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Review Article

Decoding Late Blight of Potato and Tomato: Insights into Pathogen Dynamics, Host Interactions and Emerging Solutions

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Abstract: The oomycete *Phytophthora infestans* is the source of late blight, a devastating disease that significantly impacts on tomato and potato cultivation worldwide, threatening food security and causing considerable economic losses. This review explores the epidemiological dynamics of late blight, focusing on the pathogen's life cycle, reproductive strategies, and molecular pathogenesis. Traditional management strategies, including cultural practices, host resistance, and biocontrol agents, are discussed alongside emerging sustainable technologies. Recent advancements such as CRISPR-Cas9 genome editing, RNAi (RNA interference), MAS (Marker-Assisted Selection), and biopesticides offer promising solutions to enhance resistance and reduce environmental impacts. IoT sensors and drones with thermal and multispectral imaging are highlighted for their role in real-time disease monitoring, along with the importance of integrating these tools with advanced forecasting models like BLITECAST and JHULSACAST for precision disease management. This comprehensive review offers insightful information about sustainable late blight management techniques, emphasizing the potential of combining innovative technologies with traditional practices to address this persistent agricultural challenge. It underscores the need for collaborative research, policy support, and continued investment in integrated approaches to ensure resilient potato and tomato cultivation in light of evolving threats.

Keywords: *Phytophthora infestans*, Molecular Pathogenesis, CRISPR-Cas9, RNAi, Marker-Assisted Selection, Forecasting Models

Introduction

Food security is a key component of the UN's 2030 Agenda for Sustainable Development, which acknowledges the pressing need for sustainable farming methods to satisfy the expanding world population (Ghufran *et al*., 2024). Among the various crops crucial to global nutrition and economic stability, potato (*Solanum tuberosum*) holds immense importance. A staple crop with a phenomenal growth rate, potatoes are farmed in more than 150 countries and offer vital nutrients, including vitamins B6 and C, dietary fiber, and minerals like potassium and copper (Lamichhane *et al*., 2024; Raigond *et al*., 2024). Potatoes are rich in health-promoting substances such as flavonoids, carotenoids, and polyphenols that enhance their antioxidant qualities (Bhutto *et al*., 2024).

Despite their significance, potatoes are very susceptible to destructive diseases, including late blight, as was experienced in past agricultural catastrophes such as the Irish Famine (Singh *et al*., 2023). Late blight induced by *Phytophthora infestans* is a highly virulent disease that spreads very rapidly in low temperatures and high humidity to destroy foliage in large areas, rot tubers, and, if not controlled, complete crop loss. Its economic global impact is significant, amounting to an estimated \$3 to \$5 billion annually in direct yield losses and the excessively costly fungicide treatment (Islam *et al*., 2021).

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In addition to potatoes, tomatoes (Solanum lycopersicum) are another crop that is of primary global significance and in high demand for their dietary value in the form of beta-carotene, lycopene, vitamin A, and vitamin C (Saffan *et al*., 2022). A global average annual production of almost to 177 million tons (Nkongho *et al*., 2023) makes tomatoes critical for both direct human consumption and industrial processing applications. However, tomato cultivation is also most vulnerable to late blight, adding to challenges in sustainable crop management (Lacaze *et al*., 2023).

Control of late blight needs excessive amounts of fungicides, posing risks such as environmental contamination, pathogen resistance, and human health concerns (Bouket *et al*., 2022). However, recent innovations in plant biotechnology, such as CRISPR-Cas9 (Angmo *et al*., 2023), RNAi (RNA interference) (Zhao *et al*., 2021), and MAS (marker-assisted selection) (Osei *et al*., 2019) transforming late blight management. Additionally, precision agriculture technologies, including Internet of Things (IoT)-based sensors and drones equipped with thermal and multispectral imaging, enable real-time monitoring and early detection of late blight (Mothapo *et al*., 2022; Sun *et al*., 2023). These tools, combined with advanced disease forecasting models, allow for targeted interventions, reducing fungicide dependency and mitigating environmental impacts (Narouei-Khandan *et al*., 2020).

This review seeks to explore the pathobiology of the devastating late blight disease, including the pathogen's life cycle and infection mechanisms, and to analyze the dynamics of disease outbreaks in relation to environmental factors. Additionally, it highlights innovative and sustainable management approaches aimed at reducing the consequences of late blight. By synthesizing current knowledge and identifying research gaps, the article seeks to support the development of effective and sustainable solutions to enhance global food security.

Agricultural and Economic Impact of Late Blight

Devastating plant diseases like late blight have serious negative effects on agriculture and the economy. The disease was first identified in the Andes of South America, and by the 1840s, it had spread to Europe and the US (Saville *et al*., 2016). The Irish Potato starvation (1845–1852), in which late blight resulted in severe crop failures, widespread starvation, and a sharp population drop, is most famously associated with its historical significance (Powderly, 2019). Although *P. infestans* was thought to have originated in the Andes, new study indicates that it actually started in central Mexico, from where it traveled around the world (Duan *et al*., 2021). Late blight epidemics continue to occur in Peru, the origin of both crops (Majeed *et al*., 2022).

The economic threat posed by late blight is immense, particularly to global tomato and potato production. It is one of the few plant diseases capable of completely destroying a crop, with losses reaching 100% in vulnerable cultivars. In addition to field crops, late blight also affects stored potatoes and tomatoes, causing rot and rendering them unsellable (Tsedaley, 2014). The disease thrives under conditions of high humidity and mild temperatures, spreading rapidly across fields and impacting large cultivation areas. This has made it a significant concern for regions heavily reliant on these crops, threatening food security and economic stability. Annual global losses resulting from late blight are estimated at $12 billion, with developing nations bearing approximately $10 billion of this burden (Haverkort *et al*., 2009). In Bangladesh, annual losses of potato yield from late blight range from 25 to 57% (Kessel *et al*., 2017), encouraging the adoption of decision support services such as GEOPOTATO that act to inform on the timing of fungicide applications to improve disease control and economic recovery. Moreover, a study conducted in Bangladesh from 2019 to 2021 showed that combining biological agents with the decreased use of fungicides controlled late blight and raised farmers' incomes by 7.19 and 10.98% per hectare (Islam *et al*., 2022). Late blight has been reported to reduce potato production by 5 to 90% in India, depending on climate conditions, with 15% loss per annum (mean) across the country (Lal *et al*., 2018). These region strategies show the importance of targeted approaches in mitigating the negative economic impact of late blight for both.

Geographical Distribution of Late Blight

P. infestans originated in Central and South America. Historical documentation suggests that the pathogen has been endemic to the Andes for an extensive duration & was acknowledged by indigenous populations (Austin Bourke, 1964). Mexico is esteemed as a focal point of pathogen diversity, and it was in this area that the sexual phase of the pathogen was first described. The pathogen disseminated from Mexico, culminating in outbreaks within the United States throughout the 20th century (Fry *et al*., 2015).

Potatoes and tomatoes are geographically distributed across all continents. In Africa, they can be found in countries such as Cameroon, Egypt, Kenya, Nigeria, South Africa, and Ethiopia. In Asia, notable examples include China, India, Iran, Bangladesh, and Thailand. In Oceania, they are present in Australia, New Zealand, and Papua New Guinea. In Europe, these crops are cultivated in countries like France, Germany, Spain, and the United

Kingdom. In Central America and the West Indies, they are found in Costa Rica, Cuba, and the United States. Finally, in South America, they are grown in Argentina, Brazil, Colombia, and Peru (Arora *et al.*, 2014; Cooke *et al.*, 2012). A shared ancestor between groups of pathogens and hosts, first proposed in the 19th century soon after the Irish potato famine (de Bary 1876), has been supported by recent DNA evaluations and isozyme, and by the pathogenicity resemblance between *P. infestans* isolates from Peru, the US, and Europe (Nowicki *et al.*, 2012). CAB International (Anonymous, 2003) catalogued 122 nations where late blight was documented (Fig. 1), yet it undoubtedly manifested in additional countries without formal records.

Phytophthora Infestans as the Cause of Late Blight

In 1845, Montagne identified *Botrytis infestans* as the late blight pathogen, but De Bary reclassified them as *P. infestans* in 1846 (Ifeduba and Kwon-Ndung, 2021). The term "*Phytophthora*" derived from Greek, meaning "plant destroyer" (Rhouma *et al.*, 2024). Morphologically, *P. infestans* shows closer relations to brown algae than true fungi. It is characterized by a hyaline, coenocytic mycelium that is widely branched, with hyphae generally wider and growing more slowly than typical fungi. Unlike most fungi, *Phytophthora* species are diploid, a key feature that sets them apart (Chen *et al.*, 2009). Combined with their unique cell wall composition, primarily cellulose and glucan rather than chitin, this further distinguishes them from true fungi (Rhouma *et al.*, 2024).

P. infestans is considered as a hemibiotroph as it initially grows in a biotrophic phase, feeding on living host tissue, followed by a necrotrophic phase, killing the host tissue to spread and propagate (Perfect and Green, 2001). The pathogen affects a diverse array of plant tissues, including fruit, tubers, herbaceous stems, roots, foliage, and even woody trunks. Taxonomically, it belongs to the Kingdom Chromista, Order Peronosporales, and Phylum Oomycota, which places it in a distinct taxonomic group from true fungi. The genus *Phytophthora* includes around 60 species, some of which are significant pathogens of other plants.

These include *P. cactorum*, a major apple pathogen; *P. capsicum*, which affects peppers; *P. citrophthora*, known for infecting citrus plants; and *P. cinnamomi*, a pathogen that impacts many woody plants, including conifers (Lamichhane *et al.*, 2024).

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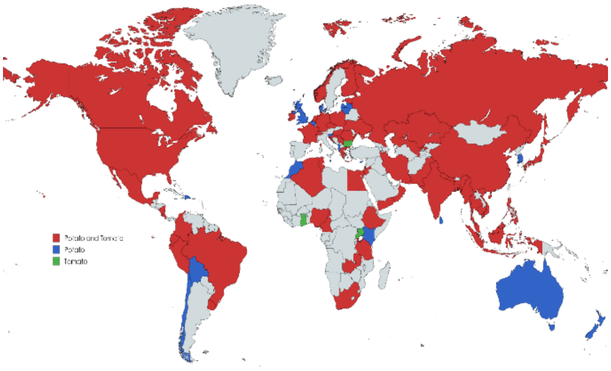

Fig. 1: Geographical distribution map of late blight affecting potatoes and tomatoes. (Red indicates regions where both potatoes and tomatoes are infected; Blue represents areas where only potatoes are infected; Green signifies regions where only tomatoes are infected)

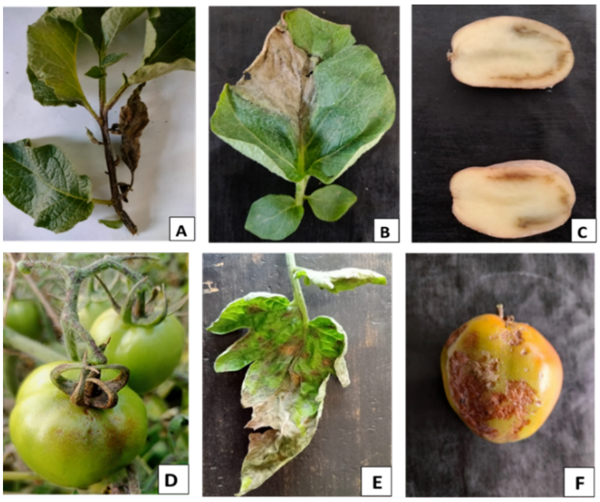

Fig. 2: Symptoms of late blight on various parts of potato and tomato plants. (A) Infected potato foliage, (B) Infected potato leaf and (C) Infected potato tuber; (D) Infected tomato fruit-bearing stem, (E) Spreading black lesions develop on tomato leaves and (F) Fruits of tomato become brown in appearance

Life Cycle and Reproductive Strategies of Phytophthora Infestans

P. infestans reproduces through both asexual and sexual mechanisms, with asexual reproduction being the dominant mode under most conditions. Asexual reproduction involves the production of distinctive, lemon-shaped sporangia formed at the tips of branched sporangiophores (Fig. 3) (Rhouma *et al.*, 2024). These sporangia can either release motile zoospores or germinate directly to produce infection hyphae. A key identifying feature of *P. infestans* sporangia is their papillate structure, which facilitates pathogen identification (Al-Adhaileh *et al.*, 2023). Morphological variability has been observed in different regions, such as Cameroon, where sporangial forms include ellipsoid, pip-shaped, and lemoniform structures (Mugao, 2023).

Sporangia typically measure 60.5 µm in length and 31.7 µm in width, contributing to the white, fluffy appearance of the mycelium (Shimelash and Dessie, 2020). Under optimal environmental conditions, such as temperatures ranging from 20 to 25°C and adequate nutrient availability, sporangia can germinate directly to infect host plants. Conversely, less favorable conditions, including temperatures between 10°C and 15°C or limited nutrients, trigger the release of biflagellate zoospores. These motile zoospores are dispersed by wind and can encyst on the surface of host plants, initiating infection & completing the asexual cycle (Schiffer-Forsyth *et al.*, 2023). The rapidity of this cycle enables *P. infestans* to effectively colonize large areas under favorable conditions (Fig. 4).

Sexual reproduction in *P. infestans* occurs through the formation of oospores, which are generated in the presence of compatible mating types, 1 and A2. This heterothallic interaction is essential for oospore production (Tsedaley *et al.*, 2014). Oospores serve as a vital survival mechanism, enabling the pathogen to persist between growing seasons. Their thick, resistant walls allow them to endure harsh environmental conditions, including extended periods in soil.

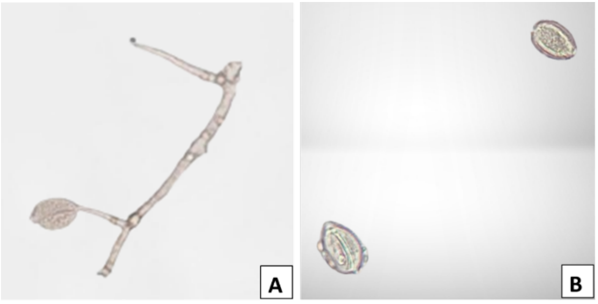

Fig. 3: Microscopic view of *Phytophthora infestans* A) Sporangia on sporangiophores (B) Limoniform sporangia

However, they are sensitive to extreme heat, such as temperatures of 40°C sustained for 12 hours (Liang *et al.*, 2020). Upon germination, oospores produce sporangia that release zoospores, restarting the infection cycle. This dual capacity for sexual and asexual reproduction enhances the pathogen's adaptability to varying environmental conditions, ensuring its survival and spread (Tsedaley *et al.*, 2014). Environmental factors significantly affect the life cycle of *P. infestans* (Fig. 4). For instance, moist and temperate conditions promote zoospore development within two hours of sporangial formation. These motile zoospores utilize their biflagellate structure to locate and infect host plants, leading to rapid disease progression. In highly susceptible potato or tomato crops, complete wilting of the leaf canopy can occur within a week (Giachero *et al.*, 2022; Rhouma *et al.*, 2016; Schiffer-Forsyth *et al.*, 2023). Sporangia are typically discharged during morning hours when temperatures rise, and humidity decreases, allowing them to spread across significant distances. However, their viability is compromised by desiccation and sunlight exposure.

Infected plant materials, such as discarded tubers or tomato fruits, act as sources of inoculum between cropping seasons. Proper management of these materials is crucial to reducing reinfection risks. The mycelium of *P. infestans* can persist in infected tubers, initiating new infection cycles in the spring when sporangia form on these tubers or on volunteer plants (Srisawad *et al.*, 2023). Integrated disease management approaches, including rotation of rotation, environmental monitoring, and the removal of infected plant debris, are essential for controlling the spread of this pathogen (Dufková *et al.*, 2021).

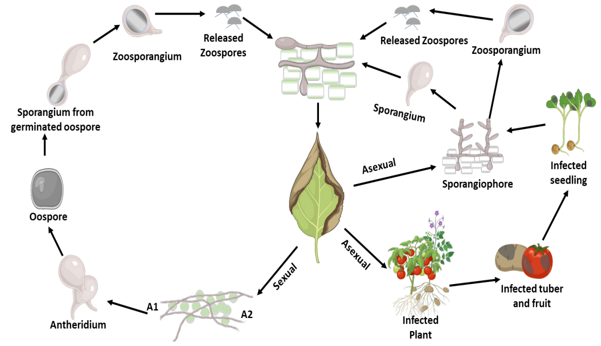

Fig. 4: Life cycle of *Phytophthora infestans*, illustrating key stages from spore release to plant infection. The diagram shows the formation of sporangia (top left), zoospore release (top center), germination and infection (center), colonization of plant tissues (bottom left), and eventual damage to the crops of tomatoes and potatoes (bottom right). The sequence demonstrates how quickly the disease spreads in favorable environmental circumstances

Population Structure of Phytophthora Infestans

P. infestans has a complex population structure influenced by its historical spread, genetic diversity, and migration patterns (Table 1). The population dynamics were profoundly influenced by the uncovering of the A2 mating type in Mexico, first reported outside its native range in Switzerland in 1981 (Dyer *et al.*, 1993). Genetic studies confirm that the global dissemination of A2 isolates in the 1980s was not a result of local evolution but rather international migration, emphasizing the need for stringent global biosecurity protocols (Goodwin and Drenth, 1997).

Table 1: Global distribution and year of revelation of *Phytophthora infestans* strains, types, and races

Country	Types, strains, or race	References
Mexico	A1 and A2	Dyer *et al.* (1993)
United States	US-1, US-6, US-7, US-8,	Goodwin *et al.* (1994)
	US-21, US-22, US-23 and US-24	Deahl *et al.* (2012)
Canada	US-22, US-23 and US-24	Danies *et al.* (2013)
Ecuador	US-1 and EC-1	Forbes *et al.* (1997)
Brazil	US-1 and BR-1	Maziero *et al.* (2009)
Ireland	HERB-1	Yoshida *et al.* (2013)
	5_A1and 8_A1	Cooke *et al.* (2012)
	13_A1, 5_A1, 6_A1and 8_A1	Rhouma *et al.* (2024)
Great Britain and Ireland	6_A1	Cooke *et al.* (2012)
Britain, Netherlands, and France	EU13_A2, US-22, US-23, and US-24	Khalid Naveed *et al.* (2017)
Netherlands	NL-003 to NL-008, NL00-1, NL-002, EU13_A2	Rajputt *et al.* (2017)
Malawi, Burundi, Mozambique, Kenya, Uganda, South Africa and Tanzania	US-1.1 to US-1.11	Rajputt *et al.* (2017)
Kenya and Rwanda	KE-1	Pule *et al.* (2013)
East Africa	EU13-A2 and KE-1	Rajputt *et al.* (2017)
Japan	JP-3 and JP-4	Akino *et al.* (2014)
Korea	KR-1	Choi *et al.* (2020)
Taiwan	US-1.1, US-1.2, US-1.3 and US-1.4 US11 and TW-1	Chen *et al.* (2009)
China	SG-1, US-1, SIB-1, and EU-13	Guo *et al.* (2010)
India	13_A2-1, 13_A2-3a,13_A2-3b, and 13_A2 3c	Rajputt *et al.* (2017)

The coexistence of A1 and A2 mating types in various regions has raised concerns about the potential for sexual reproduction, leading to the creation of oospores and isolates with novel genetic traits. Reports of oospore production have been documented in North America and Europe, although controlled experiments in Japan did not yield progeny production under artificial conditions (Kato *et al*., 1993). These findings highlight the variability in reproductive success across different environmental contexts.

Recent surveys reveal alarming trends in *P. infestans* population dynamics. Between 2009 and 2011, multiple mating types such as US-8, US-21, US-22, US-23, and US-24 were identified in the Midwestern and Eastern United States (Deahl *et al*., 2012). In Ireland, the previously dominant 13_A2 genotype saw a significant decline in 2011, replaced by genotypes 5_A1 and 8_A1, while the 6_A1 genotype gained prevalence in the United Kingdom (Cooke *et al*., 2012). In China, a unique coexistence of native genotypes with SIB-1 (JP-2) and the globally dominant US-1 strain was observed between 1998 and 2006 (Guo *et al*., 2010). Similarly, Taiwan's potato crops have been found to harbor the US-11 genotype (Chen *et al*., 2018). The rate of SIB-1 in eastern Russia and its potential for cross-border migration further underscore the dynamic nature of *P. infestans* populations (Guo *et al*., 2010).

Strains of *P. infestans* exhibit varying levels of virulence, with some strains being more aggressive and capable of overcoming host resistance more effectively. This variability is partly driven by genetic diversity, including clonal lineages and different mating types. These genetic differences affect the pathogen's virulence, competence to cause significant damage, and ability to resist control measures, such as fungicides. Some strains can develop resistance through evolutionary processes. Although control strategies-including fungicide rotation, planting resistant cultivars, and implementing cultural methods like crop rotation-are employed, they may be ineffective owing to the appearance of more virulent strains (Ludwiczewska *et al.*, 2025).

Epidemiological Dynamics and Environmental Influences

The development and spread of *P. infestans* are highly dependent on specific temperature and humidity conditions. Sporulation occurs when relative humidity exceeds 90%) (Fig.5), leading to the formation of sporangia on the undersides of leaves and infected stems, which facilitates reinfection cycles (Beninal *et al.*, 2022). The mechanism of sporangial germination is influenced by temperature; at temperatures between 21°C and 26°C, germination occurs directly through the formation of a germ tube, bypassing the zoospore stage. In contrast, at temperatures below 18°C (65°F), 6 to 8 motile zoospores are released, which require water for movement and infection (Srisawad *et al.*, 2023). The pathogen remains active within a temperature range of 3 to 26°C, although sporulation is most efficient between 18 and 22°C (64 to 72°F (Cray *et al.*, 2016).

Prolonged wet conditions, such as rain or fog, combined with alternating cool nights and warm days, create ideal environments for disease outbreaks. These conditions can rapidly devastate entire potato fields within two weeks (Giachero *et al.*, 2022). High precipitation and low temperatures exacerbate the severity of late blight by promoting sporangial dispersal and infection cycles (Bhardwaj *et al.*, 2019). Recent climate modeling studies project shifts in the geographic distribution of late blight outbreaks due to warming temperatures, which will impact sporulation and zoospore release mechanisms that depend on temperature (Hossain *et al.*, 2024).

The disease typically begins in early January under cool, foggy conditions, with various races of the pathogen predominantly found in the northern part of Bangladesh (Dey *et al.*, 2010). Late blight has been recorded in India since the late 19th century, with severe outbreaks documented in potato and tomato crops. Notably, a major epidemic in 2014 in West Bengal caused significant crop losses and socioeconomic distress among farmers (Guha Roy *et al.*, 2021). In the United States, specific clonal lineages of the pathogen, such as US-23, responsible for late blight outbreaks, have been linked to the introduction of infected seed potatoes in states like Florida (Donahoo and Roberts, 2013). Baker *et al.* (2004) noted a probability of high late blight risk being greater in the U.S. upper Great Lakes region based on 1948 to 1999 climatic data. Also in Finland, 20th century documents showed higher spring (April and May), modestly warmer summers (June–August), temperatures and smaller diurnal temperature range (Tuomenvirta and Heino, 1996; Tuomenvirta *et al.*, 2000; Tuomenvirta, 2004) also, particularly since 1980. In northern Europe and Finland, it has been attributed to an increase in cloud cover and a strengthening of the westerly flow (Tuomenvirta *et al.*, 2000).

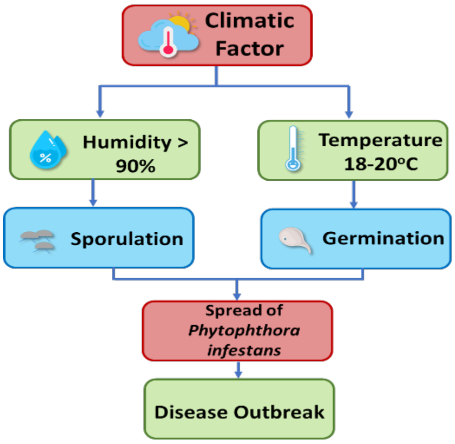

Fig. 5: Epidemiological dynamics and environmental influences on potato and tomato late blight

These climate changes may provide more favorable early season situation to potato growth, but they also provide more conditions that contribute to late blight disease. Model simulations have also indicated that in southern Finland, 10–20 days longer management time could be required to protect potato foliage against late blight, with a 1°C increase in the average temperature during the growing season, especially if soil-borne inoculum is low (Kaukoranta, 1996).

The risk of late blight extends beyond the field to storage facilities. Infected tubers and tomato fruits under high-moisture conditions provide a conducive environment for spore growth. Condensation on tuber surfaces facilitates sporangial production, contaminating adjacent tubers and triggering secondary infections, including soft rot caused by bacteria (Rogozina *et al.*, 2023).

Molecular Pathogenesis of Phytophthora Infestans

P. infestans has developed to circumvent PAMP-Triggered Immunity (PTI) by secreting effector molecules that suppress plant defenses (Fig. 6). During the biotrophic phase, *P. infestans* suppresses host immune responses and apoptosis while developing haustoria or hyphae inside viable plant cells (Koeck *et al.*, 2011). The pathogen releases a wide array of effectors, toxins like necrosis-inducing NLPs, and CWDEs, including glycosyl hydrolases, to facilitate host membrane damage and invasion. *P. infestans* secrets two kinds of effectors; intracellular (cytoplasmic) and extracellular (apoplastic) (Wang *et al.*, 2017). Key extracellular effectors include protease inhibitors such as EPI1, EPI10, EPIC1, and EPIC2B, which inhibit host defensive proteases like Rcr3pim (Song *et al.*, 2009). Intracellular effectors, particularly RXLR and CRN proteins, are critical in manipulating host immunity. RXLR effectors (Table 2) are secreted from haustoria and recognized by plant resistance proteins, triggering effector-triggered immunity (ETI). These effectors have an N-terminal RXLR-dEER motif for targeting and secretion and a flexible C-terminal domain essential for their function (Van den Ackerveken, 2017). RXLR effectors like AVR3a and AVRblb2 act as avirulence factors recognized by R genes, initiating hypersensitive responses and programmed cell death. Host plants recognize PAMPs through surface-localized receptor kinases or receptor-like proteins, forming the first line of defense (Zipfel, 2014). PTI responses include ROS production, calcium ion signaling, MAPK activation, and defense gene transcription (Boller and Felix, 2009). R proteins, encoded by R genes, provide a secondary recognition mechanism against infections by detecting effectors directly, indirectly, or via decoy pathways (van der Hoorn and Kamoun, 2008). These proteins activate immune signaling through conserved domains such as NBS, TIR, or CC (Takken and Goverse, 2012). MAPK cascades are pivotal in host defense, mediating phosphorylation events that regulate transcription factors and enzymes responsible for ROS production (Murphy *et al*., 2018).

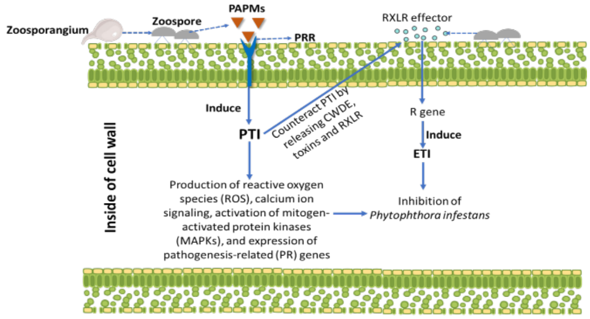

Fig. 6: Molecular pathogenesis of *Phytophthora infestans*. After sporangium encysted, zoospores were discharged and germinated. Host PRRs recognize the PAMPs released by *P. infestans*, which results in PAMP-triggered immunity. Toxins, RXLR, and CWDE are secreted by *P. infestans* to decrease PTI. ETI is triggered by certain RXLR effectors identified by the host resistance (R) gene

Sustainable Methods for Managing Late Blight

To effectively control late blight, a multimodal approach is essential. This strategy comprises three key components: the use of strategic chemical and biological controls, the cultivation of resistant plant varieties, and the adaptation of cultural practices. Furthermore, forecasting tools are available that aim to predict the optimal weather conditions for the pathogen, helping to determine the best timing for fungicide applications in the fields.

Cultural Practices

Cultural practices are a cornerstone of integrated disease management for late blight control in potato and tomato production. By preventing the establishment of *P. infestans*, cultural techniques play a crucial role in mitigating disease incidence and minimizing crop losses (Schiffer-Forsyth *et al*., 2023; Ivanov *et al*., 2021). Among the most effective strategies is the use of disease-free seed tubers, which significantly reduces the introduction of pathogens into fields (Ivanov *et al*., 2021). Additionally, preventing the accumulation of inoculum from nearby potato cull heaps or infected tomato transplants is vital for controlling late blight. Such cultural management practices focus on limiting inoculum introduction and reducing its buildup in the environment (Nowicki *et al*., 2013). Several key cultural practices are commonly employed to manage late blight. Crop rotation and the implementation of fallow periods can help minimize the prevalence of *P. infestans* by breaking the pathogen's lifecycle and limiting its buildup in soil. Removing volunteer potato and tomato plants that may harbor the pathogen further diminishes inoculum sources (Giachero *et al*., 2022). The management of cull piles is particularly crucial, as mycelia of *P. infestans* can persist in these heaps over winter and release large quantities of airborne spores at the start of the growing season, increasing the likelihood of disease outbreaks in subsequent crops. By removing infected plants and tubers, farmers reduce the potential for inoculum spread. Moreover, proper harvesting and storage techniques that regulate temperature and humidity also help limit pathogen survival and reproduction (Ivanov *et al*., 2021).

In addition to removing infected material, maintaining strong soil coverage helps shield tubers from soil-borne inoculum, while drip irrigation and other optimized watering practices help reduce conditions conducive to infection (Schiffer-Forsyth *et al*., 2023). Adequate plant nutrition is also critical, as a balanced diet can bolster the plant's natural defenses against the disease (Giachero *et al*., 2022). Weed control is another important aspect, ensuring that fungicide coverage remains effective and preventing the formation of microclimates that favor the spread of *P. infestans* (Ivanov *et al*., 2021).

Aligning row orientation with prevailing winds can facilitate the drying of foliage, further reducing the risk of infection. Regular monitoring of stored potatoes allows for early detection of disease and the removal of contaminated tubers, preventing the spread of the pathogen (Giachero *et al*., 2022). Innovative cultural practices, such as intercropping, have also shown promise in controlling late blight. For example, in the central highlands of Ethiopia, a 3:1 intercropping arrangement of garlic and potatoes (75% garlic and 25% potato) reduced the growth of *P. infestans* and enhanced potato yield (Kassa and Sommartya, 2006). This practice suggests that specific intercropping techniques could provide additional disease suppression benefits, especially in elevated environments. The physical presence of the non-host crop, such as garlic, might act as a "bio-barrier," limiting pathogen spread via wind and precipitation and reducing the amount of inoculum available to infect potato plants. Additionally, the "dilution effect" of non-host plants might lower the pathogen concentration, further reducing transmission and preventing localized outbreaks or focused epidemics (Skelsey *et al.*, 2005). These findings highlight the potential of integrating diverse cultural practices to complement traditional disease management strategies and improve the sustainability of potato and tomato production systems.

Table 2: *Phytophthora infestans* genes encoding RxLR effectors and their functions in potato and tomato

Effectors	Function	References
**Avr1*	Involved in the recognition of the host resistance responses	van der Lee *et al.* (2001)
Avr2	Contributes to suppressing host resistance	Aguilera-Galvez *et al.* (2020)
Avr3a	Plays a crucial part in virulence and immune evasion	Armstrong *et al.* (2005)
Avr3b	Interferes with the host's defense mechanisms, especially defense signaling pathways	Rietman *et al.* (2012)
Avr4	Implicated in virulence by suppressing or manipulating plant defense	Van Poppel *et al.* (2008)
Avr8	Participating in virulence and suppression of host immunity	Vossen *et al.* (2016)
Avrblb1	Contributes to host defense recognition	Song *et al.* (2003)
Avrblb2	Contributes to host defense recognition	van der Vossen *et al.* (2005)
Avrvnt1	Modulates virulence for infection success	Pais *et al.* (2018)
AvrSmira1	Targets specific host defense components to promote virulence	Rietman *et al.* (2012)
AvrSmira2	Possible involvement in the evasion of host immunity	
Avrchc1.1	Allows *P. infestans* to evade detection	Monino-Lopez *et al.* (2021)
Avrchc1.2	Likely contributes to pathogen virulence or immune suppression	
Avramr1	Interferes with host immunity by targeting defense signaling pathways	Witek *et al.* (2021)
Avramr3	Enhances pathogen survival and infection	Lin *et al.* (2021)

Host Resistance

Cultivating resistant potato and tomato cultivars reduces the need for fungicide applications, which not only lowers production costs but also helps mitigate the environmental impacts of pesticide use (Enciso-Maldonado *et al.*, 2022). Additionally, utilizing resistant cultivars helps limit changes in the population dynamics of *P. infestans*, thus reducing the risk of the pathogen developing resistance to fungicides (Rogozina *et al.*, 2023).

Currently, over 20 potato late blight resistance genes have been successfully isolated, primarily from the CC-NBS-LRR gene family, including genes such as *R1*, *R2*, *R3a*, *R3b*, *Rpi-blb2*, *Rpi-blb3*, and others (Table 3). Incorporating these genes into cultivated varieties remains environmentally friendly methods for managing late blight (Szajko *et al.*, 2020).

Late blight resistance in cultivars ranges from moderate to high, with varieties suitable for both mountainous and plains regions. Notable resistant varieties include *Kufri Giriraj*, *K. Himalini*, *K. Shailja*, and *K. Himsona* for mountainous areas, and *K. Anand*, *K. Sutlej*, *K. Badshah*, and others for plains (Central Potato Research Institute). Additionally, advanced hybrids such as *Kufri Garima*, derived from the cross between PH/F-1045 and MS/82-638, exhibit enhanced resistance to late blight (Lal *et al.*, 2013a). Although *Rpi* genes are effective against *P. infestans*, their durability varies significantly. Some genes provide long-lasting immunity, while others can be quickly overcome by pathogen populations. The *Rpi-blb1* gene from *S. bulbocastanum* is considered one of the most durable due to its broad-spectrum resistance and conservation across the wild species in which it is found (van der Vossen *et al.*, 2005). In contrast, the resistance genes identified in *S. demissum*, such as *R1* and *R3a*, have proven to be vulnerable to the selection of adapted pathogens, leading to their classification as short-lived resistance options (Ballvora *et al.*, 2002; Huang *et al.*, 2004). Additionally, *Rpi-blb2* and *Rpi-blb3* provide resistance but are also susceptible to breakdown by certain strains of *P. infestans*. Therefore, gene pyramiding is essential to enhance durability (Lokossou *et al.*, 2009; van der Vossen *et al.*, 2005). Novel genes like *Rpi-edn2* (*R9a*) and *Rpi-hcb1.1* show promising resistance, but their long-term stability is still under evaluation (Keijzer *et al.*, 2022; Aguilera-Galvez *et al.*, 2020). Polygenic resistance, which involves multiple resistance genes such as *RGA2*, *RGA3*, *R3a*, and others, has shown considerable potential in providing more durable disease tolerance (Tiwari *et al.*, 2021).

Table 3: Resistance genes against *Phytophthora infestans* (*Rpi* genes) in wild potato and wild tomato relatives

Gene	Species	Durability of Resistance	References
Rpi-avl1	*S. avilesii*	Moderate	Verzaux (2010)
Rpi-ber1	*S. berthaultii*	Narrow-spectrum	Park *et al*. (2009)
Rpi-ber1.2		Narrow-spectrum	Monino-Lopez *et al*., (2021)
Rpi-blb1	*S. bulbocastanum*	Durable, broad-spectrum resistance	Naess *et al*. (2000)
Rpi-blb2		Durable	van der Vossen *et al*. (2005)
Rpi-blb3		High durability when stacked with *Rpi-blb1* or *blb2*	Lokossou *et al*. (2009)
Rpi-bt1		Moderate	Oosumi *et al*. (2009)
Rpi-cap1	*S. capsicibaccatum*	Moderate resistance	Verzaux *et al*. (2012)
Rpi-qum1	*S. circaeifolium* ssp. *quimense*	Durability unknown	
R1	*S. demissum*	Historically beneficial, but most contemporary races have overtaken	Ballvora *et al*. (2002)
R3a; R3b		*R3b* is moderately durable in pyramids, while *R3a* is frequently defeated	Huang *et al*. (2004)
R4^{al}; *R4*^{MA}		Weak durability	Van Poppel (2010)
R5		Race-specific	Huang (2005)
R6; R7		Limited durability	
R11; R10		Moderate durability	Bradshaw *et al*. (2006)
Rpi-edn1.1	*S. edinense*	Promising	Champouret (2010)
Rpi-edn2 (R9a) ^{a}		High potential for long-lasting resistance; broad spectrum	Keijzer *et al*. (2022)
Rpi-edn3		Unknown durability	Verzaux (2010)
Rpi-hjt1.1	*S. hjertingii*	Under evaluation	Champouret (2010)
Rpi-hcb1.1	*S. huancabambense*	Broad resistance	Aguilera-Galvez *et al*. (2020)
Novel Rpi gene(s)	*S. jamesii*	Resistant in laboratory settings	Zheng *et al*. (2020)
Rpi-mch1	*S. michoacanum*	Moderate durability	Śliwka *et al*. (2012b)
Rpi-nrs1	*S. neorossii*	Moderate durability	Jones *et al*. (2009)
Rpi-pcs	*S. paucissectum*	Unknown	Villamon *et al*. (2005)
Rpi-rzc1^{a}	*S. ruiz-ceballosii*	Promising	Śliwka *et al*. (2012a)
Rpi-snk1.1	*S. schenckii*	Limited use	Champouret, (2010)
Rpi-sto1^{a};	*S. stoloniferum*	Strong field resistance	Wang *et al*. (2008)
Rpi-sto2		Moderate resistance	Champouret (2010)
Rpi-pta2		Promising in conjunction with Rpi-blb2	Wang *et al*. (2008)
Rpi-tar1	*S. tarijense*	Race-specific	Haverkort *et al*. (2016)
Rpi-tar1.3		Broader effect	Monino-Lopez *et al*. (2021)
Rpi-Smira1	*S. tuberosum* cv. Sárpo Mira	Durable in EU trials	Rietman *et al*. (2012)
Novel Rpi gene(s)	*S. tuberosum* subsp. *andigena*	Potential for resistance breeding in the future	Duan *et al*., (2021)
Rpi-ver1	*S. verrucosum*	Broad-spectrum resistance	Chen *et al*. (2018)
***Ph-1*	*S. pimpinellifolium*	Efficient in the initial phases	Bonde and Murphy (1952)
Ph-2		Partial resistance	Gallegly and Marvel (1955)
Ph-3		Durable	Chunwongse *et al*. (2002)
Ph-5.1		Potential additive resistance	Merk and Foolad 2012; Nowicki *et al*. 2012
Ph-5.2		Investigation ongoing	

To date, five main race-specific resistance genes that provide varying levels of resistance against tomato *P. infestans* strains *Ph-1*, *Ph-2*, *Ph-3*, *Ph-4*, and *Ph-5* have been discovered within Solanum pimpinellifolium, a closely related red-fruited wild relative of tomato (Table 3). The resistance gene to *P. infestans* race 0 shows very little resistance to race 1, the current dominant race (Peirce, 1971). The other resistance gene, *Ph-2* which was first found in *S. pimpinellifolium* accession West Virginia 700 (Gallegly and Marvel, 1955), suppresses the development of the disease, but not resistant to *P. infestans* in all cases (Foolad *et al*., 2008).

The best characterized resistance gene is *Ph-3*, which was initially found in a L3708 (also shown as LA1269 and

PI365957), and which displays incomplete dominant resistance to several *P. infestans* isolates (Chunwongse *et al*., 2002). Until now, *Ph-3* has been the leading resistant gene against late blight in tomatoes and has been efficiently introgressed into several breeding lines and commercial hybrid varieties of both fresh-market and processing tomatoes in several breeding programs around the world. For example, fresh-market breeding lines such as NC1 CELBR (*Ph-2* + *Ph-3*) and NC2 CELBR (*Ph-2* + *Ph-3*), and hybrid cultivars such as Plum Regal (*Ph-3*), and Mountain Merit (*Ph-2* + *Ph-3*) have been developed through the North Carolina State Tomato Breeding Program (Gardner and Panthee, 2010; Panthee *et al*., 2015).

The gene *Ph-4* in *S. habrochaites* 'LA1033' has been proposed as a candidate region for quantitative trait locus (AVRDC, 1998; Lough, 2000). The *Ph-5* gene, identified in *S. pimpinellifolium* PI 270443, confers resistance to 7 race/species of the late blight pathogen (Foolad *et al*., 2008). Nevertheless, *Ph-5* is regulated by two loci, one on chromosome 1 (*Ph-5-1*) and another on chromosome 10 (*Ph-5-2*) (Merk and Foolad, 2012; Nowicki *et al*., 2012), which complicates its practical application.

However, introgression of other late blight resistance QTLs into cultivated tomato varieties is a labor-intensive task and several of them may even display undesirable characteristics (Brouwer *et al*., 2004). However, these QTLs may provide a more durable solution than that based on major resistance genes alone. To counter the threat to established *P. infestans* resistance genes due to the appearance of new strains (Stellingwerf *et al*., 2018), breeders are utilizing gene stacking approaches to stack more resistance genes together. This strategy increases the genetic barriers that the pathogen must overcome, as it requires mutations in several avirulence (Avr) loci for *P. infestans* to successfully evade this enhanced resistance.

Microbial Biocontrol

Microbial biocontrol is an important and sustainable strategy in managing the late blight disease of potato and tomato caused by *P. infestans*. For long-term disease control, it is essential to continue researching and developing alternative approaches, such as host resistance and biocontrol techniques. While *in vitro* studies help in understanding the mechanisms behind microbial biocontrol, translating these results to field applications remains a challenge. However, certain fungal species, such as *Trichoderma*, have demonstrated significant potential in combating late blight. *Trichoderma* spp., including *T. harzianum* and *T. asperellum*, exhibit various mechanisms, such as coiling around the pathogen and releasing enzymes, secondary metabolites, and toxins to inhibit pathogen growth (Kariuki *et al*., 2020). Notably, *T. harzianum* and *T. asperellum* have been shown to increase tomato plant growth by more than 30 and 19%, respectively, while also reducing late blight symptoms by up to 40% (Table 4) (Mollah and Hasan, 2023).

Despite their bioactive potential, bacterial and fungal Biocontrol Agents (BCAs) are not always effective under field conditions. For instance, *Trichodex*®, a commercial product containing *T. harzianum*, reduced *P. infestans* growth by 40% in vitro but had no significant effect on late blight in greenhouse and detached leaf tests (Stephan *et al*., 2005). This highlights the need for new selection techniques, possibly focusing on the synthesis of siderophores and biosurfactants, which may enhance in planta efficacy (Bailly and Weisskopf, 2017).

Other microorganisms also play a significant role in microbial biocontrol of late blight. The antagonistic oomycete *Pythium oligandrum*, for instance, demonstrates mycoparasitism by secreting enzymes that degrade cell walls and consuming various fungi and oomycetes for nutrition. Interestingly, this mycoparasitic behavior may have evolved through gene duplication and horizontal gene transfer, further supporting its effectiveness as a biocontrol agent (Liang *et al*., 2020). Numerous naturally occurring microorganisms, including *Penicillium aurantiogriseum*, *Myrothecium verrucaria*, *Acremonium strictum*, and various *Trichoderma* species, have also shown promising antagonistic effects (Lal *et al*., 2013b). In addition to fungi, bacteria such as *Bacillus*, *Pseudomonas*, and *Streptomyces* exhibit significant biocontrol properties. For example, *Bacillus* species inhibit the growth of *P. infestans*, while *Pseudomonas* species Produce Volatile Organic Compounds (VOCs) such as hydrogen cyanide and aldehydes, which contribute to disease suppression. Some *Pseudomonas* strains also generate cyclic lipopeptides that target the zoospores of *P. infestans* and compete for iron through siderophore production (Caulier *et al*., 2018). In vitro studies, along with molecular and genomic research, offer valuable insights into the mechanisms of BCAs. For example, research on *Pseudomonas* has identified specific genetic loci that control aggression toward *P. infestans*, paving the way for the development of hyper-aggressive strains for future applications (De Vrieze *et al*., 2020).

Moreover, understanding the evolutionary history of BCAs, such as the horizontal gene transfer events that enable *Pythium* spp. to acquire hyperparasitism, is crucial for the establishment of more effective biocontrol strategies (Caulier *et al*., 2018). An important strategy in the biocontrol of *P. infestans* is the degradation of the pathogen's cell wall, which is composed primarily of β-D-glucans and cellulose. Many BCAs secrete enzymes that break down these cell wall components, and combining such agents may offer greater efficacy in managing late blight (Liang *et al*., 2020).

Table 4: Microbial biocontrol agents and their role in late blight management

Agent	Effect	References
Trichoderma harzianum	40% less disease, and the release of cell wall-breaking enzymes	Chowdappa *et al*. (2013)
Trichoderma asperellum	Reduces late blight, enhances plant growth, and secretes secondary metabolites	Kariuki *et al*. (2020)
Pythium oligandrum	Exhibits mycoparasitism and produces cell wall-degrading enzymes	Liang *et al*. (2020)
Trichoderma viride	Inhibits growth through enzyme secretion and antagonistic interactions	Purwantisari *et al*. (2018)
Penicillium sp.	Demonstrates antagonistic effects	f *et al*. (1991)
Chaetomium brasilense	Generates cell wall degrading enzymes	Gupta *et al*. (2004)
Acremonium strictum	Inhibits pathogen growth	
Pseudomonas fluorescens	Produces volatile organic compounds (VOCs), cyclic lipopeptides, and siderophores to inhibit pathogen growth	Slininger *et al*. (2007)
Pseudomonas sp.	Secretes VOCs like hydrogen cyanide, produces bio-surfactants that impede *P. infestans* growth	Caulier *et al*. (2018)
Bacillus subtilis	Activates defense enzymes and reduces late blight	El-Naggar *et al*. (2016)
Streptomyces sp.	Secretes enzyme and competes for nutrients	Fu *et al*. (2022)
Aspergillus flavus	Behaves antagonistically with *P. infestans*	Lal *et al*. (2013b)
Aspergillus niger	Shows inhibitory effects on the proliferation of pathogen	

Furthermore, endophytic bacteria, which are naturally occurring antagonists in healthy plants, have shown promise in the biocontrol of late blight. For example, 2800 microorganisms resembling *Bacillus* and *Pseudomonas* were extracted from potato agroecosystems, and several of these strains significantly alleviated disease symptoms in greenhouse trials. One particular strain, *B. subtilis* 30B-B6, demonstrated effectiveness in a small-scale field trial (Caulier *et al*., 2018).

Regulatory approval is necessary to get from lab-scale promise to real-world implementation. The European Protection Agency (EPA) and the European Food Safety Authority (EFSA) conduct thorough evaluations, including risk assessments to determine impacts on human health, non-target organisms, and the environment, and efficacy tests to confirm their capacity to disease control like late blight. The agencies also assess environmental factors, e.g., persistence and mobility of microbial compounds and their capacity to disrupt ecological balance (EFSA, 2019). Upon approval, BCAs must undergo commercialization in the form of labeling with proper directions, compatibility with existing agricultural practice, and training of farmers on safe handling. Post-marketing surveillance is currently monitoring the long-term safety and effectiveness of these agents. With growing demand for sustainable management, microbial BCAs are highly promising as a substitute for chemical fungicide, provided they meet stringent regulatory standards (Ball, 2015).

When used as preventative measures, biocontrol agents like *Penicillium* sp., *T. viride*, *T. harzianum*, and *Chaetomium* sp. demonstrated promise against *P. infestans*; but, when used as curative measures, they were ineffective (Dey *et al*., 2010). While *P. infestans* was present on potato plants seven days before the antagonist was applied in the therapeutic procedure, a spore suspension of antagonists was sprayed on the plants 7 days before the *P. infestans* inoculation as a preventive step.

Fungicidal Application

Strategic fungicide application can contribute importantly to plant protection in situations of high disease-induced stress or when new races of pathogens are emerging (Ivanov *et al*., 2021). Fungicide use, ranging from early inorganic products such as Bordeaux mixture to advanced systemic fungicides such as Mandipropamid and Azoxystrobin, has been key in the management of late blight. Systemic fungicides like metalaxyl, mefenoxam, and newer chemicals inhibit pathogen growth through interference with essential metabolic processes, namely RNA polymerase-1 (Davidse *et al*., 1983). However, resistance to them has been induced at a very rapid pace in agricultural ecosystems.

Table 5: Chemical management strategies and fungicide efficacy against late blight of potato and tomato

Category	Fungicide/ Strategy	Mode of action/Effectiveness	Comparative Efficacy (Multi-season)	References
First Generation Fungicides	Copper sulfate, hydrated lime, water (Bordeaux mixture)	Inorganic fungicide; prevents infection and disease spread	Moderately effective in the early stages of infection	Ryley and Drenth (2024);
Systemic Fungicides	Metalaxyl (Ridomil 2E), Mefenoxam (Ridomil Gold EC)	Decreases sporulation and mycelial development within tissues by inhibiting RNA polymerase-1	High efficacy at first, but after several seasons of use, resistance development was observed	Gisi and Cohen (1996); Davidse *et al*. (1983)
	Dimethomorph, Propamocarb	Affects pathogen growth and reproduction	In both early and late stages, dimethomorph is effective; in all seasons, propamocarb provides moderate protection	Alvarez-Romero *et al*. (2024)
Contact Fungicides	Mancozeb, Chlorothalonil (Bravo), Mancozeb + Cymoxanil (Curzate)	Broad-spectrum protectants; inhibits spore germination and disease spread	In heavy rain, effectiveness decreases	Lal *et al*. (2018);
Novel Fungicides	Fenamidone	Target cytochrome bc1 in mitochondrial complex III; interferes with respiration	Under moderate disease pressure, efficacy was maintained for two to three growing seasons	Kamel *et al*. (2024)
	Cymoxanil	Block cytochrome bc1 in mitochondrial complex III from exchanging electrons	Better in mixes for year-round effectiveness	Mahajan *et al*. (2024)
	Ametoctradin (Initium)	Non-systemic fungicide; inhibits ATP synthesis by affecting mitochondrial respiration	High effectiveness over several seasons when used in combination or rotation	Jackson *et al*. (2024)
Fungicide Mixtures	Metalaxyl + Mancozeb (Ridomil MZ), Cymoxanil + Mancozeb, Dimethomorph + Mancozeb	Combines systemic and contact fungicides to broaden activity spectrum and slow resistance development	Remains highly effective for more than three seasons.	Lal *et al*. (2018)
Alternative Strategies	β-Aminobutyric acid (BABA), Phosphoric acid	SAR (Systemic Acquired Resistance) activators; induce plant defense genes (e.g., PR-1 protein, β-1,3 glucanase,)	Year-to-year variations in performance; integrated programs are more successful	Lal *et al*. (2018)
Micronutrients	ZnSO4, CuSO4, Ferric chloride, Ferrous ammonium sulfate	Inhibit pathogen growth and spore germination; delay disease onset when used with resistant cultivars	Only supplemental control	Bhat *et al*. (2007)
Spray Schedules	Mancozeb 75% WP, Cymoxanil 8% + Mancozeb 64% WP Dimethomorph 50% WP,	Scheduled prophylactic sprays followed by systemic fungicides effectively reduce terminal disease severity and yield loss	Following schedules results in a 30–40% increase in yield and a >60% decrease in disease in multi-season field experiments	Lal *et al*. (2017a)

Fungicide Efficacy Studies	Ametoctradin + Dimethomorph (w/w), Mandipropamid, Azoxystrobin	Efficient in combating novel *P. infestans* clonal lines (e.g., US-23, US-24)	Seasonally, Ametoctradin + Dimethomorph is quite successful	Seidl Johnson *et al.* (2015)
Environmental Concerns	Reduced fungicide use and EU delisting of products	Focus on integrated pest management (IPM), potato breeding, and forecasting models to reduce fungicide dependence	Long-term studies demonstrate that using integrated approaches reduces the use of fungicides by 40–50% while controlling disease	Fry (2007)
Prophylactic Strategies	Chlorothalonil, Mancozeb, or Dimethomorph mixtures	Preventative applications before disease onset followed by systemic fungicides for better control	Effective for several years when properly timed with disease predictions	Chakraborty and Mazumdar (2012)

Ofurace (Orafce 50WP), metalaxyl, and mancozeb (Ridomil MZ) have exhibited strong suppression of late blight (Lal *et al*., 2018). A newly formed fungicide, fenamidone, targets *P. infestans*' cytochrome bc1 in mitochondrial complex III. Similarly, cymoxanil-type fungicides block electron transfer in mitochondrial complex III (Mahajan *et al*., 2024). Dimethomorph and fenamidone proved to be the most potent in vitro treatments for late blight (Kamel *et al*., 2024). Systemic fungicides supplemented with prophylactic sprays significantly decrease disease intensity and delay resistance development (Lal *et al*., 2015). A new blend, dimethomorph (20.27% w/w) + ametoctradin (27%), was highly effective in controlling late blight of potatoes in studies carried out in India (Lal *et al*., 2017b). Initium (ametoctradin) targets specifically *P. infestans* by inhibiting mitochondrial complex III, which blocks ATP synthesis (Jackson *et al*., 2025). New molecular tools and fungicide classes, such as QiI fungicides such as ametoctradin, have been found to be effective in controlling resistant *P. infestans* populations (Jackson *et al*., 2025).

Comparative studies have evaluated fungicide efficacy over different seasons. Earlier studies showed metals such as metalaxyl and mancozeb to perform well initially but in the third or fourth consecutive growing season there was partial or total resistance, especially in dense fungicide-applied areas (Fry *et al*., 1993). Seidl Johnson *et al*. (2015) compared effectiveness of fungicides against three US clonal lines of *P. infestans* (US-22, US-23, US-24) in isolated tomato leaf tests. Preventive applications of these fungicides effectively managed late blight caused by novel *P. infestans* clonal lineages, with the US-24 lineage being managed by fewer applications of fungicides compared to US-23 or US-22. Field trials showed that combinations of fungicides, e.g., mandipropamid with cymoxanil or dimethomorph, were very effective in managing new clonal lineages, with disease severity reduced by over 80% (Alvarez-Romero *et al*., 2024). A seven-spray regimen of three sprays of Mandipropamid 23.4% SC and four sprays of Ametoctradin 27% + Dimethomorph 20.27% SC effectively managed late blight severity ($p < 0.05$) in India's North Eastern Himalayan region, increasing tuber yields from 21.58 t/ha to 21.86 t/ha with a BCR of ~1:1.97 (Dey *et al*., 2024). Field tests in Nepal between 2015–2016 showed Dimethomorph, Fenamidone + Mancozeb, and Mancozeb reduced AUDPC by up to 90, 68, and 47%, respectively, with significantly superior improvements in tuber yields compared to non-treated controls (Khadka *et al*., 2020).

Long-term fungicide efficacy was quantified using trials conducted in Europe and North America. Despite metalaxyl and mancozeb controlling late blight at first, repeated application led to resistance (Fry *et al*., 2015). West Bengal experiments indicated that control of late blight was best when a prophylactic spray of mancozeb (0.25%) was supplemented with dimethomorph+mancozeb or cymoxanil+mancozeb (0.3%) at early infection stage, followed by a supplemental mancozeb spray (0.25%) seven days post-systemic fungicide application (Chakraborty and Mazumdar, 2012). Victory 72 WP was launched in West Shoa in Ethiopia to fight fungicide resistance in potato and tomato (Amin *et al*., 2013). Studies showed that lower doses of systemic fungicides like Ridomil were economical without compromising efficacy (Tsedaley, 2014). Preventative mancozeb and chlorothalonil sprays followed by systemic fungicides were superior to post-symptomatic application (Lal *et al*., 2015). The result of a comparative trial of 12 fungicides with *P. infestans* clonal groups indicated that effective application of such fungicides in conventional and also organic crop management systems is feasible. Preventative sprays produced better control in contrast to curative sprays, where major focus was given to active management practices (Seidl Johnson *et al*., 2015).

P. infestans resistance to fungicides is a result of primary genetic mutations at the target location, allowing the pathogen to become tolerant to treatment. Quick emergence of metalaxyl-resistant isolates in Switzerland, Ireland, and the Netherlands has demonstrated *P. infestans*' ability to adapt rapidly (Gisi and Cohen, 1996). Resistance development is accelerated by excessive use of a single mode of action, which provokes increased selection pressure on the pathogen. Studies have demonstrated that metalaxyl-resistant isolates are more likely to produce oospores when subjected to fungicides, increasing further the cycles of resistance. New surveillance techniques revealed mutations in genes such as Cytochrome b and RNA polymerase I, responsible for lowered sensitivity to fungicides, showing the genetic nature of resistance mechanisms (Mahajan *et al*., 2024). Repeated application of the same mode of action fungicides induces selection for resistance strains, eventually reducing overall effectiveness. For example, resistance to traditional oomycete-targeting fungicides necessitated alternative mechanisms such as SDHI fungicides (fluopyram) (Kamel *et al*., 2024).

Fungicide resistance prevention involves integrating several management strategies. Preventative application of chlorothalonil and mancozeb followed by systemic or translaminar fungicides retarded the resistance more than curative spraying (Lal *et al*., 2015). A spraying programme beginning with mancozeb 75% WP (0.2%) before disease onset, followed by two sprays of dimethomorph 50% WP (0.2%) + mancozeb 75% WP (0.2%) at a gap of 7–10 days, recorded the lowest terminal severity of the disease (24.55%) and the maximum disease control (74.45%) (Lal *et al*., 2017a). Development of new fungicides such as QiI fungicides (ametoctradin) and SDHI fungicides (fluopyram) has facilitated resistance development ease to manage (Jackson *et al*., 2025). Genomic surveillance techniques now allow for real-time monitoring of resistance development, enhancing the precision of intervention methods (Mahajan *et al*., 2024). One of the most important ways to overcome resistance is fungicide rotation with different modes of action, and the use of fungicide mixtures. Blending mandipropamid with cymoxanil or dimethomorph has been effective in reducing disease severity and managing resistant *P. infestans* isolates (Alvarez-Romero *et al*., 2024) (Table 5). Integrated approaches incorporating new chemistries, resistant cultivars, and predictive modeling offer science-based solutions for sustainable late blight management.

Alternative Chemicals

Various alternative substances, aside from fungicides, have also been tested for their effectiveness in treating late blight in potatoes. Compounds such as $FeCl_3$, $NH_4Fe(SO_4)_2 \cdot 12H_2O$, and zinc sulphate at a concentration of 10 mM demonstrated complete inhibition of both growth and spore germination of *P. infestans*. In contrast, substances like $(NH_4)_2MoO_4$, $CuSO_4$, and $K_2S_2O_4$ at a concentration of 1 mM achieved only partial inhibition of growth and spore germination (Bhat *et al*., 2007).

The use of micronutrient-based foliar sprays, such as zinc sulphate and copper sulphate (0.2%), in combination with host resistance, delayed the onset of late blight by 12 days, subsequently reducing disease severity and improving yield. Additionally, combining a sub-phytotoxic dose of boron with lower rates of propineb + iprovalidicarb proved more proficient than fungicide-only treatments (Frenkel *et al*., 2010).

Systemic acquired resistance (SAR) activators, such as phosphorous acid and β-aminobutyric acid (BABA), have also shown promise in controlling late blight. These activators reduced disease severity by 40% to 60% and stimulated the upregulation of defense-related genes and *P. infestans* effector proteins, including β-1,3-glucanase, protease inhibitors, PR-1 proteins, thaumatin proteins, xyloglucanase, and others (Lal *et al*., 2018).

Several factors determine the effectiveness of induced resistance (IR) including the plant genotype, environmental conditions, and application methods (Sharma *et al*., 2010; Liljeroth *et al*., 2010) (Fig. 7); therefore, IR alone does not provide full protection. However, IR can contribute to total protection when included in other disease control methods. For instance, the use of BABA in conjunction with fungicides is known to reduce fungicide application by up to 25%, which is an advantage in terms of sustainability for disease management (Liljeroth *et al*., 2010). Although many fungicides have been developed to control late blight throughout the past 15 years, there have been reports of fungicide resistance to fungicides, such as dimethomorph (Stein and Kirk, 2004).

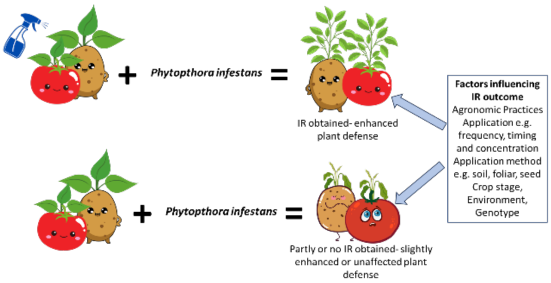

Fig. 7: Factors influencing the results of induced resistance (IR) in plants, late blight of potato and tomato as an example

A comprehensive study conducted between 1998 and 2000 evaluated 258 *P. infestans* isolates assembled from Brazilian potato and tomato fields including 87 isolates from potatoes to assess fungicide resistance (Reis *et al*., 2005). Statistical analysis of agar and leaf-disc sensitivity tests revealed a significant level of insensitivity to the systemic fungicide metalaxyl among potato isolates. In the agar test, 35% of 210 isolates were found to be insensitive, 36% intermediately insensitive, and 29% sensitive, with US-1 and BR-1 genotypes showing similar resistance trends. Leaf-disc assays corroborated these results, indicating that 24.3% of 240 isolates were insensitive while 40.7% remained sensitive. In contrast, no resistance was observed against the protectant fungicides chlorothalonil and cymoxanil, as greater than 75% of the isolates exhibited ED50 values below 1.0 µg/ml. Further supporting this trend, European surveys conducted between 1996 and 1997 reported even higher levels of metalaxyl resistance in potato isolates, with 48% categorized as resistant, 18% as intermediate, and 34% as sensitive (Knapova *et al*., 2002). Notably, only 2% of tomato isolates displayed resistance. Most resistant strains in these studies were associated with the A1 mating type, suggesting possible host-specific adaptation. These findings collectively underscore the widespread emergence of metalaxyl-resistant *P. infestans* strains, particularly in potato populations, and highlight the critical need for continuous resistance monitoring and the adoption of integrated fungicide management strategies to ensure effective and sustainable control of late blight. The integration of systemic fungicides with contact fungicides, exemplified by mancozeb, serves to mitigate the progression of resistance and enhance control efficacy. Numerous nations have enacted regulations aimed at limiting the frequency of fungicide applications. For example, within the European Union, it is advised that no singular fungicide be utilized more than twice consecutively to avert the accumulation of resistance (Fry, 2007).

Emerging Technologies in Late Blight Management

The prevalence of late blight worldwide today makes it clear that more work has to be done, despite the fact that a lot of effort has been made to combat *P. infestans* by employing pesticides and identifying resistance genes. Along with the ongoing enhancement of current methods to deal with late blight, new technologies have emerged (Fig. 8). The prevalence of late blight worldwide today makes it clear that more work has to be done, despite the fact that a lot of effort has been made to combat *P. infestans* by employing pesticides and identifying resistance genes.

Botanicals

A range of commercially available phytochemicals were assessed as potential environmentally acceptable biopesticides. Zeylenone, carvacrol, matrine, and eugenol were among those that demonstrated potential (Zhang *et al*. 2021; He *et al*. 2021). The use of 0.3 percent eugenol, for example, yielded a greater yield and demonstrated a protective effect on potato crops that was comparable to, if not superior to, that of conventional chemical pesticides like mancozeb (80 percent WP) in a comparative field test (Dong and Zhou, 2022). They also discovered that eugenol may significantly slow down the growth of *P. infestans* on oatmeal agar. Eugenol's protective effects can be further enhanced by transporting it using nanomaterial carriers (Wang *et al*. 2021). Zeylenone, which was extracted from *Uvaria grandiflora*, influences the energy intake of *Phytophthora* and could eventually employed for botanical fungicide (He *et al*. 2021).

CRISPR-Cas Genome Editing for Improving Resistance

With the advancement of CRISPR-Cas genome editing technology, precise alterations to plant genomes have been made possible, revolutionizing the process of creating resistant crop types. Through the introduction of resistance genes or mutations that strengthen innate immune responses, CRISPR-Cas9 enables the targeted editing of particular genes in tomatoes and potatoes. To increase ETI or the identification of PAMPs, for instance, genes linked to NLR proteins or PRRs can be altered. Stronger immune pathway activation brought on by these genetic changes may help the plants better resist *P. infestans* diseases (Li *et al*., 2022; Angmo *et al*., 2023). Moreover, susceptibility (S) genes that promote pathogen infection can be silenced using CRISPR-Cas9 (Zaidi *et al*., 2018).

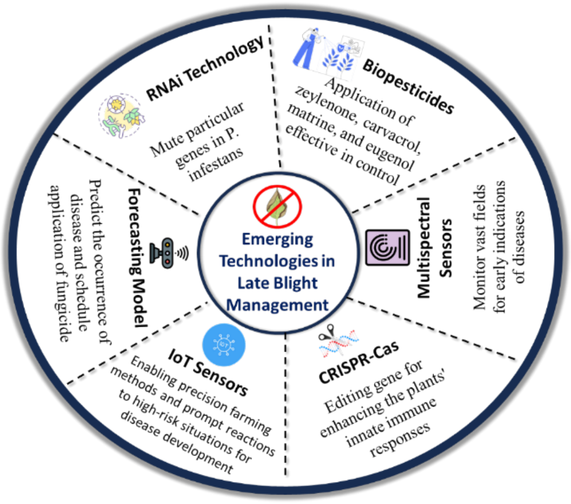

Fig. 8: Emerging technologies in late blight management. Innovations including remote sensing, pathogen monitoring, drones for crop surveillance, and advanced bioinformatics for managing potato late blight

The genes BSL1 and DMR6, for example, are known susceptibility (S) genes, and altering them may improve resistance to oomycete infections. Since DMR6 (Downy Mildew Resistance 6) functions as a negative regulator of plant defense mechanisms, mutations in this gene have been linked to greater resistance in a number of plant species. Similarly, pathogen susceptibility has been linked to BSL1 (BSU-like 1), which interacts with the brassinosteroid signaling system. CRISPR Cas editing can effectively decrease disease vulnerability by disrupting these genes (Kraśniewska *et al*., 2020). Editing genes that decrease host defense mechanisms, such as DMR6 or BSL1, has showed potential in boosting resistance against oomycete pathogens. It is possible to considerably lessen tomatoes' and potatoes' vulnerability to late blight by deleting or altering these genes. These illustrations demonstrate how CRISPR-Cas9 genome editing provides a potent, effective, and sustainable way to increase tomato and potato resistance to late blight. Researchers & breeders can expedite the creation of resilient cultivars by utilizing this technique, guaranteeing increased agricultural output and resistance to changing disease threats. Despite its promise, the CRISPR/Cas system faces several significant limitations in disease resistance breeding. One major challenge is the dynamic nature of pathogens, which continuously evolve to overcome existing resistance mechanisms. A notable example is the trade-off observed in disease resistance: disabling the StNRL1 gene enhanced resistance to late blight but simultaneously increased susceptibility to early blight, suggesting the gene plays a dual role in pathogen response. Another critical issue is the implicit for off-target mutations associated with CRISPR/Cas9, which, although minimized through bioinformatics tools, still necessitate extensive screening to ensure precision. Additional obstacles include low transformation efficiency and difficulties in in vitro plant regeneration, which hinder the broader application of this technology in potato breeding (Norouzi *et al*., 2024). Furthermore, CRISPR/Cas9-mediated mutagenesis of the SlMYBS2 gene in tomatoes, aimed at combating *P. infestans*, revealed further drawbacks. The edited mutant plants (slmybs2-c) exhibited reduced resistance, characterized by increased necrosis, larger lesion sizes, suppressed expression of defense-related genes, and excessive accumulation of reactive oxygen species (ROS), which likely contributed to cellular damage rather than protection. These findings underscore the complexities and limitations of using CRISPR/Cas9 for durable disease resistance (Liu *et al*., 2021).

RNA Interference (RNAi)

RNAi is a new and innovative technology that has recently been added to the potential toolkit of PLB (potato late blight) control. RNAi was initially discovered to be a part of the antiviral defense system of plants, but it is now believed to be essential for many other environmental adaptation mechanisms in plants, including defense against arthropod herbivores and fungal diseases (Zhao *et al*., 2021). Some *Phytophthora* effectors can disrupt the plant's RNA-silencing pathway, according to recent studies (Qiao *et al*., 2013). The first proof of host-induced gene suppression in *P. infestans* by potatoes was presented by Jahan *et al*. (2015), indicating the necessity of the cross-kingdom molecular process. RNAi is a part of the potato-*Phytophthora* pathosystem. RNA interference (RNAi) technology can silence specific genes in *P. infestans* that are critical to its virulence, reducing the pathogen's ability to infect and providing a new method of biological control (Dong and Zhou, 2022). Recent advancements in RNA interference (RNAi) technology have facilitated the development of late blight-resistant potato cultivars by silencing genes encoding essential effector proteins used by *P. infestans* to suppress plant defenses. This approach has led to the creation of genetically engineered potato lines containing RNAi constructs, based on an inverted repeat strategy, specifically targeting the R3a homolog in *P. infestans*. This method has effectively reduced late blight severity by disrupting the pathogen’s infection cycle and interfering with its molecular pathogenesis (Drozda *et al*., 2022; Berindean *et al*., 2024).

In parallel, the role of circular RNAs (circRNAs), particularly circRNA45 and circRNA47, has gained increasing attention for their involvement in plant defense responses. These circRNAs are upregulated during infection and act as molecular sponges for microRNAs such as miR477-3p, thereby modulating the expression of disease resistance genes. Transient overexpression of circRNA45 and circRNA47 in tomato plants has been shown to reduce lesion size, demonstrating their potential to enhance plant immunity (Hong *et al*., 2020).

Small RNAs also play a pivotal role in plant-pathogen interactions. Notably, miR8788 targets the plant gene StABH1, which is involved in defense signaling. Downregulation of StABH1 by miR8788 facilitates pathogen infection; however, silencing miR8788 through miRNA target mimicry has produced knockdown strains with impaired growth on potato plants, leading to improved resistance. These findings were supported by transformation techniques using plasmid DNA and RNA extractions from *P. infestans* strains (Hu *et al*., 2020).

Furthermore, the regulatory influence of microRNAs such as miR1918 has been underscored due to its association with genes linked to susceptibility. Transgenic tomato plants expressing specific small RNAs targeting *P. infestans* genes have shown enhanced resistance. qRT-PCR analyses have confirmed an inverse correlation between miR1918 levels and the expression of target genes, reinforcing its role in modulating plant defense responses (Jahan, 2015).

RNA interference (RNAi) technology presents promising potential for plant disease management, but it is not without significant limitations. One of the primary drawbacks is the variability and instability of RNAi constructs, which can lead to inconsistent resistance across successive plant generations. Additionally, RNAi-mediated gene silencing may cause unintended off-target effects, impacting non-target genes and resulting in undesirable phenotypes (Dubrovina and Kiselev, 2019). Unlike gene knockout techniques, RNAi only downregulates gene expression, which may be insufficient when combating highly virulent *P. infestans* isolates. Moreover, the silencing effect can diminish over time due to epigenetic modifications or the plant's own defense mechanisms against foreign RNA, undermining its long-term effectiveness (Sun *et al.*, 2016). The efficacy of RNAi is also influenced by double-stranded RNA (dsRNA) concentrations—while certain levels inhibit pathogen growth, others might paradoxically promote it. Environmental factors such as growth medium and temperature further affect outcomes, complicating the extrapolation of laboratory results to field conditions. Most studies to date have been conducted in controlled environments using detached leaves or seedlings, which may not accurately represent the complex interactions in natural field settings. There is also concern that repeated RNAi applications could lead to resistance development in pathogens. Finally, regulatory hurdles and public apprehension surrounding genetically modified organisms pose additional barriers to the widespread adoption of RNAi-based approaches. Addressing these challenges through continued research is crucial for enhancing the viability of RNAi in sustainable agricultural disease management (Porwal *et al.*, 2020).

Molecular Breeding Through Marker-Assisted Selection (MAS)

The use of molecular breeding, such as MAS, has become essential for improving tomato and potato crops' resilience to late blight. MAS uses genetic markers associated with late blight resistance genes to enable the accurate identification and selection of resistance characteristics. With the help of this technology, breeders can quickly introduce desired features into market cultivars, avoiding the time-consuming and frequently inaccurate traditional breeding procedures. MAS can be used to develop high-yielding, disease-resistant cultivars by introducing resistance genes, such as *Ph3* and *Ph5* from wild tomatoes or *Rpi-vnt1*, *Rpi-blb1*, and *Rpi-blb2* from wild potato species, into susceptible types (Angmo *et al.*, 2023; Osei *et al.*, 2019). Furthermore, MAS facilitates the pyramiding of several resistance genes into a single cultivar in order to produce long-lasting and universal resistance. The idea of combining several *Rpi* genes in potatoes or *Ph* genes in tomatoes to increase resistance to *P. infestans* is backed by research showing that these resistance (R) genes can identify various pathogen effectors, offering a more comprehensive and long-lasting defense (Vossen *et al.*, 2016). Targeting different *P. infestans* effector proteins, pyramiding *Rpi-blb1*, *Rpi-blb2*, and *Rpi-vnt1* in potatoes has been demonstrated to increase resistance (Vossen *et al.*, 2016). MAS was used to identify the resistance genes *Rpi-abpt* and *Rpi-blb1* in a study that involved 72 potato lines that were produced by crossing the susceptible cultivar 'ACI Pakri-1' with a donor that was resistant to late blight. According to field assessments, the susceptible parent showed 100% foliage destruction at 63–65 days after planting (DAP), while the chosen resistant lines showed just 1–25% degradation at 85 DAP (Islam *et al.*, 2018). Likewise, tomatoes that have Ph3 and Ph5 genes combined have stronger defenses against different types of pathogens (Foster *et al.*, 2009). In tomato conducting MAS-based breeding with *Ph-3*, resistant cultivars demonstrated up to a 70% reduction in disease incidence in comparison with non-resistance (Foolad *et al.*, 2008). These statistical outcomes underscore the efficacy of MAS in generating long-lasting cultivars resistant to late blight, which mitigates the need for fungicides and improves the productivity of crops.

The MAS was effective in identifying recombinants with the desired resistance traits. Out of 1152 F2 plants screened, 11 were identified as having potential recombination events between *Ph-3* and Sw-5, and three of these were confirmed to have resistance to late blight pathogens (Robbins *et al.*, 2010). Similarly, the high saturation of the potato molecular map with over 350 uniformly distributed markers enables precise identification of resistance genes and QTLs. This robust genetic framework enhances the effectiveness of Marker-Assisted Selection (MAS) in breeding *P. infestans*-resistant potato cultivars, improving crop resilience and yield (Barone *et al.*, 2004). Additionally, MAS makes it easier to create resistant cultivars without sacrificing important agronomic characteristics like fruit quality, yield, or stress tolerance. The efficiency of MAS is further increased when combined with modern methods like high-throughput genotyping, which makes it a crucial tactic in late blight resistant breeding initiatives. Therefore, MAS is a revolutionary method for preventing tomato and potato late blight. MAS speeds up the creation of resilient cultivars, guaranteeing sustainable agricultural production and food security, by incorporating resistance traits from wild relatives and implementing them in commercial breeding programs.

Use of Sensors

By facilitating real-time monitoring and precise interventions, the incorporation of sensor technology has completely transformed the treatment of late blight in tomato and potato crops. Field-installed Internet of Things (IoT) sensors continuously gather information on temperature, humidity, soil moisture, and plant health—all of which are important variables affecting the development of late blight. Real-time microclimate data from these sensors can be used to forecast times when disease outbreaks are most likely to occur. IoT technologies facilitate precision farming by enabling farmers to take targeted and timely measures, such modifying irrigation schedules or optimizing fungicide applications to lessen the conditions that encourage the growth of pathogens.

In potato fields, hyperspectral imaging sensors were utilized in studies through Unmanned Aerial Vehicles (UAVs) for the detection of late blight. The sensitivity of the disease monitoring was remarkably improved with the proposed CropdocNet model having a detection rate of 98.6% (Shi *et al*., 2022). Two-drone coordination was utilized in another study to track potato late blight severity. It improved disease severity monitoring accuracy through complete field coverage in addition to early data collection (Sun *et al*., 2023) Environmental factors causing the outbreak of late blight have also been monitored through IoT-based models. To notify farmers in real time when the conditions are favorable for the development of the disease, one of the systems had wireless sensors for temperature, humidity, and leaf wetness (Wang *et al*., 2024). These technologies do not only improve the speed and accuracy of late blight detection but also enable targeted intervention, which can mitigate crop loss and improve yield.

Drones with thermal and multispectral imaging sensors are effective instruments for monitoring potato and tomato farms on a wide scale. Frequently before visual symptoms manifest, these drones are able to identify early indicators of late blight, such as variations in canopy temperature or chlorophyll fluorescence. Farmers can reduce the need for widespread pesticide applications and conserve resources by using this data to detect diseased areas and implement tailored treatments (Sun *et al*., 2023; Mothapo *et al*., 2022).

LAMP can be utilized to develop web-based dashboards, databases, and APIs for visualizing and managing IoT sensor data. In the context of disease detection, the LAMP assay successfully identified *P. infestans* in asymptomatic potato leaves as early as 24 hours post-inoculation. This rapid detection capability is crucial for timely intervention and effective management of late blight (Si Ammour *et al*., 2017). To sum up, sensor technologies such as Internet of Things systems and sensors installed on drones—offer revolutionary ways to control tomato and potato late blight. These tools promote sustainable agriculture by facilitating accurate, data-driven farming methods that improve crop health, resource efficiency, and disease detection.

Advanced Disease Forecasting Models

To anticipate the probability of late blight outbreaks, sensor data is frequently included into sophisticated disease forecasting models, including BLITECAST and JHULSACAST. By using these forecasts, farmers can minimize losses and lessen their effects on the environment by making well-informed decisions about crop management (Parola, 2022). To predict the presence of late blight disease, a number of forecasting models have been developed. Van Everdingen originally created "Dutch rules" (Van Everdingen, 1926) to predict the onset of late blight and to schedule fungicide applications under Holland conditions. Many forecasting systems, such as SIMCAST, BLITECAST, PhytoPre, NegFry, ProPhy, PROGEB, Web-Blight, China Blight, Bio-PhytoPre, Plant Plus, PhytoPRE + 2000, and others, have been developed for different regions of the world (Arora *et al*., 2014). To predict the onset of potato late blight, the BLITE-SVR forecasting system was developed. This model was developed using 13 various kinds of meteorological data, and the effectiveness of BLITE-SVR was contrasted with that of linear regression, pace regression, and the conventional moving-average method. The prediction accuracy for the first instance of late blight in potatoes was 64.3% for BLITE-SVR, 42.9% for the conventional moving-average method, 35.7% for linear regression and 42.9% using pace regression (Gu *et al*., 2016). An online Decision Support System (DSS) was developed to manage late blight in potatoes and tomatoes (Small *et al*., 2015). To predict disease dynamics based on crop data, weather, and management strategies, this system combines several models. Subsequent to the ascertainment of the geographical coordinates applicable to their production unit, the system systematically collects meteorological data from the closest operational weather station, in conjunction with acquiring localized forecast data from the National Weather Service's National Digital Forecast Database (Small *et al*., 2015).By predicting the frequency and severity of late blight using a range of meteorological variables, these models assist farmers in determining when to use fungicides (Henderson *et al*., 2007). Forecasting is important in chemical control due to the potential to provide information about the spray application process, including optimum amount, timing, and frequency of treatment. A variety of approaches to predict the optimal timing for the first fungicide application, as well as for subsequent applications, are more convenient and reduce the number of sprays needed for good blight control (Litschmann *et al*., 2020).

Conclusion and Future Perspectives

Late blight, caused by *P. infestans*, continues to threaten global food security by causing substantial losses in potato and tomato production. The pathogen's complex epidemiology, characterized by adaptive reproductive strategies and potent virulence mechanisms, presents significant challenges for effective management. While traditional methods such as cultural practices, host resistance, and biocontrol have shown some success, the integration of innovative and sustainable technologies is critical for long-term control. Emerging tools like CRISPR-Cas9 genome editing, RNAi, molecular breeding through MAS, biopesticides, and IoT-enabled sensors are transforming late blight management strategies. Advanced disease forecasting models also enable precise, data-driven interventions, optimizing resource use and reducing environmental impacts.

Future research should focus on developing broad-spectrum resistance by pyramiding multiple resistance-associated genes into commercial cultivars using genome editing and MAS techniques. Enhancing the efficacy of natural biopesticides, such as zeylenone and carvacrol, through advanced delivery systems like nanomaterials could provide eco-friendly alternatives to chemical controls. The expanded use of digital agriculture tools, including IoT sensors, drones, and real-time analytics integrated with forecasting models, can further advance precision farming and disease management. A deeper understanding of the molecular mechanisms *governing P. infestan*s pathogenesis and host-pathogen interactions will be instrumental in designing novel resistance strategies. Moreover, the effects of the disease progress on the progression of late blight in the context of climate change must be analyzed and climate-resilient management strategies must be implemented to secure future agriculture productivity.

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Mahabuba Mostofa: Drafting, data collection and data analysis.
Dodi Al Sharif: Drafting, data collection and data analysis.
Md Motaher Hossain: Conception, Research design, and draft reviewing.

Ethics

This paper is original and not submitted elsewhere. The corresponding author agrees that all authors have seen and approved the final version of the manuscript and there is no ethical problem to disclose.

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