance breeding strategies, contributing to global efforts to improve food security and make agriculture more sustainable in the face of ongoing challenges like climate change and emerging pathogens [10].

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Received: 02-Dec-2024, Manuscript No: acst-25-159456, Editor Assigned: 06-Dec-2024, pre QC No: acst-25-159456 (PQ), Reviewed: 16-Dec-2024, QC No: acst-25-159456, Revised: 20-Dec-2024, Manuscript No: acst-25-159456 (R), Published: 30-Dec-2024, DOI: 10.4172/2329-8863.1000772

Citation: Cairns JE (2024) Exploring genomic selection for accelerated breeding of disease-resistant wheat varieties. Adv Crop Sci Tech 12: 772.

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### Discussion

The exploration of genomic selection (GS) for accelerating the breeding of disease-resistant wheat varieties holds immense promise, but its full potential requires overcoming several technical and practical challenges. One of the major benefits of genomic selection is its ability to significantly reduce the breeding cycle by predicting disease resistance traits early in the plant's development, before phenotypic resistance becomes evident. This early selection can lead to faster development of resistant varieties and more efficient use of resources, particularly in large-scale breeding programs.

However, the implementation of GS is not without challenges. One of the key limitations is the need for a comprehensive and high-quality genomic dataset. Accurate prediction models depend on the availability of large, diverse, and well-characterized populations with detailed genotypic and phenotypic data. Without a robust database, GS models may be less accurate, leading to suboptimal selection. Moreover, the complexity of disease resistance traits, which often involve multiple genes and gene-environment interactions, presents a challenge for genetic prediction. Unlike simpler traits controlled by single genes, disease resistance is polygenic and influenced by environmental factors, making it harder to predict consistently.

Another challenge is the cost and accessibility of advanced genomic technologies. While high-throughput sequencing and genotyping have become more affordable, the infrastructure and expertise required to implement these techniques can be a barrier for many breeding programs, especially in developing countries. Additionally, GS requires substantial computational resources and bioinformatics capabilities to analyze and interpret the large volumes of data generated.

Despite these challenges, the integration of GS with other breeding technologies, such as gene editing and high-throughput phenotyping, could further enhance the accuracy and speed of developing diseaseresistant wheat varieties. The combination of genomic selection with genome-wide association studies (GWAS) could help identify novel resistance genes, which can be used to develop more diverse and resilient wheat varieties. Furthermore, leveraging machine learning and artificial intelligence to optimize genomic prediction models could enhance the precision of GS, making it a more reliable tool for breeders.

One significant advantage of GS in wheat breeding is its potential to address multiple disease threats simultaneously. Instead of focusing on individual diseases, GS can incorporate markers for various disease resistance traits at once, improving the overall resilience of the crop. As pathogens evolve and new diseases emerge, the ability to rapidly adapt wheat varieties to these changes through genomic selection could help ensure a stable and sustainable wheat supply.

In conclusion, while there are hurdles to overcome, the application of genomic selection for accelerated breeding of disease-resistant wheat varieties offers a transformative approach to crop improvement. The ongoing development of genomic tools, better understanding of disease resistance genetics, and integration of advanced technologies will likely make GS a key strategy for improving wheat's resistance to diseases, ensuring food security, and making wheat production more sustainable in the face of climate change and increasing pathogen threats.

#### Conclusion

The exploration of genomic selection (GS) for accelerated breeding of disease-resistant wheat varieties represents a significant leap forward in modern agricultural practices. As global wheat production faces mounting pressure from a variety of diseases, the traditional breeding methods, although effective, are often too slow and resource-intensive to keep pace with the evolving challenges. Genomic selection offers the potential to overcome these limitations by allowing breeders to make more informed, accurate selections based on genetic data, thus speeding up the development of disease-resistant varieties.

One of the primary benefits of GS is its ability to predict disease resistance early in the breeding cycle, even before visible symptoms appear, which can substantially shorten breeding timelines. This approach is particularly valuable for diseases like wheat rust, Fusarium head blight, and powdery mildew, which can devastate crops in short periods. By incorporating genomic data, breeders can more efficiently select for multiple resistance traits simultaneously, which increases the resilience of wheat varieties to a range of diseases. Moreover, GS helps create more genetically diverse breeding populations, improving the long-term stability and sustainability of wheat varieties.

However, the effective application of genomic selection in wheat breeding requires overcoming some critical challenges. The complexity of disease resistance, which is controlled by multiple genes and influenced by environmental factors, makes accurate prediction difficult. Furthermore, the cost of high-throughput genotyping technologies and the need for large, well-characterized breeding populations remain significant barriers for some breeding programs. Nonetheless, the continued advancement in genomics, bioinformatics, and machine learning holds the potential to improve the accuracy and efficiency of GS, making it a more accessible and practical tool for breeders worldwide.

As research into genomic selection continues, its integration with other innovative techniques such as genome editing, high-throughput phenotyping, and multi-environment trials will likely enhance its effectiveness in developing disease-resistant wheat varieties. Ultimately, genomic selection has the potential to not only accelerate the breeding process but also to address the challenges posed by climate change, emerging pathogens, and shifting agricultural demands. By enabling the rapid development of wheat varieties with enhanced disease resistance, genomic selection could play a key role in ensuring global food security, boosting crop yields, and making wheat production more resilient in the face of an unpredictable agricultural landscape.

In conclusion, while there are hurdles to overcome, the application of genomic selection in wheat breeding represents a promising and transformative approach. By harnessing the power of genomics, we can pave the way for a new era of crop improvement, where diseaseresistant wheat varieties can be developed more quickly and with greater precision, ultimately benefiting both farmers and consumers worldwide.

#### **Conflict of interest**

None

### Acknowledgment

None

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