

Plant Genomics: A New Frontier in Disease Resistance Breeding

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Diseases caused by fungi, bacteria, viruses and nematodes continue to reduce crop productivity and threaten food security worldwide. Although conventional breeding has produced many disease resistant varieties, the process is often slow and may not keep pace with rapidly evolving pathogens. Recent advances in plant genomics have made it easier to identify resistance genes and use them more effectively in breeding programmes. Tools such as marker-assisted selection (MAS), QTL mapping, genome wide association studies (GWAS), genome editing and artificial intelligence now help breeders work faster and select promising lines more accurately. Although challenges related to cost, regulation and data management remain, integrating genomics with conventional breeding offers an efficient and sustainable approach for developing climate resilient and disease resistant crops. This review examines how plant genomics is influencing disease resistance breeding and considers its future role in crop improvement.

Keywords: Plant genomics, disease resistance, marker-assisted selection, genome editing, crop improvement, sustainable agriculture

Introduction

Plant diseases remain a major challenge in agriculture because they reduce both yield and crop quality. Every year, fungal, bacterial, viral and nematode pathogens cause significant economic losses worldwide and threaten global food security. Climate change has intensified this problem by creating conditions that favour the spread of disease and the emergence of new pathogen races. For this reason, developing disease resistant varieties is now a major priority in plant breeding (Singh *et al.*, 2023). For decades, breeders improved resistance by crossing plants and selecting the best offspring over several generations. This approach has been effective but it is also time consuming and labour intensive. Moreover, pathogens continuously evolve making previously resistant varieties susceptible after a few years.

Advances in plant genomics have changed crop improvement by allowing scientists to study plant genomes in much greater detail. Modern genomic tools help identify resistance genes, useful molecular markers and beneficial alleles much faster than traditional methods. Using DNA based methods, breeders can identify resistant plants at an early stage rather than waiting for maturity or visible disease symptoms. This has greatly improved the speed and precision of developing disease resistant varieties. Genomics does not replace conventional breeding rather than it strengthens and supports it. The integration of genomics with advanced technologies such as artificial intelligence (AI), high throughput phenotyping and speed breeding is helping researchers develop improved crop varieties capable of meeting the growing challenges of climate change, emerging pathogens and increasing food demand.

Genomics Revolutionizing Disease Resistance Breeding

The shift from conventional breeding to genomics assisted breeding represents an important step in modern crop improvement. Unlike traditional breeding which depends mainly on visible plant characteristics, genomics allows breeders to select plants based on their genetic makeup. This approach not only saves time but also increases the accuracy of selecting desirable traits. One of the earliest and most widely adopted genomic tools is Marker-Assisted Selection (MAS). Molecular markers are short DNA sequences closely linked to genes controlling disease resistance. These markers serve as genetic indicators, allowing breeders to identify resistant plants without direct exposure to the pathogen (Pati *et al.*, 2025). MAS has been successfully used to develop bacterial blight resistant rice, rust resistant wheat and Fusarium wilt resistant chickpea, significantly reducing the time required to develop improved varieties (Soorni *et al.*, 2025; Kumar *et al.*, 2023).

For complex traits controlled by multiple genes, researchers use Quantitative Trait Loci (QTL) mapping and Genome Wide Association Studies (GWAS). QTL mapping helps identify chromosomal regions associated with disease resistance while GWAS analyses natural genetic variation across diverse germplasm to discover genes linked to important traits. These approaches have improved our understanding of disease resistance mechanisms and provided valuable information for breeding programmes in crops such as rice, wheat, maize, soybean and chickpea. Another valuable source of disease resistance is found in crop wild relatives. During domestication, many cultivated crops lost useful genetic diversity because of repeated selection for yield and quality. Wild relatives, however, have evolved under diverse environmental conditions and often carry resistance to important pests and diseases. Advances in genomics have made it easier to identify useful genes from these wild species and transfer them into cultivated crops through pre breeding programmes, thereby broadening the genetic base of modern varieties.

Among recent innovations, genome editing using CRISPR-Cas technology has attracted considerable attention (Amoroso & Andolfo, 2026). Unlike conventional breeding, which transfers large portions of DNA, CRISPR enables precise modification of specific genes associated with disease resistance or susceptibility. Researchers have successfully used genome editing to improve resistance against bacterial, fungal and viral diseases in several crop species. Although the technology is still evolving, it shows strong potential for faster and more precise crop improvement. Modern disease resistance breeding also benefits from high throughput phenotyping (HTP) which uses drones, sensors, imaging systems and thermal cameras to evaluate thousands of plants rapidly and accurately. These technologies can detect disease symptoms at very early stages, allowing breeders to identify promising genotypes more efficiently than conventional visual observations (Crossa *et al.*, 2025; Ma *et al.*, 2025; Sheikh *et al.*, 2024).

At the same time, artificial intelligence (AI) and bioinformatics are improving how breeders analyse and interpret genomic data. AI algorithms can process large datasets generated from DNA sequencing and phenotyping, helping researchers identify superior breeding lines and predict disease resistance with greater accuracy. This reduces both the time and cost involved in crop improvement. Another breakthrough is speed breeding, which accelerates plant growth by controlling light, temperature and other environmental conditions. Several crops, including wheat, barley and chickpea, can produce multiple generations within a single year. When combined with genomics assisted selection, speed breeding enables breeders to develop disease resistant varieties much faster than conventional methods. Together, these tools have made plant breeding faster, more targeted and more data driven than before. Rather than replacing conventional breeding, plant genomics complements traditional methods and provides breeders with powerful tools to develop high yielding, climate resilient and disease resistant crop varieties for sustainable agriculture.

Challenges and Future Prospects

Despite these advances, several practical challenges still limit the wider use of genomics in disease resistance breeding. Although the cost of DNA sequencing has decreased

considerably over the past decade, large scale genome sequencing and high throughput phenotyping platforms remain expensive for many breeding programmes, particularly in developing countries. Likewise, drones, hyperspectral cameras and automated phenotyping systems require substantial investment and skilled manpower. Another important concern is the regulation of genome edited crops. Technologies such as CRISPR-Cas can precisely modify plant genes without introducing foreign DNA, yet regulatory policies differ across countries. Clear biosafety guidelines and better public understanding will be essential for broader acceptance of genome edited crops. Plant pathogens also continue to evolve, producing new races capable of overcoming resistance genes. This makes durable resistance especially important, including gene pyramiding, the use of quantitative resistance and regular monitoring of pathogen populations.

Furthermore, disease resistance is often influenced by genotype $\times$ environment (G $\times$ E) interactions. A variety that performs well in one region may become susceptible under different environmental conditions due to variations in temperature, humidity and pathogen populations. Therefore, evaluating breeding materials across multiple environments remains essential before releasing new varieties. Another emerging challenge is the management of large genomic datasets. Modern sequencing technologies generate enormous amounts of information that require efficient bioinformatics tools, high performance computing and trained personnel for accurate analysis (Crossa *et al.*, 2025). Strengthening computational infrastructure and promoting data sharing will further enhance genomics assisted breeding. Even with these limitations, plant genomics is likely to play an increasingly important role in future breeding programmes. Continuous improvements in sequencing technologies, artificial intelligence, precision phenotyping and genome editing are expected to make disease resistance breeding faster, more accurate and more affordable. The integration of these technologies with conventional breeding will play a vital role in developing resilient crop varieties for sustainable agriculture.

Success Stories of Genomics Assisted Disease Resistance Breeding

Crop	Disease	Genomic Approach	Outcome
Rice	Bacterial blight	Marker-assisted backcrossing	Successful pyramiding of Xa21, xa13 and xa5 genes for broad spectrum resistance (Pradhan <i>et al.</i> , 2015)
Wheat	Stem rust (Ug99)	Molecular markers and genomics assisted breeding	Identification and deployment of resistance genes against Ug99, protecting wheat production (Singh <i>et al.</i> , 2011; Singh <i>et al.</i> , 2025)
Chickpea	Fusarium wilt	GWAS, QTL mapping and Marker-Assisted Selection	Identification of resistance associated genomic regions and development of improved breeding lines (Soorni <i>et al.</i> , 2025)

These examples demonstrate how plant genomics has successfully accelerated disease resistance breeding in major food crops. While marker assisted selection remains a reliable approach for transferring major resistance genes, newer technologies such as GWAS, genome editing and artificial intelligence are further improving breeding efficiency. Their integration with conventional breeding offers a practical pathway for developing high yielding and disease resistant varieties.

Conclusion

Plant genomics has become an important tool for improving disease resistance in crops. By combining molecular genetics with modern breeding approaches, it enables breeders to identify resistance genes more accurately and develop improved varieties in a much shorter time than conventional breeding alone. Technologies such as marker-assisted selection, GWAS, genome editing, high throughput phenotyping and artificial intelligence are helping

improve breeding programmes worldwide. Although challenges related to sequencing costs, regulatory policies, pathogen evolution and data management still exist, ongoing technological advancements are steadily overcoming these limitations. Future breeding programmes should focus on integrating genomics with conventional breeding, speed breeding and precision phenotyping to develop durable, climate resilient and disease resistant crop varieties. An integrated approach of this kind can improve agricultural productivity while also supporting long term food security and sustainability.

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