Integrative
Plant Biotechnology
ISSN: 3007-2735 (Online), 3007-2727 (Print)

Review Article

Intelligent Reprogramming of Crops for Resistance Against Emerging Plant Pathogens: From Conventional Breeding to Genome Editing

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Article History
Received: August 24, 2025
Accepted: September 21, 2025
Published online: September 25, 2025

Cite this article
Asghar, J., Jan, A., Hamayun, M., Ali, K., Rehman, A. U., Ahmed, M., Ullah, I., Basit, A., & Saddam, S. (2025). Intelligent reprogramming of crops for resistance against emerging plant pathogens: From conventional breeding to genome editing. Integrative Plant Biotechnology, 03, 253-268.

ABSTRACT

Emerging plant pathogens are threat to global food security. Plant pathogens are rapidly spreading due to increasing globalization, agricultural intensification and rapidly changing climatic conditions. These emerging pathogens are rapidly adapting to overcome host resistance. Therefore, necessitating the development of sustainable disease management strategies. Breeding for resistance is an important approach for sustainable disease management. The advancement in molecular genetics, genomics, and biotechnology have revolutionized the field of breeding for resistance. Precise incorporation of resistant genes into elite cultivars has been possible due to advanced breeding techniques such as Marker-assisted selection, genomic selection, and genome editing tools. However, there are still several challenges in plant breeding. The development of resistant varieties is further complicated by public perception and regulatory hurdles surrounding genetically modified crops. However, using integrated pest management such as resistant varieties along with cultural, biological and chemical control methods can enhance the durability of resistance. The development of resilient crop varieties has been possible with Advances in omics technologies, high-throughput phenotyping, and pathogen detection methods. Besides the development of resilient variety, it is essential to deliver resistant varieties to farmers. International collaboration, open-access breeding networks, and public-private partnerships play important role in delivering the resistant varieties to farmers. Resistance breeding needs to be proactive to face the challenges of emerging plant pathogens and global food security. This review highlights the factors causing spread of emerging plant pathogens, discuss modern approaches, key challenges and future direction of resistant breeding.

Keywords: Emerging plant pathogens, Disease resistance breeding, Marker-assisted selection, Genomic selection, Genome editing

INTRODUCTION

Emerging plant pathogens such as nematodes, fungi, bacteria, viruses, and oomycetes are becoming a major threat to agricultural systems. According to Kantor *et al.* (2024), these pathogens possess challenges for plant health and food production systems. Pathogens host range have increased causing increased pathogen incidences geographically. Further globalization, climate change, and intensification of agricultural practices are generally increasing the introduction

https://doi.org/10.55627/pbiotech.003.03.1496

and establishment of these emerging pathogens in new ecological systems (Hossain *et al*., 2024). Emerging plant pathogens have significantly reduced crop yield and quality worldwide. Moreover, rising global population and demand for food products are further affecting food security. Staple food supplies are threatened by outbreaks of emerging pathogens such as virulent races of rust fungi in wheat and bacterial wilt of banana in banana plantations (Gai and Wang, 2024; Virk *et al*., 2024). The management of plant pathogens has become increasingly challenging in recent years due to rapid evolution of pathogen populations. Environmental pressure on plants such as changing temperatures, elevated atmospheric carbon dioxide is weakening the plant resistance and pathogens are adapting to these conditions within few cropping cycles. Therefore, development of environment and insect resistant varieties is crucial for food security (Dracatos *et al*., 2023).

Breeding for resistance is environmentally and economically sustainable method of plant disease management. Breeding plants for resistance has been revolutionized by advances in molecular genetics, genomics and biotechnology. Modern breeding techniques such as marker assisted selection (MAS), genomic selection (GS), and genome editing tools (CRISPR/Cas9) are efficient to develop elite cultivars with precise incorporation of resistant genes (Yıldırım *et al*., 2023). Resistance breeding has progressed from traditional methods such as phenotypic selection to precise molecular breeding, detecting cloned resistance (R) genes and pathogen effectors that facilitate resistance breeding, as conceptualized in the gene-for-gene model (Figure 1). Laying the groundwork for a new era of plant disease resistance breeding. The advancement in resistance breeding is the solution to present and future emerging pathogen threats (Pedrozo *et al*., 2025; Švara *et al*., 2024; Dracatos *et al*., 2023). This review paper discusses the factors of emerging plant pathogens, explores the advances in breeding for resistance, identify the key challenges and future direction for sustainable crop protection.

EMERGING PLANT PATHOGENS: CHARACTERISTICS AND CHALLENGES

Factors Driving Emergence of Pathogens

The emergence and spread of plant pathogens are driven by a combination of environmental, economic, and agricultural factors. Climate change is playing central role as it modifies the temperature regimes, precipitation patterns, and atmospheric composition, including elevated CO_2 levels. The changes speed up life cycles of pathogens, make them more fertile, and expand their geographic boundaries (Kumar and Mukhopadhyay, 2024; Nitta *et al*., 2024). Warm winters allow pests and pathogens to overwinter in the areas where they were previously unable to overwinter and changed rainfall patterns enable environmental factors to contribute to the occurrence of epidemics (Kumar and Mukhopadhyay, 2024). In addition, plant health can be negatively affected by the reactive nitrogen gases and other pollution materials in the atmosphere, which increase susceptibility to emerging diseases (Alfizar and Nasution, 2024). Trade and globalization have significantly contributed in movement of plant material (seeds, fruits, nurseries) across continents. It facilitates the process of agricultural diversification, although it also enables the interruption of ecological barriers to plant pathogens and their vectors (Brooker *et al*., 2023). Pathogens establish in new introduced regions rapidly due to absence of their natural predators or resistant local strains (Oraon *et al*., 2024). The agricultural intensification also increases the risk of pathogens emergence. Economically efficient large-scale monocultures lead to the creation of genetically identical host environments that allow the development of pathogens and their evolution (Fan *et al*., 2025). Crop rotation and shifts in cropping patterns whereby crops are cultivated into different ecological zones due to market demand and population pressure subject crops to new pathogens outbreaks (Mihrete and Mihretu, 2025).

Table 1 summarizes the most threatening emerging plant pathogens and pests affecting staple crops worldwide, underscoring the diversity of causal agents and their devastating consequences. The listed pathogens, ranging from fungi such as *Puccinia graminis* (Singh *et al*., 2015; Soko *et al*., 2018) and *Magnaporthe oryzae* (Nalley *et al*., 2016) to viruses like ACMV (Combala *et al*., 2024) and BBTV (Watanabe *et al*., 2013), bacteria such as *Ralstonia solanacearum* (Kurabachew and Ayana, 2017) and *Xanthomonas vasicola* (Uwimana *et al*., 2024), and even parasitic weeds like *Striga hermonthica* (Midega *et al*., 2017) illustrate the broad spectrum of biotic stresses confronting global agriculture. Bacterial blight of cotton (*Xanthomonas citri* pv. *malvacearum*) (Shah *et al*., 2025; Anwer *et al*., 2024) and brown spot of rice (*Bipolaris oryzae*) (Shamshad *et al*., 2024; Qi *et al*., 2025) are also recognized as serious emerging threats, causing significant yield and quality losses in major cotton- and rice-growing regions worldwide. Their modes of spread, including windborne spores, insect vectors, contaminated tools, and seedbanks, facilitate rapid dissemination across regions, often leading to severe yield reductions and economic losses. The data highlights not only the vulnerability of staple crops such as wheat, rice, banana, cassava, and maize but also the urgent necessity of breeding for durable resistance as a central strategy to safeguard global food security.

Table 1. Major emerging plant pathogens, their hosts, geographic distribution, modes of spread, and associated economic impacts

Pathogen name	Pathogen type	Primary host crop(s)	Current geographic distribution	Mode of spread	Estimated yield loss / economic impact	Key references
Puccinia graminis f. sp. *tritici*	Fungus (basidiomycete)	Wheat	East Africa, Middle East, spreading to Asia	Windborne spores	Up to 80% yield loss in susceptible varieties	(Singh *et al*., 2015; Soko *et al*., 2018)
African cassava mosaic virus (ACMV)	Virus (Geminiviridae)	Cassava	Sub-Saharan Africa, expanding in Asia	Whitefly vector	24–75% yield reduction; up to US$2.7 billion losses regionally	(Combala *et al*., 2024)
Xanthomonas vasicola pv. *musacearum* (BXW)	Bacterium	Banana	East and Central Africa	Insect vectors, tools, planting material	Up to 100% yield loss; ~US$25 billion potential losses in SSA over 10 years	(Uwimana *et al*., 2024)
Phytophthora infestans	Oomycete	Potato, tomato	Global; notable in Latin America, Asia, Africa	Wind- and rain-borne sporangia	Up to 100% yield loss in unmanaged fields	(Fry *et al*., 2015; Shattock, 2002)
Magnaporthe oryzae	Fungus (Ascomycete)	Rice	Asia, emerging globally	Windborne spores, irrigation	Major losses; often 10–30% in outbreaks	(Nalley *et al*., 2016)
Ralstonia solanacearum	Bacterium	Potato, tomato, Solanaceae	Tropical and subtropical areas	Soil, water, infected tools	Significant losses; up to 60–80% under conducive conditions	(Kurabachew and Ayana, 2017)
Puccinia graminis f. sp. *hordei*	Fungus	Barley	Global, particularly Europe, North America	Windborne spores	Frequent yield losses, often 20–50% in susceptible areas	(Hatta *et al*., 2020)
Banana bunchy top virus (BBTV)	Virus	Banana, plantain	Asia, Pacific, Africa	Aphid/vector, planting material	Severe yield reductions; plant stunting leads to crop failure	(Watanabe *et al*., 2013)
Fusarium graminearum (FHB)	Fungus	Wheat, barley	Global, especially North America	Airborne spores	Up to 30% yield loss; high quality penalties due to mycotoxins	(Boutigny *et al*., 2013)
Striga hermonthica	Parasitic weed	Cereals (maize, sorghum)	Sub-Saharan Africa	Seedbank, host proximity	Infestation on 5 million ha, losses >70%	(Midega *et al*., 2017)

https://doi.org/10.55627/pbiotech.003.03.1496

Xanthomonas citri pv. *malvacearum*	Bacterium	Cotton	Africa, Asia, some parts of USA	Seedborne, rain splash, contaminated tools	Up to 40% yield loss in severe epidemics	(Shah *et al*., 2025; Anwer *et al*., 2024)
Bipolaris oryzae	Fungus (Ascomycete)	Rice	Asia, Africa, Latin America	Seed and, air and water borne conidia	16-43% yield loss; grain quality reduction	(Shamshad *et al*., 2024; Qi *et al*., 2025)

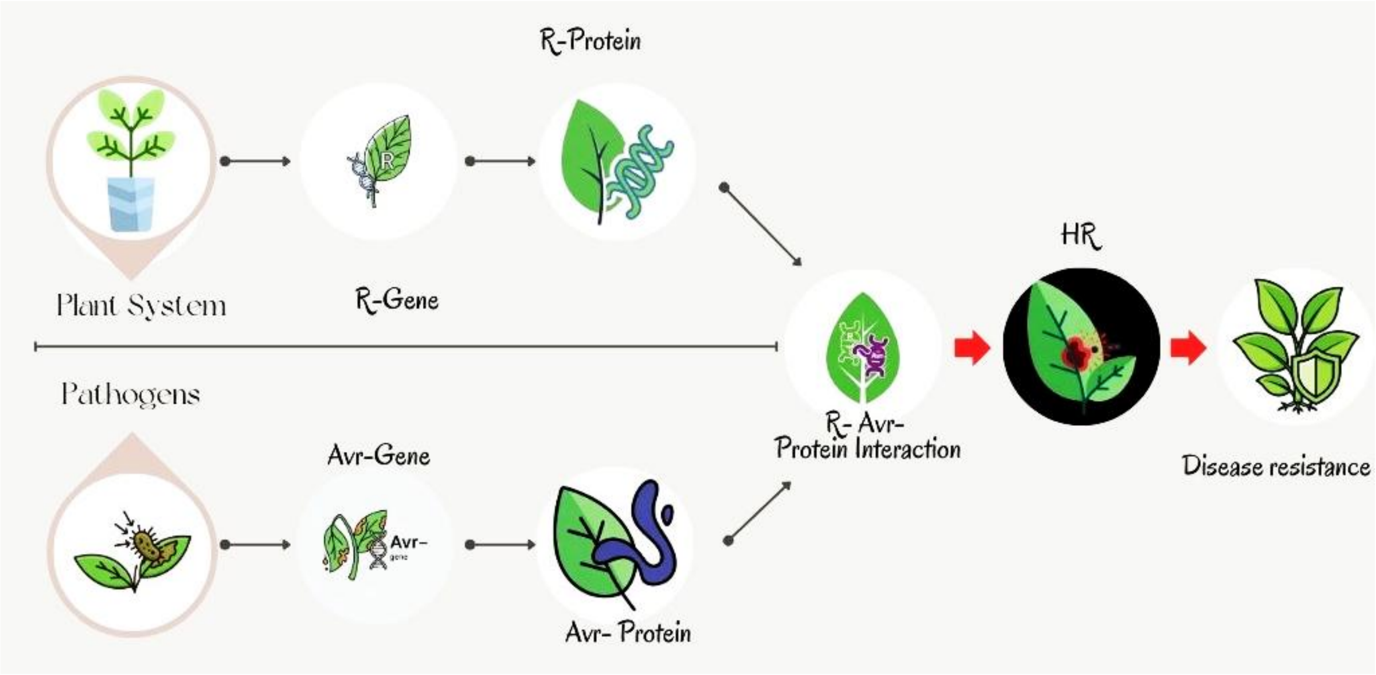

Figure 1: The gene-for-gene model of plant disease resistance, illustrating the interaction between plant resistance (R) genes and pathogen avirulence (Avr) genes, leading to hypersensitive response (HR) and resistance.

Pathogen Adaptation and Resistance Breakdown

Even when resistant cultivars are achieved, pathogens can overcome defenses, by several mechanisms. A typical approach is mutation within a virulence gene, which modifies the molecular targets recognized by the plant immune receptors and this inhibits discovery as illustrated in the gene-for-gene model (Figure 1). There is also another mechanism based on effector diversification whereby the pathogens alter the effector proteins which are important to manipulate the host cellular activity. The mechanisms behind pathogen evasion of host recognition allows the pathogen to neutralize previous resistance genes (Zdrzałek *et al*., 2024). The durability of host resistance depends on both host genetics and pathogen adaptability. Polygene quantitative resistance is more durable than monogenic resistance (Çelik Oğuz and Karakaya, 2021) This durability is largely explained by the activation of complex host defense signaling cascades (Figure 2). Nevertheless, the prevention of quantitative resistance can also be eliminated over time as pathogens obtain low-cost escape mutations that do not reduce pathogen fitness (Chen *et al*., 2024).

BREEDING FOR RESISTANCE: APPROACHES AND TECHNOLOGICAL ADVANCES

Conventional Breeding Methods

Traditional breeding still constitutes a major direction in breeding disease-resistant crop varieties. Backcross breeding, mass selection, pure-line selection, and recurrent selection are methods that have widely been used in enhancing the adaptation and resistance characteristics in plants (Anand *et al*., 2023). The method of backcrossing is preferable to self-pollinated crops, whereas recurrent selection and hybridization are common among cross-pollinating species (Ajayi *et al*., 2024). In the past, the methods have recorded remarkable successes. In common beans, traditional breeding has been successful in increasing environmental adaptation to diverse conditions coupled with increased resistance to major pathogens (Cha *et al*., 2024).

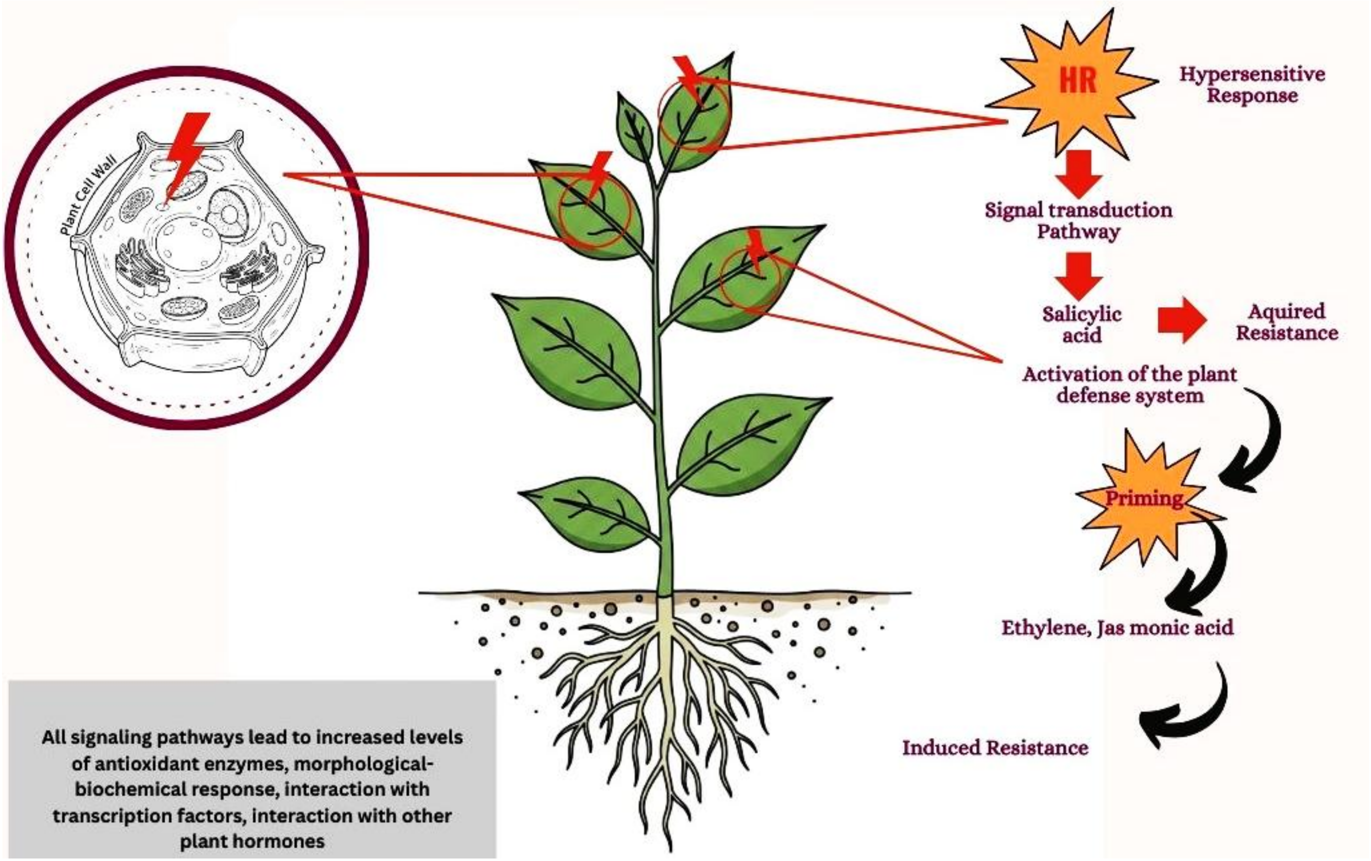

Figure 2. Stages of plant defense signaling pathways, including hypersensitive response (HR), salicylic acid-mediated acquired resistance, and priming-induced resistance through jasmonic acid and ethylene pathways.

However, it is time-consuming, especially against traits such as drought-tolerance or resistance to complex diseases. Limitations are dependent upon the existing genetic variability, long generation time and predisposed to genotype × environment interactions. Although various disadvantages of conventional breeding are present, this breeding method costs less, and the infrastructure does not require much specialized equipment as modern molecular techniques and is still required when combined with newer technology (Isıyel *et al*., 2024). Conventional approaches such as backcrossing and recurrent selection remain widely used for incorporating resistance traits. For example, recent work has demonstrated the successful introgression of multiple *Sr* genes (Sr22, Sr33, Sr35, Sr45) into wheat, significantly improving resistance to stem rust under diverse environments (Hatta *et al*., 2020). Similarly, recurrent selection continues to be applied in maize breeding, yielding enhanced resistance to foliar diseases across different environments (Ćeran *et al*., 2024) as elaborated in Table 2.

Modern Breeding Tools

Limitations of conventional procedures have led to development of molecular and genomic tools that shorten breeding cycles, enhance the selection accuracy. Speed breeding time decreases between generations through manipulated environmental conditions such as ideal light, temperature, and day length so that up to five or six crop generations may be harvested in a year (Kumar and Walia, 2024). This accelerates genetic gains and can be used in conjunction with genomic for faster introduction of traits (Potts *et al*., 2023). In marker-assisted selection (MAS), readily available molecular markers associated with desirable traits can be used to select individuals at an early stage of growth, preferably as seedlings, and minimize the requirement of extensive phenotypic screening (Song *et al*., 2023). MAS is especially helpful for our understanding of single-major gene-based traits and finds a broader application on wheat crops, barley and rice (Mapari and Mehandi, 2024).

Genomic selection (GS) is an advancement of this concept by using genome-wide data on markers to predict the breeding value of all individuals in a population (Michel *et al*., 2021). GS is the most effective on polygenic characteristics, including quantitative disease resistance, and in some scenarios, GS has been found to be more predictive than MAS, which was demonstrated in Fusarium head blight resistance in wheat (Mapari and Mehandi, 2024).

Table 2. Examples of resistance breeding approaches applied in major crops.

Approach	Crop and Disease	Key Achievement	Key References
Conventional backcrossing	Wheat - stem rust (*Puccinia graminis*)	Resistant cultivars developed with Sr22, Sr33, Sr35, Sr45 genes introgressed from wild relatives	Hatta *et al*., 2020
Conventional recurrent selection	Maize - multiple foliar diseases	Improved resistance and stability under different environments	Ćeran *et al*., 2024
Marker-Assisted Selection (MAS)	Rice -bacterial blight (*Xanthomonas oryzae* pv. *oryzae*)	Introgression of Xa4, Xa21, Xa33 genes for durable resistance	Derbyshire *et al*., 2024
MAS (QTL-based)	Wheat - stripe rust	Deployment of QTLs for adult plant resistance in elite germplasm	Wang *et al*., 2023
Genomic Selection (GS)	Wheat - Fusarium head blight	Enhanced prediction accuracy and faster selection compared to MAS	Poland and Rutkoski, 2016; Ćeran *et al*., 2024
High-Throughput Phenotyping (HTP)	Rice - blast	UAV-based hyperspectral imaging for early resistance screening	Khan *et al*., 2022
Gene pyramiding	Wheat - stripe rust (*Puccinia striiformis*)	Additive resistance from pyramiding multiple adult plant resistance genes	Wang *et al*., 2023
QTL Mapping	Maize - northern leaf blight	Identification and deployment of QTLs linked with quantitative resistance	Samantara *et al*., 2022
Genome editing (CRISPR/Cas9)	Rice - bacterial blight	Editing of SWEET susceptibility genes improved durable resistance	Erdoğan *et al*., 2023
Genome editing (CRISPR/Cas9)	Wheat - powdery mildew	CRISPR knockout of TaMLO genes for durable resistance	Yıldırım *et al*., 2023
Utilization of wild relatives	Wheat - stripe rust	Resistance introgressed from *Aegilops tauschii* and wild einkorn	Derbyshire *et al*., 2024
Utilization of landraces	Rice - blast	Mining resistance alleles from Asian landraces for durable Pi genes	Umakanth *et al*., 2017; Kaur *et al*., 2022

High throughput phenotyping (HTP) is the integration of imaging and sensor technology and automation to measure quickly and non-destructively a high volume of plants. The identification of genotype phenotype relationships in disease resistance can be made by integrating genomic information and data obtained from RGB imaging, hyperspectral cameras, LiDAR and thermal sensors. HTP reduces phenotyping cost and accelerates selection decisions (Sabag *et al*., 2024; Thapa *et al*., 2024). The relative strengths and limitations of these strategies are captured in Figure 3, which highlights differences in cost, speed, and durability.

Marker-assisted selection has been particularly effective for rice bacterial blight, where genes such as *Xa4, Xa21,* and *Xa33* have been pyramided into elite cultivars to deliver durable resistance (Derbyshire *et al*., 2024). More recently, genomic selection has gained traction for predicting polygenic resistance traits; studies in wheat have shown superior performance in managing Fusarium head blight compared to traditional MAS (Ćeran *et al*., 2024). High-throughput phenotyping is also revolutionizing selection, with UAV-based hyperspectral imaging used successfully to detect early blast infections in rice (Khan *et al*., 2022) as given in Table 2.

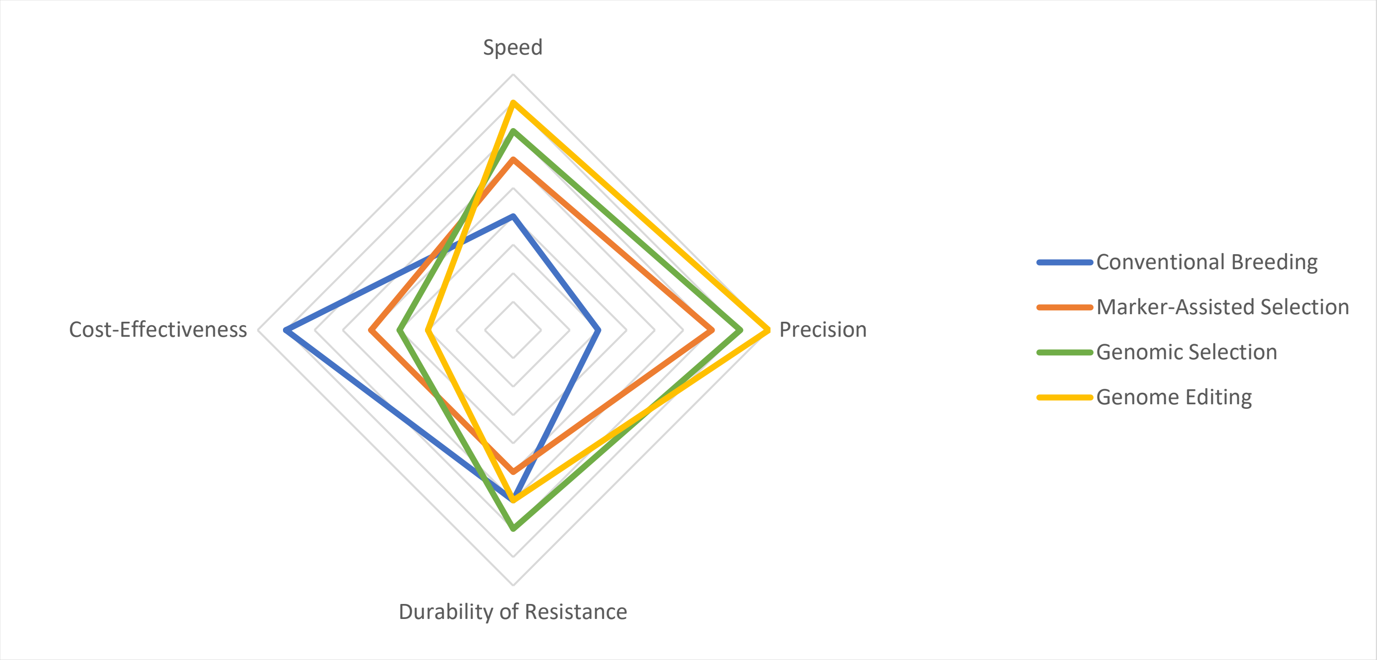

Figure 3. Comparison of breeding strategies for disease resistance based on speed, precision, durability, and cost-effectiveness.

Gene Pyramiding and Multiline Varieties

Gene pyramiding involves combining multiple resistance genes in a single cultivar for broad-spectrum and durable resistance. This method may offer the advantage that it is less likely that resistance will break down since several defence mechanisms have to be countered simultaneously by pathogens. Sequential combination of QTLs conferring rice blast resistance has yielded long lasting, non-race-based resistance (Liu *et al*., 2024). The combination of several genes conferring adult-plant resistance has delivered additive effects of stripe rust resistor in wheat (Younas *et al*., 2024; Wang *et al*., 2023). Multiline varieties are a combination of a variety of lines (each with different resistant genes) planted together as a single variety. Such genetic heterogeneity of a crop stand can delay epidemic development and enhance long-term stability of resistance and minimize the use of chemical pesticides (Tong *et al*., 2024). Pyramiding multiple resistance genes has proven effective in delivering additive and durable resistance. Recent studies in wheat demonstrated that stacking adult-plant resistance genes substantially reduced stripe rust severity across diverse environments (Wang *et al*., 2023). Such gene combinations provide broad spectrum protection, delaying pathogen adaptation as reported in Table 2.

Quantitative Trait Loci (QTL) Mapping for Durable Resistance

The quantitative disease resistance (QDR) which is often regulated by several genes is more lasting than the qualitative resistance. The mapping of QTLs related to QDR makes it possible to apply MAS to enable selection of complex resistance characteristics by breeders. Crops that have benefited greatly due to QTL-based approaches in the improvement of resistance include wheat, barley, common bean, tomato, and pepper (Womack *et al*., 2020). Another advantage linked to the incorporation of QTLs is that there is decreased risk of adaptation in pathogens due to the distribution of defence response to several genetic locations (Mungalu *et al*., 2020). Breeders are mainly focusing on QTL mapping. For example, mapping QTLs for northern leaf blight (NLB) resistance in maize have been recently identified and deployed in breeding programs for incorporation into elite germplasm (Samantara *et al*. 2022). The importance of QTL mapping for complex and polygenic traits is evident (Table 2).

Integration of Phenotypic and Genotypic Data

With the combination of high-quality phenotypic data and genotypic information, breeding outcomes could be predicted better. Genotyping-by-sequencing (GBS) and genome-wide association studies (GWAS) are some of the techniques that can aid in the identification of molecular markers associated with the traits of the resistance (Qureshi *et al*., 2025). With the help of bioinformatics, these markers are also associated with the phenotypes observed and allow the superior selection of traits and a reduction in the length of breeding cycles (Kumar *et al*., 2024). The integration of high-quality phenotypic data with genotyping-by-sequencing (GBS) and genome-wide association studies (GWAS) enabling superior trait prediction. Recent advances emphasize the utility of bioinformatics pipelines in linking markers with resistance phenotypes, reducing breeding cycles and increasing efficiency (Derbyshire *et al*., 2024) as elaborated in Table 2.

Genome Editing

Genome editing technologies like CRISPR/Cas9, transcription activator-like effector nucleases (TALENs) and zinc-Finger nucleases (ZFNs) have revolutionized agriculture with the targeted editing of the genes being targeted. These tools can insert, delete or edit disease resistance genes without excessive linkage drag and preserve useful agronomic characteristics (Sahito *et al*., 2024; Erdoğan *et al*., 2023).

Nevertheless, there are obstacles. Deployment can be prevented by off-target mutations, regulatory uncertainty and hazard to perception (Oguejiofor *et al*., 2023). Countries have different regulatory regimes to genome-edited crops, which limit the pace and magnitude of uptake. Genome editing tools have delivered major breakthroughs in plant disease resistance. In wheat, CRISPR/Cas9-mediated knockout of *TaMLO* genes has conferred durable resistance against powdery mildew, while in rice, editing of *SWEET* susceptibility genes has significantly enhanced resistance to bacterial blight (Erdoğan *et al*., 2023; Yıldırım *et al*., 2023). These examples highlight the transformative role of precise genome engineering in modern resistance breeding Table 2.

Utilization of Wild Relatives and Landraces

Wild crop relatives and traditional landraces can serve as very useful reservoirs of resistance breeding. They usually have resistance genes that have been lost in domestication. Allele mining, genomic selection, and chromosome segment substitution line (CSSL) development methods assist in the isolation and transfer of the resistance's traits of such sources (Huang *et al*., 2023; Li *et al*., 2023). However, introgression can be complex due to crossing barriers, chromosome incompatibility, and linkage drag, in which these undesirable traits come with useful alleles (Kashyap *et al*., 2022). Careful breeding strategies and molecular tools are required to reduce these problems while maintaining yield and quality. Crop wild relatives and landraces remain invaluable reservoirs of resistance genes. For example, resistance alleles against stripe rust have been introgressed from *Aegilops tauschii* and other wild wheats into modern cultivars (Derbyshire *et al*., 2024). Likewise, allele mining in Asian rice landraces continues to provide durable *Pi* genes against blast (Kaur *et al*., 2022) as presented in Table 2. Figure 3 shows that genome editing is more efficient than other strategies in terms of speed, precision, and durability of resistance, though it is less cost-effective than conventional breeding (Marium *et al*., 2025). Genomic selection ranks high in durability and precision, while marker-assisted selection offers moderate performance across traits (Sharma *et al*., 2024). Conventional breeding remains the most cost-effective but lags in speed and precision. Modern molecular approaches (genome editing, genomic selection) provide more precise and durable resistance compared to traditional methods (Pandey *et al*., 2022).

KEY CHALLENGES IN RESISTANCE BREEDING

Balancing Resistance with Yield and Quality

Achieving disease resistance without loss of yield, quality, other essential agronomic traits remain one of the most consistent limitations in resistance breeding. Traits associated with resistance may in some cases be associated with reductions in yields, or poor-quality traits when they are introduced between wild relatives or landraces (Derbyshire *et al*., 2024). A way to keep this trade-off in check is by using multi-trait selection mixed designs like index selection, tandem selection and independent culling. Genomic selection model with genetically correlated traits usage can provide a more advanced dual methodology of enhancing resistance levels and hence preserving the level or even the qualities of yield (Rehman *et al*., 2024). One such case is a successful balancing gene, rice Xa4 gene, leads to resistance to bacterial blight and enhances cell wall thickening due to which lodging resistance is also increased without a reduction in produce (Yuan *et al*., 2024).

Accelerating Breeding Cycles

The emerging pathogens evolve rapidly, and this requires a breeding response to be able to adjust to its evolvement. Combined with the genomic selection, and marker-assisted breeding, speed breeding (SB) can even shorten breeding cycles to a fraction of the time (Ćeran *et al*., 2024). We can also use metabolomics-aided breeding to also deploy a biosensor to determine metabolite biomarkers that are associated with variability in resilience to stress (Mashabela *et al*., 2022). However, these will require control-environment space, precision of environmental manipulations as well as intense technical know-how (Potts *et al*., 2023).

Infrastructure, Funding, and Resource Limitations

As we have seen so far, resistance breeding requires long term investment in infrastructure as well. Such as controlled growth chamber, well advanced phenotyping systems, cutting edge bioinformatics systems. Much of the breeding programs, especially those in developing nations, cannot afford to have multi-year selection pipelines (Dong and Fan, 2024). In the case of promising technologies, such as CRISPR/Cas9, the bottleneck commonly resides in the fact that the lab capacity is not sufficient, and the projects need funding to expand into significant breeding programs. Environmental regulation, climatic patterns of change and shifts in land use are matters that also limit the operation of global breeding networks disrupting coordinated deployment strategies of genes (Lallawmkimi *et al*., 2024; Xing and Wang, 2024).

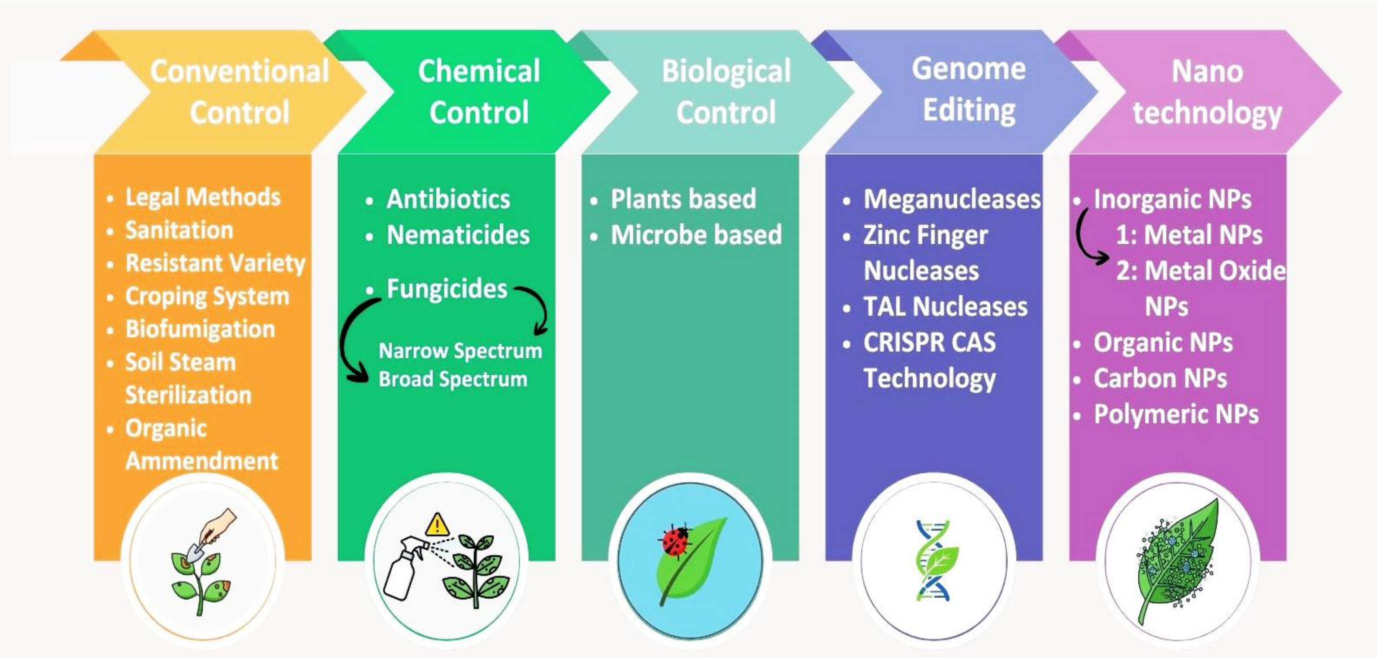

Figure 4. Overview of plant disease control methods, ranging from conventional practices and chemical applications to biological control, genome editing, and nanotechnology-based approaches

Regulatory Hurdles and Public Perception

The regulatory approval system is complex, lengthy and even costly in case of the varieties developed by biotechnology (Hallerman *et al*., 2024). In other jurisdictions, non-harmonized procedures and divergent biosafety guidelines slow the passage to release of resistant cultivars. The use of misinformation and widespread scepticism on the part of the population towards genetically modified (GM) crops also restricts adoption. To find solutions to these problems, direct communication, informational campaigns, and the presentation of the positive effects of decreasing the use of pesticides on the environment are needed (Kolur *et al*., 2024).

Non-transgenic approaches such as cis-genesis and precise genome editing may help overcome public resistance by avoiding the transfer of genes from unrelated species (Lironcurti *et al*., 2023). However, genome editing faces uncertain regulatory status in many countries, necessitating adaptive policies that distinguish it from traditional GM technology (Wray-Cahen *et al*., 2024).

INTEGRATED MANAGEMENT FOR DURABLE RESISTANCE

Integrated Pest Management (IPM)

Although genetic resistance is an effective means of combatting plant pathogens, it works best when included in larger management systems that integrate multiple approaches (Figure 4). IPM involves use of resistant varieties integrated with complementary controlling practices including cultural, biological and chemical control methods in a bid to minimize the influence of the pathogen and postponement of resistance degradation. The rise of biotechnology fueled by genetically modified insect-resistant crops including Bt cotton and Bt maize has substantially curbed the use of pesticides while also ensuring that production remains high (Jan *et al*., 2025). Crop rotation, field sanitation and destruction of the alternative hosts can break the life cycle of the pathogen, and reduce the pathogen load (Gyawali *et al*., 2023). In cases when chemical interventions are required, they are used in a way that will not have much negative effect on the environment, and their use will reduce the pace at which pesticide resistance occurs (Galli *et al*., 2024).

Disease Forecasting and Early Warning Systems

The ability to forecast diseases and early warning systems are essential to safeguard against emerging pathogens - especially those that spread quickly. Forecasting is more effective when it is associated with the full range of control techniques available (Figure 4). You can predict outbreaks with these systems. Also, you can use them to guide early interventions using models and reports (Sumithra *et al*., 2025). When new diseases are discovered more quickly, it helps to prevent epidemics on a larger scale and further limit the economic costs and damage to the environment in response to any emergency. By putting together weather-based forecasting models along with inspecting the pathogen population has gotten better rust disease management in wheat-growing regions (Vashisht *et al*., 2023).

Recent case studies highlight these advances. The identification of more than 40 different races of a pathogenic fungus strain, *Puccinia striiformis*, in Egypt is indicative of the scale of the threat and the grave risk that pathogen diversity poses to agricultural crops around the world. Esmail *et al*. (2025) note the discovery of these races in over 40 states in Egypt. This is a good example of the need for continuous monitoring of pathogens that threaten agricultural crops around the world. Comparable research on *Puccinia triticina* (wheat leaf rust) has found the emergence of new virulent races after 2020 that quickly overcome the effectiveness of previously effective resistance genes (Omara *et al*. 2021). The examples highlight the need for integrated forecasting platforms connecting pathogen surveillance with resistance deployment strategies.

Agroecological Approaches

This supports the notion that when breeding for crop resistance takes place within agroecological farming systems, the result will be sustainable and resilient crop production. Biodiversity, ecosystem services, and resource efficiency are key goals of agroecology which can be enhanced particularly using genetic varieties and systems of rotations (Akanmu *et al*., 2023). These systems can be supported by developing low-input varieties with multi-stress resistance. It is also important to ensure compatibility with organic and conservation agriculture. Intercropping or agroforestry combined with resistance breeding can limit the spread of pathogens besides improving soil health and moisture retention. These agroecological strategies complement other disease control methods highlighted in Figure 4, ensuring sustainability and resilience. Agroecological strategies can be effective when combined with resistance breeding. For instance, deploying varietal mixtures has been shown to slow down the breakdown of resistance in cereals by reducing uniform selection pressure on pathogen populations (Yazdani *et al*., 2025). Such approaches ensure that resistance remains durable while supporting ecosystem resilience.

FUTURE PERSPECTIVES

Role of Omics and Advanced Phenotyping

Breeding and resistance are being transformed by advances in genomics, transcriptomics proteomics and metabolomics. Such omics technologies can be used to identify host resistance genes and regulatory networks in response to both biotic and abiotic stresses, and how host-pathogen interactions occur (Naqvi *et al*., 2024), these regulatory networks often map onto signaling pathways such as those depicted in Figure 2. The combination of the multi-omics data can help in more specific selecting and decrease the time of resilient cultivar development (Haidar *et al*., 2024). Artificial intelligence and high-throughput imaging High-throughput phenotyping (HTP) increases breeding efficiency. LiDAR, hyperspectral, and thermal-sensing platforms may be used to assess disease symptoms, canopy structure, and stress response within both real-world and experimental settings (Cembrowska-Lech *et al*., 2023). These tools, when combined with genomic information, have the potential to fill the genotype-phenotype gap and increase accuracy of predicting complex traits related to resistance (Nguyen *et al*., 2023).

Recent advancements emphasize the increasing utilization of AI and ML in resistance breeding. Several simulation tools have been developed in recent years, which were not available at the beginning of genomic selection. For instance, using deep learning models trained on hyperspectral and phenotypic datasets for wheat and rice has significantly improved the prediction of disease resistance over traditional methods. Combining omics, phenotyping, and AI is reducing breeding cycle time and increasing prediction efficiency (Ma *et al*., 2025; Farooq *et al*., 2024).

Advances in Pathogen Detection Technologies

It is important to identify the pathogens early and correctly to manage the pathogens. By using metagenomics, it became possible to recognize known as well as unknown pathogens in one sample at a time and without the prior hypothesis regarding a sample by using next-generation sequencing (Jabran *et al*., 2024). The introduction of nano-based biosensors and Raman spectroscopy into agricultural supply chain is being developed to provide real-time monitoring of diseases (Oon *et al*., 2023; Bhowmik *et al*., 2025). Using lightweight diagnostics, like loop-mediated isothermal amplification (LAMP) microchips, which are quick, sensitive, and can be performed on-site, can aid in the deployment of these kinds of diagnostics in low resource settings (Yadav and Yadav, 2025). New approaches will also be used wastewater surveillance to monitor community pathogens and bacteriophage-sensor solutions to detect plant pathogens in a short period (Panhwar *et al*., 2023). Early detection and intervention can be done with the help of these technologies, minimizing economic losses and inhibited pathogen spread.

Continuous genomic surveillance networks are increasingly important. By combining real-time metagenomics with global data-sharing platforms, outbreaks of rust fungi and viral pathogens can now be predicted with higher accuracy (Lappan *et al*., 2024). This integration allows resistance breeding programs to anticipate pathogen shifts rather than react after resistance breakdown.

International Collaboration and Germplasm Exchange

International collaboration is crucial for management of emerging plant pathogens. Plant disease diagnostic networks, genomic surveillance networks, and germplasm exchange networks allow the rapid distribution of resistant varieties across countries (Engels *et al*., 2024; Islam, 2024). Collaboration networks in breeding-networks with open access, resistance breeding can be accelerated more speedily than in other breeding networks, as seen in cases like those facilitated by CGIAR. Nonetheless, some issues persist, which include phytosanitary limitations, intellectual property rights, and inconsistent diagnostic practices (Jha *et al*., 2023).

Recent collaborative initiatives emphasize not only germplasm exchange but also open-access breeding databases that integrate multi-omics and phenotypic data globally (Lappan *et al*., 2024). Such platforms allow breeders in resource-poor regions to access advanced tools and materials, increasing equity in resistance breeding.

Policy Support and Public–Private Partnerships

The regulatory frameworks must be in tandem with technological innovations. Genome edited crops, specifically through cisgenesis or precision editing technologies, should be assessed at science-based, proportionate regulations to prevent the occurrence of unjust delays (Dowd-Uribe *et al*., 2023). A clear policy definition between conventional GM crops and targeted genome edits will lead to increased levels of trust and adoption. Partnerships between the public and private sectors can help deploy research innovations. According to Van Asseldonk *et al*. (2023) Public-private partnerships can align the incentive of both the public research organizations and the seed companies, thus enabling faster access to resistant varieties by growers especially smallholders. Partnerships between varieties that address the environmental and market needs of the specific locality of the technology are needed (Zuberi *et al*., 2023). Many recent PPP initiatives have enhanced the delivery of resistant cultivars in Africa and South Asia by linking CGIAR centers with regional seed companies (Yazdani *et al*., 2025). Such partnerships illustrate how innovative pipelines can align with local agroecological and market opportunities.

CONCLUSION

Emerging plant pathogens threaten global food security due to changing climatic conditions, rapid globalization and intensification of agriculture. The rapid evolution of plant pathogens is overcoming host resistance in a few cropping seasons. Therefore, it is essential to have resilient breeding methods. Development of resistant breeding techniques is critical in sustainable disease management. Modern molecular breeding techniques such as genomic selection, genome editing and use of wild relatives in breeding have provided more tools for sustainable breeding. Combining these modern tools with standard breeding techniques enables development of durable resistance providing high yield and quality traits. Resistant breeding with integrated pest management techniques enforced with early warning systems and agroecology provides even better durability in breeding. However, challenges persist in such breeding approaches are balancing desired resistant traits with yield and quality traits, regulatory hurdles of genetically modified crops and consumer perception of genetically modified crops. To overcome these challenges, it is necessary to develop specific policies, develop public private partnerships and open communications for building trust and acceptance. Besides that, rapid pathogen detection, use of omics technologies and novel phenotyping techniques should be used to control emerging plant pathogens. following these management approaches, plant breeders, pathologists and policymakers can keep pace with emerging plant pathogens and protect global food security.

AUTHOR CONTRIBUTIONS

All authors contributed to the conception and design of the study. Data collection, and literature review were mainly performed by Jabir Asghar, Ameer Jan, Muhammad Hamayun, Khatir Ali, Atiq u Rehman, Mushtaq Ahmed, Izaz Ullah, Abdul Basit, and Shaikh Saddam. The first draft of the manuscript was prepared by Jabir Asghar, and all authors contributed to manuscript revision. Jabir Asghar and Ameer Jan were responsible for formal analysis and visualization. Critical revisions, validation, and editing were provided by Muhammad Hamayun, Khatir Ali, Atiq u Rehman, Mushtaq Ahmed, Izaz Ullah, Abdul Basit, and Shaikh Saddam. All authors read and approved the final manuscript.

CONFLICT OF INTEREST

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

ACKNOWLEDGEMENTS

We are grateful to Vice Chancellor Prof. Dr. Mumtaz Baloch University of Makran, Panjgur for Encouraging and Supporting in this Scientific write up.

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