



Breeding Disease Resistant Crops for Sustainable Agriculture

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Plant diseases caused by fungi, bacteria, viruses and nematodes are major constraints to crop production, food quality and farm profitability. The Food and Agriculture Organization has estimated that plant pests and diseases can cause losses of up to 40% of global crop production annually. Increasing pathogen diversity, changing climate, intensive monocropping and repeated dependence on chemical pesticides have made disease management increasingly challenging. Developing disease-resistant varieties is therefore one of the most economical and environmentally compatible components of integrated crop protection. Modern breeding has progressed from selection and hybridization to marker-assisted selection, quantitative trait locus (QTL) analysis, genomic selection and genome editing. Practical examples from chickpea, wheat and rice demonstrate how conventional breeding can be combined with molecular technologies to improve resistance while retaining desirable agronomic performance. However, resistance is not necessarily permanent because pathogen populations evolve. Durable protection therefore requires the combination of diverse resistance genes, quantitative resistance, modern breeding technologies and appropriate crop-management practices.

Keywords: disease resistance, conventional breeding, marker-assisted selection, quantitative trait loci, gene pyramiding, genomic selection

Introduction

Plant diseases reduce yield and quality and can substantially increase the cost of crop production. Fungal, bacterial, viral and nematode pathogens can become particularly damaging when susceptible varieties are cultivated repeatedly over large areas. The Food and Agriculture Organization has estimated that plant pests and diseases can cause losses of up to 40% of global crop production, highlighting the importance of effective disease management (Food and Agriculture Organization of the United Nations, 2021). Climate change adds another layer of complexity because temperature, humidity and rainfall influence both crop susceptibility and pathogen development (Xiong *et al.*, 2022). Genetic resistance provides an important alternative to repeated chemical protection. Resistant cultivars can reduce disease development throughout the crop cycle and are particularly valuable in regions where repeated pesticide application is costly or difficult. Plant immunity and disease resistance involve complex interactions between host genetic factors and pathogen-derived signals, making the genetic improvement of resistance an important component of crop breeding (Zhao *et al.*, 2022). Nevertheless, resistance should not be considered a permanent or stand-alone solution. Pathogens evolve rapidly, and a resistance gene that is highly effective against one pathogen population may become less effective when new races or virulent variants arise (Nelson *et al.*, 2018).

Disease resistance is broadly expressed through two genetic patterns. Qualitative resistance is often associated with major resistance genes and can provide strong protection against particular pathogen races. Quantitative resistance, in contrast, generally involves several genes or genomic regions and may reduce disease severity rather than completely preventing infection. Quantitative resistance is often considered to have greater potential for durability because it is less dependent on recognition of a single pathogen genotype (Nelson *et al.*, 2018; Roumen *et al.*, 2017). Consequently, modern breeding increasingly aims to combine major resistance genes with quantitative resistance and other complementary mechanisms.

Conventional Breeding Approaches

Conventional breeding remains the basis of disease-resistance improvement because useful resistance originates from genetic diversity. Resistant landraces, breeding lines, cultivars and crop wild relatives can serve as donors. The general process involves identifying suitable resistant parents, crossing them with agronomically superior material and selecting resistant progeny over successive generations. Selection is particularly useful when resistant plants can be reliably identified under natural or artificial disease pressure. Hybridization allows resistance to be combined with yield, maturity, quality and adaptation traits. Backcross breeding is especially valuable when a resistance trait must be transferred into an otherwise superior cultivar. Similar breeding principles have been applied across major crops, where diverse resistance sources are combined with elite agronomic backgrounds to develop improved cultivars (Lin *et al.*, 2022). However, conventional selection may require several generations, particularly when resistance is quantitatively inherited or disease expression is strongly influenced by environmental conditions.

An important limitation is linkage drag, in which undesirable traits from a resistance donor are transferred together with the desired resistance. Marker-assisted selection can help reduce this problem by allowing breeders to select for the target genomic region while recovering the elite genetic background.

Molecular Breeding Approaches

Marker-Assisted Breeding and QTL Analysis

Marker-assisted selection (MAS) uses DNA markers associated with resistance loci to identify desirable plants before complete phenotypic evaluation. Marker-assisted backcrossing (MABC) combines molecular selection with conventional backcrossing. Foreground selection identifies individuals carrying the target resistance region, whereas background selection helps accelerate recovery of the recurrent-parent genome. A strong example is chickpea improvement for Fusarium wilt. Mannur *et al.* (2019) used the resistant donor WR315 to improve the cultivars Annigeri 1 and JG 74. Background selection resulted in 90-95% recurrent-parent genome recovery in BC₂F₁ Annigeri 1 derivatives and 90-97% recovery in BC₃F₁ JG 74 derivatives. Multilocation testing identified Super Annigeri 1, which showed an 8% yield increase over Annigeri 1 together with improved Fusarium wilt resistance. Thus, molecular breeding did not replace conventional breeding; rather, it made the backcrossing process more precise.

For complex resistance, QTL mapping is particularly important. QTL analysis identifies genomic regions associated with variation in disease response and can provide markers for breeding. A recent chickpea study by Soorni *et al.* (2025) analyzed 32 Fusarium wilt resistance QTLs and identified seven meta-QTL regions across four linkage groups. Candidate genes associated with pathogen perception, signaling and transcriptional regulation were also identified. Selected BC₃F₂ plants subsequently showed 90-96% similarity to the recurrent parent. Such studies illustrate the transition from simply identifying resistant plants toward understanding the genomic architecture underlying resistance.

Gene Pyramiding for Broader Resistance

Pathogen populations can overcome individual resistance genes. Gene pyramiding therefore aims to combine two or more resistance genes, preferably with complementary recognition spectra or mechanisms, in a single cultivar. Combining multiple resistance sources can reduce

dependence on a single resistance mechanism and may improve the durability of disease resistance (Roumen *et al.*, 2017). The development of PBW723, also known as Unnat PBW343, provides an important Indian example. PBW343 was a highly successful wheat cultivar but subsequently became vulnerable to rust. Sharma *et al.* (2021) used marker-assisted breeding to combine rust-resistance genes in the PBW343 background. PBW723 showed improved resistance and was released for cultivation in the North-Western Plain Zone. Its average yield in Punjab was reported as 58.0 q/ha, and approximately 8-9% of Punjab's cultivated wheat area was occupied by the variety three years after release.

The significance of gene pyramiding extends beyond the individual cultivar. It demonstrates how molecular markers can help breeders recover an elite genetic background while incorporating new resistance sources. However, a gene pyramid should not automatically be described as permanently durable. Pathogen evolution can still reduce its effectiveness, making continuous monitoring and diversification of resistance sources necessary (Nelson *et al.*, 2018).

Genomic Selection

Marker-assisted selection is highly effective when markers are closely associated with major resistance genes or well-characterized QTLs. However, quantitative disease resistance may involve many genes, each contributing a small effect. Genomic selection (GS) addresses this challenge by using genome-wide markers to predict the breeding value of individuals. Such genome-wide approaches are increasingly relevant for complex disease resistance, where many loci contribute to the final phenotype (Lin *et al.*, 2022). The major advantage of GS is that selection can begin before extensive multi-environment phenotyping. This can shorten breeding cycles and increase selection intensity. Its success, however, depends on an appropriate training population, reliable phenotypic data and a sufficiently strong relationship between genomic predictions and field performance. Therefore, genomic selection should be viewed as a complement to, rather than a replacement for, good disease phenotyping.

Genome Editing

Genome editing has introduced another dimension to disease-resistance breeding. Clustered regularly interspaced short palindromic repeats (CRISPR)-associated systems can modify specific DNA sequences. Instead of transferring a resistance gene from another genotype, breeders can sometimes modify a susceptibility gene or regulatory sequence required by the pathogen. Recent advances in targeted genome modification have expanded the potential of precision breeding for disease resistance and other crop traits (Li *et al.*, 2024). Recent developments in base editing and prime editing have expanded the range of possible genetic modifications. However, genome editing is not a universal solution. Susceptibility genes may have important roles in plant development, yield or metabolism, and their modification can produce undesirable effects. Edited plants must therefore be evaluated for resistance, agronomic performance, quality, environmental stability and potential off-target effects before deployment. Regulatory requirements also differ among countries and should be considered during product development (Tuncel *et al.*, 2025).

From Resistance Breeding to Integrated Disease Management

Genetic resistance is most effective when combined with other components of integrated disease management. Healthy seed, crop rotation, field sanitation, appropriate sowing practices, disease forecasting, biological control and judicious pesticide use can reduce pathogen pressure and delay resistance breakdown. Such integration is particularly important because disease resistance can vary with pathogen population structure and environmental conditions. Beneficial microorganisms such as *Trichoderma*, *Bacillus* and *Pseudomonas* can contribute through competition, antibiosis, production of antimicrobial compounds and activation of plant defence responses. *Trichoderma* species have received particular attention as multifunctional plant-beneficial microorganisms, while beneficial *Bacillus* and *Pseudomonas* strains can suppress pathogens through several biological mechanisms (Woo *et al.*, 2023; Dimkić *et al.*, 2022). However, their performance can vary with crop genotype, soil, climate and formulation. Biological control should therefore complement rather than

automatically replace genetic resistance or chemical protection. The deployment strategy is equally important. Large-scale cultivation of genetically uniform varieties can create strong selection pressure on pathogen populations. Diversifying varieties and resistance genes, monitoring pathogen races and avoiding excessive dependence on one resistance source can help maintain resistance over longer periods (Nelson *et al.*, 2018; Roumen *et al.*, 2017).

Future Perspective

The next phase of disease-resistance breeding will depend on integrating several technologies rather than relying on a single method. High-throughput phenotyping can improve disease assessment by using imaging, sensors and automated data analysis, allowing breeders to evaluate large populations more rapidly and objectively (Song *et al.*, 2021). Genomic surveillance can help monitor pathogen populations and identify emerging virulence before major epidemics occur. Speed breeding can accelerate generation advancement and shorten the time required to move promising breeding materials through successive generations (Gudi *et al.*, 2022). Genomic selection can further increase the efficiency of selection for complex resistance. Genome-wide resources, including improved reference genomes and pangenomes, can help breeders discover resistance alleles that are absent from standard reference genomes. Climate change also requires a broader breeding target. Future varieties should combine disease resistance with tolerance to drought, heat and other environmental stresses. Climate change can alter pathogen distribution, disease development and host-pathogen interactions, making the stability of resistance across environments increasingly important (Xiong *et al.*, 2022). Importantly, resistance must be tested across environments because temperature and moisture can alter both disease development and the expression of resistance.

Conclusion

Disease-resistant varieties remain one of the strongest foundations of sustainable crop protection. Conventional selection, hybridization, backcrossing and introgression continue to provide the genetic framework for crop improvement, while marker-assisted selection, QTL analysis, gene pyramiding, genomic selection and genome editing have increased the precision and speed of breeding. The development of Super Annigeri 1 in chickpea, PBW723 in wheat and disease-resistant rice carrying *Pi2*, *xa5* and *Xa23* demonstrates the practical value of integrating conventional and molecular approaches. Nevertheless, no single resistance gene or breeding technology can guarantee permanent protection. Durable disease management requires diversified resistance sources, quantitative resistance, continuous pathogen monitoring and integration with appropriate agronomic and biological practices. The future of disease-resistant agriculture therefore lies not simply in developing a resistant variety, but in designing resistant, productive and climate-resilient cropping systems. Combining genetic diversity with modern genomics, precision breeding, improved phenotyping and integrated disease management can reduce disease-related losses while decreasing unnecessary dependence on pesticides and strengthening the sustainability of crop production.

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