



Early Blight of Potato Caused by *Alternaria solani* (Sorauer): A Critical Review of Epidemiology, Weather Relations, Disease Assessment and Management

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Abstract

Early blight, caused principally by the necrotrophic fungus *Alternaria solani*, remains one of the most persistent foliar constraints on potato (*Solanum tuberosum* L.) production across temperate and subtropical growing regions. The disease progresses through repeated infection cycles governed closely by temperature, leaf wetness duration and relative humidity, and it interacts with crop phenology in ways that complicate both its prediction and its control. This review synthesises recent literature on the taxonomy and biology of the

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causal organism, the weather variables that regulate sporulation and infection, the tools available for disease assessment ranging from visual scoring to molecular diagnostics and deep learning-based image analysis, the forecasting and decision support systems developed to time fungicide applications, and the chemical, genetic, biological and cultural strategies used to manage the disease. Particular attention is given to the species complex now recognised within large-spored *Alternaria*, to the divergence of fungicide sensitivity associated with quinone outside inhibitor and succinate dehydrogenase inhibitor chemistries, and to the quantitative and largely polygenic nature of host resistance. Evidence from multi-year field trials indicates that realised yield losses vary considerably with soil type, cultivar maturity and season, complicating generalisations about economic impact. The review concludes that sustainable management depends on the integration of resistant or partially resistant cultivars, weather-informed spray timing, judicious fungicide rotation and improved diagnostic sensitivity, rather than reliance on any single tactic. Gaps remain in the genetic basis of durable resistance, in the transferability of forecasting models across climatic zones, and in the practical deployment of digital diagnostic tools at farm scale.

Keywords: *Alternaria solani*; potato early blight; epidemiology; weather relations; disease forecasting; integrated disease management.

1. Introduction

1.1 Potato Production and the Challenge of Foliar Disease

Potato is grown on every populated continent and occupies a central place in global food security because of its high caloric yield per unit area, its adaptability to diverse agroecological zones and its role as both a subsistence and a commercial crop. Productivity is nonetheless constrained by a wide range of fungal, oomycete, bacterial and viral pathogens, among which foliar blights are particularly damaging because they reduce the photosynthetic canopy during the period of tuber bulking. Early blight, caused mainly by *Alternaria solani* (Ellis & G. Martin) L.R. Jones & Grout, is one of the two dominant foliar blights of potato worldwide, the other being late blight caused by the oomycete *Phytophthora infestans*. Where late blight tends to attract disproportionate research and extension attention because of its capacity for explosive epidemics, early blight is frequently underestimated even though it occurs in nearly every potato-growing region and can, under favourable conditions, cause substantial premature defoliation; global estimates place uncontrolled yield loss from the disease at 40 to 50 percent (Li et al., 2024). Recent field-based evidence further indicates that early blight severity is influenced by soil and crop-management conditions, supporting field-specific integrated management recommendations rather than uniform intervention schedules (Stridh et al., 2024).

The disease complex historically labelled "early blight" is now understood to be caused by more than one large-spored *Alternaria* species, although *A. solani* remains the dominant and most economically important agent on potato in most surveyed regions (Schmey et al., 2024). The consequences of infection extend beyond simple defoliation: reduced leaf area lowers the interception of solar radiation, accelerates canopy senescence and, in susceptible cultivars exposed to early-season infection, can depress both total and marketable tuber yield. Recent field-scale research has also shown that ultra-high-resolution unmanned aerial vehicle imagery combined with supervised deep learning can support the detection of *A. solani* symptoms under field conditions, broadening the available approaches to disease surveillance (Wieme et al., 2024).

1.2 *Alternaria solani* and Early Blight: An Overview

Alternaria solani is a necrotrophic ascomycete that survives between seasons as mycelium and conidia in infected crop debris, seed tubers and alternative solanaceous hosts, and that produces asexual conidia which disperse aerially to initiate new infections on emerging foliage. Symptoms typically begin as small, dark, irregularly shaped lesions on the oldest, lowest leaves, which under favourable conditions enlarge into necrotic spots exhibiting the concentric ring pattern often used as a field diagnostic feature (Niu et al., 2022). As lesions coalesce, infected leaflets senesce and abscise, and in severe epidemics the loss of canopy can be substantial before harvest. At the molecular level, functional analysis of *A. solani* CFEM effectors has linked specific secreted proteins with pathogen virulence and host defence activation, adding mechanistic detail to current understanding of the potato-pathogen interaction (Qiu et al., 2024).

Diagnosis based on symptoms alone is complicated by the existence of a broader disease complex on Solanaceae. Field surveys using multilocus phylogenetic methods have repeatedly recovered several large-spored *Alternaria* taxa co-occurring on the same potato leaves, including *A. solani*, *A. linariae* (synonym *A. tomatophila*), *A. protenta* and *A. grandis*, and their relative frequency differs geographically (Ivanović et al., 2022). A second, taxonomically distinct group of small-spored *Alternaria* species, principally *A. alternata*, causes a related but generally milder condition often termed brown spot, and the two conditions are frequently referred to jointly as an early blight–brown spot disease complex because their early symptoms are difficult to distinguish in the field (Schmey et al., 2024). This taxonomic heterogeneity has practical consequences for epidemiological modelling, for resistance breeding and for the interpretation of fungicide efficacy trials, because studies that do not molecularly confirm the causal agent may conflate the biology of genuinely distinct organisms. Recent evaluation of *Bacillus subtilis* in combination with chlorothalonil further illustrates how biological and chemical tactics may be investigated as complementary components of early blight management (Noh et al., 2024).

1.3 Scope, Research Gap and Objectives

Despite a substantial and growing literature on potato early blight, published synthesis has tended to treat epidemiology, diagnostic technology and management as separate bodies of work, and relatively few reviews have attempted to connect the mechanistic understanding of weather-driven infection with the practical tools now available for disease assessment and decision support. Recent advances in genome sequencing of *A. solani* populations, in transcriptomic dissection of host–pathogen interactions, in quantitative trait locus mapping of partial resistance, and in image-based and molecular diagnostics have not yet been consolidated alongside the longer-established literature on forecasting models and fungicide programmes. There is, in particular, a need to reconcile evidence on the magnitude of yield loss, which varies markedly between studies and growing systems, with the practical guidance offered to growers on when and how to intervene.

This review addresses that gap by bringing together recent primary literature on four interlinked themes: the epidemiology of *A. solani* and its relationship with weather variables; the methods available for assessing and diagnosing disease severity, from visual scales to molecular and computer vision-based tools; the forecasting and decision support systems developed to optimise fungicide timing; and the chemical, host-genetic, biological and cultural strategies employed in disease management. The specific objectives are to characterise the environmental conditions most consistently associated with infection and sporulation across production regions; to compare the diagnostic and forecasting tools currently available and their reported accuracy; to evaluate the evidence base for resistance breeding, fungicide resistance management and biological control; and to identify the principal knowledge gaps that constrain the development of more sustainable, regionally adapted management programmes.

2. Methods for Literature Selection

2.1 Information Sources and Search Strategy

Literature was identified through systematic searching of four general bibliographic databases, Web of Science Core Collection, Scopus, Google Scholar and PubMed, supplemented by five field-specific indexing databases selected for their coverage of agricultural and plant pathological literature: CAB Abstracts, AGRICOLA, AGRIS, BIOSIS Previews and the Directory of Open Access Journals. PubMed was retained despite its clinical orientation because a substantial proportion of molecular plant pathology and transcriptomic research on *A. solani* is indexed there through its coverage of open-access life-science journals. Reference lists of retrieved articles were also examined to identify additional relevant studies not captured by the electronic search, a form of citation chaining that is a recognised complement to database searching in narrative synthesis.

2.2 Search Terms and Temporal Scope

Search strings combined the causal organism and disease terms with topic-specific qualifiers using Boolean operators, for example ("*Alternaria solani*" OR "early blight") AND ("potato" OR "*Solanum tuberosum*") AND (epidemiology OR weather OR forecast* OR "disease severity" OR fungicide OR resistance OR management OR diagnos*). Truncation and wildcard operators were applied where supported by the database interface, and searches were broadened where a topic was underrepresented in the initial title, abstract and keyword search.

The search covered literature published between 1 January 2000 and 9 April 2026, a window selected to capture the substantial expansion of molecular, genomic and precision-diagnostic research on *A. solani* that has occurred since the early 2000s while remaining broad enough to include the weather-based forecasting literature that underpins current decision support systems. A small number of methodologically foundational studies published before this window were retained where they were repeatedly cited within the retrieved literature and where their findings continued to underpin current practice.

2.3 Eligibility Criteria and Screening Workflow

Records were included if they reported primary research or synthesis on the biology, epidemiology, diagnosis, forecasting or management of early blight in potato, or on the taxonomy and population biology of *A. solani* and closely related large-spored *Alternaria* species where directly relevant to potato pathology. Studies were excluded if they addressed early blight exclusively in tomato or other solanaceous crops without extending findings to potato, if they were published in non-peer-reviewed outlets, conference proceedings without full peer review, trade publications, preprints or patents, or if the full text could not be verified against the original source. No language restriction was applied at the search stage, but articles not available in English were excluded at full-text screening because translation resources were not available for quality assessment. Duplicate records retrieved across databases were identified by matching digital object identifiers, author lists and publication years and were removed prior to full-text review. Screening proceeded in two stages: an initial title and abstract review to remove clearly irrelevant records, followed by full-text assessment of the remaining articles against the eligibility criteria described above. Where multiple studies addressed a similar question, preference was given to more recent, higher-impact or more methodologically rigorous studies, while older or smaller studies were retained where they represented the most influential contribution on a given subtopic.

2.4 Rationale for a Narrative Review Approach

A narrative rather than a systematic review format was adopted because the subject matter spans several methodologically heterogeneous domains, including field epidemiology, molecular diagnostics, plant breeding genetics and computational image analysis, for which a single quantitative synthesis protocol such as meta-analysis would not be appropriate. Narrative reviews of this kind are recognised as a flexible and rigorous means of integrating heterogeneous evidence across disciplinary boundaries when the objective is to characterise the state of knowledge and identify research priorities rather than to estimate a pooled effect size (Sukhera, 2022). This flexibility is balanced against a recognised risk of selection bias, mitigated here through the explicit, reproducible search strategy and eligibility criteria described above, an approach consistent with recommended practice for transparent narrative synthesis in peer-reviewed literature (Ferrari, 2015).

3. Biology, Taxonomy and Disease Cycle of *Alternaria solani*

3.1 Taxonomic Position and the Large-spored *Alternaria* Complex

Alternaria solani belongs to the family Pleosporaceae within the order Pleosporales, a lineage of predominantly necrotrophic and saprotrophic ascomycetes. The genus *Alternaria* is taxonomically complex, and morphological identification based on conidial shape and chain formation has historically been unreliable at the species level within the large-spored section that includes *A. solani*. Multilocus sequence typing using nuclear loci such as glyceraldehyde-3-phosphate dehydrogenase, calmodulin and RNA polymerase II subunit genes has clarified that several morphologically similar taxa can co-occur on potato foliage within a single field, with the relative frequency of each species differing between production areas (Ivanović et al., 2022). A comprehensive review of the genus concluded that the early blight and brown spot disease complexes on potato and tomato are best understood as caused by a diverse assemblage of large- and small-spored *Alternaria* taxa rather than by a single uniform pathogen, since both organisms frequently occur on the same plant and their early symptoms are difficult to differentiate (Schmey et al., 2024).

3.2 Genomic and Population Characteristics

Whole-genome sequencing of European *A. solani* isolates has revealed extensive population-level genetic diversity that is not strongly structured by geography, together with evidence of recombination suggestive of cryptic sexual or parasexual processes that could accelerate adaptive change within the pathogen population

(Einspanier et al., 2022). This genomic plasticity is of direct practical relevance because it provides a mechanism through which fungicide-resistance mutations, discussed in Section 7, can spread and recombine within populations rather than arising and persisting as isolated clonal lineages. At a finer scale, multi-omics characterisation of isolates collected across several growing seasons in Yunnan Province, China, confirmed that *A. solani* and *A. alternata* co-occur as the principal and conditional causal agents respectively: of 85 *Alternaria* isolates recovered from typical early blight lesions, 35 were confirmed as *A. solani* and 50 as *A. alternata* by morphological and ITS sequence comparison, and the study identified candidate pathogenicity-related genes associated with infection (Li et al., 2024).

3.3 Infection Process and Disease Cycle

Infection begins with the germination of a conidium on the leaf surface, typically within a film of free moisture, followed by the formation of an appressorium that facilitates penetration of the host epidermis, either directly or through natural openings such as stomata and wounds. Transcriptomic profiling of the early hours of infection, spanning from one hour after inoculation, when conidia have only just begun to germinate, through to forty-eight hours post-inoculation, when widespread cell necrosis is under way, has shown that the fungus undergoes marked transcriptional reprogramming during appressorium formation and penetration, followed by a further wave of expression change coinciding with the transition to necrotrophic colonisation (Brouwer et al., 2021). Comparative transcriptome sequencing in Chinese isolates has further refined understanding of the genes activated during this transition from early colonisation to overt necrotrophic damage, providing candidate targets for future intervention strategies (Jiang et al., 2023).

Once necrotic lesions have formed, sporulation resumes on the lesion surface, producing new conidia that disperse by wind and rain splash to initiate secondary infection cycles on younger foliage throughout the growing season, a pattern that makes early blight a polycyclic disease capable of multiple generations within a single crop. Between seasons the fungus persists as mycelium and conidia in infected crop debris left on or near the soil surface, and it can also be seed-borne, providing sources of primary inoculum for the following season. Lesions can additionally develop on tubers, producing brown skin protrusions with circular to irregular depressions that eventually soften and rot, reducing marketability and serving as a further overwintering reservoir of inoculum (Li et al., 2024).

Table 1 draws together the taxonomic and biological features most directly relevant to accurate diagnosis of early blight and to the interpretation of subsequent epidemiological and management evidence. A recurring theme is that morphological identification alone is insufficient to distinguish the several *Alternaria* species capable of producing early blight-like symptoms, and molecular confirmation is increasingly treated as a prerequisite for epidemiological and breeding studies that aim to attribute observed variation specifically to *A. solani*.

Table 1. Taxonomic, morphological and biological features relevant to the diagnosis of potato early blight

Feature	Description	Diagnostic or practical relevance	Source references
Principal causal species	<i>Alternaria solani</i> , large-spored, Pleosporaceae	Dominant agent on potato in most surveyed regions	Schmey et al. (2024); Ivanović et al. (2022)
Co-occurring large-spored species	<i>A. linariae</i> , <i>A. protenta</i> , <i>A. grandis</i>	Morphologically similar to <i>A. solani</i> ; require molecular confirmation	Ivanović et al. (2022); Schmey et al. (2024)
Small-spored complex member	<i>A. alternata</i>	Causes related but generally milder brown spot; frequently co-isolated	Schmey et al. (2024); Li et al. (2024)
Confirmatory molecular markers	GAPDH, calmodulin, RNA polymerase II (<i>Rpb2</i>) gene sequences	Resolve species identity where morphology is ambiguous	Ivanović et al. (2022)
Genomic population structure	High diversity, evidence of recombination across European isolates	Provides a mechanism for rapid spread of fungicide-resistance alleles	Einspanier et al. (2022)
Infection process	Conidial germination, appressorium formation, penetration, necrotrophic colonisation	Underpins timing of protective fungicide application	Jiang et al. (2023); Brouwer et al. (2021)
Survival structures	Mycelium and conidia in crop debris, seed tubers	Sources of primary inoculum between seasons	Li et al. (2024)

4. Epidemiology and Weather Relations

4.1 Environmental Drivers of Infection and Sporulation

Temperature and moisture availability are the dominant environmental determinants of *A. solani* infection and sporulation, and the relationship between these variables and disease progress has been characterised across a range of production environments. Field studies in Gujarat, India, recorded a strong positive correlation between disease intensity and both maximum temperature and evaporation, alongside a significant negative correlation with evening relative humidity, illustrating that the relationship between humidity and disease is not uniformly positive but depends on the time of day at which humidity is measured and on its interaction with temperature (Patel et al., 2024). A separate multi-year study conducted in Uttar Pradesh similarly linked the timing of first disease appearance to specific combinations of maximum and minimum temperature together with relative humidity, reinforcing that both the onset and the rate of epidemic development are climatically conditioned (Ghalib et al., 2025).

Aerobiological monitoring conducted in north-western Spain across six potato growing seasons found significant positive correlations between minimum and average temperature, and between mean temperature during the leaf wetness period, and the concentration of airborne *Alternaria* conidia, with leaf wetness duration emerging as a particularly strong predictor of spore concentration through a significant linear regression relationship (Meno et al., 2020). Findings of this kind, in which spore formation and release respond jointly to temperature and moisture rather than to either variable alone, have direct implications for the design of weather-based forecasting models, discussed further in Section 6.

4.2 Leaf Wetness, Temperature Thresholds and Infection Risk

Beyond ambient humidity, the duration of leaf surface wetness is widely regarded as the single most important proximate driver of infection, because free moisture is required for conidial germination and appressorium formation. Field-adapted thresholds developed for north-west Spain found that airborne *Alternaria* concentrations exceeding 50 spores per cubic metre were consistently associated with days on which mean air temperature exceeded 18 degrees Celsius and leaf wetness persisted for more than seven hours, with leaf wetness proving decisive in estimating spore concentration (Meno et al., 2020). These thresholds were derived to support a modified version of the widely used tomato forecaster (TOMCAST) model, discussed in Section 6.1, in which daily infection risk is summarised from the combined effect of leaf wetness duration and temperature during the wet period.

4.3 Seasonal and Spatial Dynamics, Plant Phenology and Climate Change

Disease pressure typically intensifies as the growing season progresses, coinciding with crop maturation and subsequent canopy senescence, both of which are associated with a decline in plant defence status and an increase in host susceptibility. Comparative evaluation of forecasting approaches based on plant phenology, pathogen requirements and combinations of the two found that plant-based indicators, including growing degree-day accumulation, generally achieved the lowest prediction error for the onset of first symptoms, and that combining a pathogen-based threshold with a plant-based indicator produced a more accurate prediction than either approach used alone (Meno, Abuley et al., 2022). This pattern is consistent with the general biology of the pathogen, in which older, senescing leaves at the base of the canopy are typically the first to show symptoms before infection progresses upward through the plant (Li et al., 2024).

The prospect of a warming climate has drawn increasing attention because *A. solani* has a comparatively high optimal temperature range for growth relative to some other foliar pathogens of potato, implying that warmer growing seasons could extend the period of favourable conditions in some production regions (Meno, Abuley et al., 2022). Because disease pressure interacts with soil type, cultivar maturity class and local weather in ways that differ between sites and years, however, projecting the net effect of climate change on early blight severity is not straightforward, and empirical monitoring across a range of environments remains necessary to detect emerging shifts in disease pressure.

Table 2 draws together the weather variables most consistently implicated across independent studies conducted in India, Spain and China. Although the precise numerical thresholds differ between studies, reflecting

differences in cultivar, latitude and measurement methodology, the underlying pattern is consistent: infection risk rises with warm daytime temperatures and extended periods of leaf surface wetness, while disease pressure is further amplified as the crop matures and canopy senescence increases host susceptibility. This convergence across geographically distant studies supports the use of temperature and leaf wetness as the core predictive variables in the forecasting systems described in Section 6.

Table 2. Documented relationships between weather variables and *Alternaria solani* epidemiology across production regions

Weather variable	Reported relationship with disease	Growing region	Source references
Maximum temperature and evaporation	Strong positive correlation with disease intensity	Gujarat, India	Patel et al. (2024)
Evening relative humidity	Significant negative correlation with disease intensity	Gujarat, India	Patel et al. (2024)
Maximum and minimum temperature, relative humidity	Combination of variables linked to timing of first symptom appearance	Uttar Pradesh, India	Ghalib et al. (2025)
Minimum and average temperature	Significant positive correlation with airborne spore concentration	North-west Spain	Meno et al. (2020)
Leaf wetness duration and temperature	Spore concentrations exceeding 50 spores per cubic metre associated with more than 7 hours of leaf wetness above 18 degrees Celsius	North-west Spain	Meno et al. (2020)
Crop maturity and senescence	Older, lower leaves show symptoms first as susceptibility increases with canopy ageing	Yunnan, China	Li et al. (2024)
Plant developmental stage	Growing degree-day and phenology-based indicators outperform purely weather-based prediction of symptom onset	North-west Spain	Meno, Abuley et al. (2022)

5. Disease Assessment: Symptom-Based, Molecular and Digital Approaches

5.1 Visual Scoring and Severity Indices

The simplest and most widely used approach to disease assessment remains visual scoring, in which trained assessors estimate the proportion of leaf area affected using a standardised scale, from which a percentage disease index is calculated. Field studies in northern India, for example, applied a nine-point score chart across fifty randomly selected leaves per plot to quantify seasonal disease progress in relation to weather conditions (Ghalib et al., 2025). Similar approaches underpin the relative area under the disease progress curve, an index calculated by integrating repeated visual assessments across the growing season and used extensively in cultivar screening and breeding trials to identify significant differences in resistance among genotypes (Xue et al., 2019). Visual scoring is inexpensive and requires no specialised equipment, but it is inherently subjective, dependent on assessor training and experience, and poorly suited to detecting infection before symptoms become macroscopically visible.

5.2 Molecular and Serological Diagnostics

Molecular diagnostics address the principal limitation of visual assessment by enabling detection of the pathogen before, or independently of, visible symptom development. Quantitative real-time polymerase chain reaction assays targeting species-specific transcripts have achieved detection sensitivity down to a single spore within a whole potato leaf, more than a thousand times more sensitive than detection based on genomic DNA, offering a substantial improvement over conventional methods and enabling identification of infection during the symptomless latent period (Niu et al., 2022). Such assays are particularly valuable for epidemiological monitoring and for validating forecasting models, because they allow researchers to confirm the presence of the pathogen in the crop canopy in advance of the visible lesions on which conventional scoring depends. At the population level, multilocus sequencing of diagnostic gene regions has also been essential for resolving which *Alternaria* species is responsible for a given outbreak, a distinction that visual symptoms alone cannot reliably provide (Ivanović et al., 2022).

5.3 Imaging, Machine Learning and Precision Detection

The past decade has seen rapid growth in image-based and computational approaches to disease detection and severity quantification, driven by the increasing availability of smartphone cameras and the maturation of convolutional neural network architectures. A model trained on 4,200 field-captured smartphone images achieved an overall classification accuracy of 99 percent in distinguishing healthy, early blight-affected and late blight-affected potato leaves, while additionally categorising severity into low, moderate and severe classes for each disease (Dame et al., 2025). Complementary work applying explainable artificial intelligence techniques to transfer learning-based classifiers has sought to address the interpretability limitations that often accompany deep learning models in agricultural applications, combining high classification accuracy with model transparency intended to help end users trust and interpret each prediction (Alhammad et al., 2025). These computational tools remain constrained by their dependence on large, well-labelled training datasets and by the need for further validation under the variable lighting, background and canopy structure conditions encountered in commercial fields, in contrast to the more controlled image acquisition conditions under which many published models have been trained and tested.

Table 3 highlights a trade-off that runs through the disease assessment literature: methods that are inexpensive and rapid to deploy at scale, such as visual scoring, generally lack the sensitivity and objectivity of molecular and computational approaches, while the latter require greater investment in equipment, expertise or training data. In practice, the two categories of method are complementary rather than substitutable, with visual scoring remaining the standard for field-level decision making and epidemiological monitoring, and molecular and imaging tools increasingly used to validate forecasting models, confirm causal species identity and support research into resistance mechanisms.

Table 3. Comparison of disease assessment and diagnostic approaches for potato early blight

Approach	Basis of assessment	Principal advantage	Principal limitation	Source references
Visual severity scoring	Percentage leaf area affected, standardised score charts	Low cost, no equipment required	Subjective, assessor-dependent, symptom-dependent	Ghalib et al. (2025); Xue et al. (2019)
Relative area under disease progress curve	Repeated visual assessments integrated over the season	Captures cumulative disease pressure for cultivar screening	Labour-intensive, requires multiple field visits	Xue et al. (2019); Xue et al. (2022)
Quantitative real-time PCR	Species-specific transcript or DNA amplification	Detects infection during the symptomless latent period	Requires laboratory infrastructure and trained personnel	Niu et al. (2022)
Multilocus gene sequencing	GAPDH, calmodulin and <i>Rpb2</i> sequence comparison	Resolves species identity within the <i>Alternaria</i> complex	Not practical for routine field-level diagnosis	Ivanović et al. (2022)
Deep learning image classification	Convolutional neural network analysis of leaf images	High accuracy, rapid, scalable via smartphone	Dependent on training data quality and field variability	Dame et al. (2025); Alhammad et al. (2025)

6. Forecasting and Decision Support Systems

6.1 Weather-Based Forecasting Models

Weather-based forecasting has long been advocated as a means of reducing unnecessary fungicide applications by restricting sprays to periods when environmental conditions are genuinely conducive to infection. The most widely adapted framework internationally is the tomato forecaster model, commonly abbreviated TOMCAST, which accumulates daily severity values calculated from the interaction of leaf wetness duration and mean temperature during the wet period, ranging from zero when conditions are unfavourable for spore formation to four when conditions are highly favourable, with a fungicide application recommended once accumulated severity values reach a predefined threshold (Meno et al., 2020). Adaptation of the model to potato production in north-west Spain incorporated aerobiological monitoring alongside the conventional weather-based calculation, lowering the minimum temperature threshold to reflect cooler local conditions, and this combined

approach allowed the first significant disease peak of the season to be predicted several days in advance in most growing seasons (Meno et al., 2020).

6.2 Integration of Plant Phenology and Pathogen Biology

Purely meteorological models have been shown to underperform models that incorporate plant developmental stage, because host susceptibility itself changes over the season independently of weather. Comparative evaluation of plant-based, pathogen-based and combined forecasting approaches found that plant-based indicators achieved the lowest prediction error for the timing of first symptom appearance among the pathogen-only models tested, and that combining a pathogen-based threshold with a plant-based growth indicator produced a more accurate prediction of disease onset than either approach used alone (Meno, Abuley et al., 2022). This finding indicates that host developmental state is not merely a passive backdrop to infection but an active determinant of when a canopy becomes vulnerable, a point with direct implications for the timing of the first protective fungicide application.

6.3 Fungicide Strategy, Pathogen Population Response and Regional Validation

Beyond the choice of forecasting variables, the pattern and sequence of fungicide use itself interacts with pathogen population biology in ways that decision support systems need to accommodate. Multi-season field monitoring of *A. solani* populations under different fungicide application strategies demonstrated that the composition of the pathogen population can shift measurably over the course of a single growing season depending on which fungicides are applied and in what sequence (Odilbekov et al., 2019). This finding reinforces the case, developed further in Section 7, for pairing forecasting-based spray timing with deliberate fungicide rotation rather than treating weather-based scheduling and resistance management as separate concerns. Threshold-based programmes, in which fungicide timing is linked to field-derived disease severity thresholds rather than a fixed calendar interval, have been shown to reduce overall fungicide input while maintaining acceptable disease control, offering a practical route to reducing selection pressure for resistance without sacrificing efficacy (Leiminger & Hausladen, 2012). A recurring conclusion across regional adaptations of these models, from Spain to elsewhere, is that the general framework transfers reasonably well between climatic zones, but that specific temperature and severity value thresholds require local recalibration before a model can be recommended for operational use in a new environment.

Table 4 summarises the principal forecasting frameworks and related decision support evidence discussed in the reviewed literature. A consistent conclusion emerging across these studies is that no single indicator, whether purely meteorological or purely phenological, provides optimal prediction in isolation, and that the most useful systems integrate weather thresholds with information on crop development stage while remaining attentive to how the resulting spray sequence shapes pathogen population dynamics.

Table 4. Weather-based forecasting and decision support models evaluated for potato early blight

Model or approach	Basis of prediction	Reported performance or outcome	Source references
TOMCAST (tomato forecaster)	Accumulated daily severity values from leaf wetness and temperature	Fungicide application timed to accumulated severity value threshold	Meno et al. (2020)
TOMCAST with aerobiological data	Weather thresholds combined with airborne spore monitoring	Improved prediction of the first significant disease peak by several days	Meno et al. (2020)
Plant phenology and growing degree-day models	Crop developmental stage and thermal accumulation	Lower prediction error for onset of first symptoms than pathogen-only models	Meno, Abuley et al. (2022)
Combined phenology and pathogen threshold models	Integration of plant-based and pathogen-based indicators	More accurate prediction of disease onset than either approach alone	Meno, Abuley et al. (2022)
Disease-oriented threshold values	Field-derived thresholds linking disease severity to spray timing	Reduced fungicide input relative to fixed-interval programmes	Leiminger & Hausladen (2012)
Fungicide-strategy population monitoring	Tracking of pathogen population composition under different spray sequences	Population composition shifts measurably within a single season according to fungicide strategy	Odilbekov et al. (2019)

7. Management Strategies

7.1 Chemical Control and Fungicide Resistance Management

Fungicide application remains the primary means of early blight control in most commercial potato production systems, reflecting the continued absence of highly resistant, agronomically acceptable cultivars for widespread cultivation. Economic evaluation of fungicide programmes in northern India found that scheduled applications of protectant and systemic fungicides, including mancozeb, hexaconazole, difenoconazole and chlorothalonil, significantly reduced disease severity relative to untreated controls while remaining cost-effective under prevailing input prices (Sharma et al., 2022). However, the sustained reliance on a limited number of fungicide chemistries has driven the emergence of resistance, most notably to quinone outside inhibitor and succinate dehydrogenase inhibitor fungicides, two mode-of-action classes that have been widely deployed against *A. solani* since the early 2000s. Molecular surveys of German isolates identified specific point mutations in the succinate dehydrogenase complex, designated SdhB-H278Y and SdhC-H134R, that confer reduced sensitivity to boscalid and related succinate dehydrogenase inhibitor fungicides, with the practical impact of these mutations demonstrated to extend from in vitro assays through greenhouse trials to reduced field efficacy (Metz et al., 2019). Whole-genome sequencing of a broader European isolate collection subsequently confirmed that these resistance-associated mutations occur against a backdrop of substantial underlying genetic diversity and recombination, a combination that increases the risk of resistance spreading more rapidly than would be expected from a purely clonal population structure (Einspanier et al., 2022). Continuous monitoring of pathogen populations within a single growing season has further shown that the composition of *A. solani* populations can shift measurably in response to the specific sequence and combination of fungicides applied, underscoring the importance of planned fungicide rotation rather than repeated use of a single active ingredient or mode-of-action class (Odilbekov et al., 2019).

7.2 Host Plant Resistance and Breeding

Genetic resistance offers a potentially more durable and environmentally favourable alternative to chemical control, but progress has been constrained by the polygenic, quantitative nature of resistance in cultivated potato and by an unfavourable genetic correlation between resistance and late maturity. Evaluation of 217 tetraploid cultivars in Pennsylvania found broad-sense heritability for early blight resistance of 0.89, but also identified a strong negative correlation between resistance and foliage maturity, meaning that many of the most resistant lines were also undesirably late-maturing (Xue et al., 2019). Subsequent quantitative trait locus mapping using a tetraploid population derived from a resistant clone, and employing a genetic linkage map covering more than 1,469 centimorgans with over 9,000 single nucleotide polymorphism markers, identified quantitative trait loci for resistance that were statistically independent of the loci controlling maturity, indicating that maturity-independent resistance is genetically achievable even though it has been difficult to combine with acceptable agronomic type in released cultivars (Xue et al., 2022). Complementary quantitative trait locus mapping in a separate Swedish tetraploid population identified loci associated with resistance expressed in both foliage and tubers, extending the genetic characterisation of resistance beyond the leaf canopy to the harvested organ of direct economic value (Odilbekov et al., 2020).

Wild relatives of cultivated potato represent an important reservoir of resistance genes not fully exploited in commercial breeding programmes. Interspecific crosses between diploid cultivated potato and the wild species *Solanum berthaultii* and *S. commersonii* subspecies *malmeanum* produced progeny populations exhibiting, respectively, quantitatively inherited and unusually dominantly inherited resistance, the latter finding being notable because resistance to necrotrophic pathogens is typically expected to behave as a recessive or quantitative trait (Wolters et al., 2021). These findings collectively suggest that although fully immune cultivars remain elusive, meaningful gains in partial, maturity-independent resistance are achievable through the deliberate exploitation of wild germplasm combined with marker-assisted selection informed by the quantitative trait locus studies described above.

7.3 Molecular Basis of Resistance and Susceptibility

Transcriptomic comparison of potato genotypes differing in susceptibility has begun to clarify the molecular pathways underlying partial resistance. Comparative transcriptome sequencing of three cultivars with contrasting susceptibility identified extensive upregulation of jasmonic acid and ethylene biosynthesis pathway

genes, together with enrichment of WRKY, ERF, bHLH, MYB and C2H2 transcription factor families among the differentially expressed genes, implicating these regulatory networks in the plant's defence response to necrotrophic colonisation (Sajeevan et al., 2023). Comparable work using seedlings with contrasting resistance levels identified more than 11,000 differentially expressed genes across the infection time course, with the greatest number of changes detected ten days post-infection, and used co-expression network analysis to nominate hub genes potentially useful as markers for resistance screening (Li et al., 2025). Collectively, these transcriptomic studies point toward jasmonate- and ethylene-mediated defence signalling as central to the potato response against *A. solani*, offering candidate pathways for future marker development and, potentially, targeted breeding or gene editing approaches.

7.4 Biological Control and Induced Resistance

Biological control agents, principally species of *Trichoderma*, have attracted growing research interest as a means of reducing reliance on synthetic fungicides while offering an additional mode of disease suppression compatible with integrated management programmes. Combined application of *Trichoderma viride* and *T. harzianum*, whether singly or as a dual consortium, achieved mycelial inhibition of *A. solani* exceeding 90 percent in vitro and was associated with elevation of systemic defence responses and measurable growth promotion in glasshouse trials, with scanning electron microscopy confirming visible antagonistic damage to fungal hyphae and conidia (Kumar et al., 2022). Biological control efficacy, however, is frequently reduced under field conditions relative to the glasshouse trials in which many candidate agents are first evaluated, reflecting the difficulty of establishing and maintaining antagonist populations under variable environmental exposure, and this gap between controlled and open-field performance remains a persistent constraint on the practical deployment of biocontrol agents at commercial scale.

7.5 Cultural Practices and Integrated Disease Management

Cultural practices, including crop rotation away from solanaceous hosts, use of pathogen-free seed tubers, balanced nutrient management and avoidance of plant stress, are widely recommended as components of an integrated approach because they reduce primary inoculum load and improve host vigour without contributing to selection pressure for fungicide resistance. A dedicated review of holistic pest management approaches for early blight concluded that no single tactic, whether chemical, genetic, biological or cultural, is sufficient on its own to achieve durable and economically sustainable control, and argued instead for management programmes that combine weather-informed spray timing, partially resistant cultivars, biological inputs and cultural sanitation within a coordinated framework, noting that moisture and environmental stress significantly influence the severity of outbreaks and that combining tactics addresses the disease at multiple points in its cycle (Jindo et al., 2021). This conclusion is reinforced by the evidence discussed above that fungicide application strategy itself shapes pathogen population structure over time (Odilbekov et al., 2019), implying that cultural and genetic tactics reducing overall reliance on any single fungicide mode of action serve a resistance-management function in addition to their direct effect on disease severity.

Table 5. Summary of early blight management strategies and reported efficacy

Strategy	Mechanism or basis	Reported outcome	Key constraint	Source references
Protectant and systemic fungicides	Direct inhibition of fungal growth or respiration	Significant reduction in disease severity; cost-effective under trial conditions	Risk of resistance development with repeated use of one mode of action	Sharma et al. (2022); Leiminger & Hausladen (2012)
Fungicide resistance monitoring	Detection of <i>Sdh</i> and cytochrome <i>b</i> mutations	Identifies emerging resistant genotypes to guide product choice	Requires molecular diagnostic capacity	Metz et al. (2019); Einspanier et al. (2022)
Cultivar resistance breeding	Selection for quantitative trait loci independent of maturity	Maturity-independent resistance loci identified but not yet widely deployed	Polygenic nature complicates breeding; resistance often linked to late maturity	Xue et al. (2019); Xue et al. (2022); Odilbekov et al. (2020)
Wild species introgression	Interspecific crosses with resistant wild relatives	Quantitative and, in one case, dominant resistance identified	Introgression of undesirable linked traits; lengthy breeding cycles	Wolters et al. (2021)

Strategy	Mechanism or basis	Reported outcome	Key constraint	Source references
Marker-assisted selection informed by transcriptomics	Candidate defence pathway and hub gene identification	Jasmonate and ethylene pathways implicated in resistance response	Markers not yet validated for routine breeding use	Sajeevan et al. (2023); Li et al. (2025)
Biological control (<i>Trichoderma</i> spp.)	Mycelial antagonism and induced systemic defence	Over 90 percent in vitro mycelial inhibition; growth promotion observed	Reduced and variable efficacy under field conditions	Kumar et al. (2022)
Cultural practices and integrated management	Reduction of primary inoculum and host stress, combined with other tactics	Recommended as the coordinating framework for sustainable control	Effectiveness difficult to isolate from other concurrent tactics	Jindo et al. (2021)

Table 5 illustrates that the available management tactics differ substantially in their maturity of development and readiness for field deployment. Fungicide-based control remains the most immediately actionable strategy but carries an inherent resistance-management burden, while genetic and biological approaches offer more sustainable long-term prospects but require further research investment before they can substitute for, rather than merely supplement, chemical control.

8. Yield Losses and Economic Significance

Quantifying the yield loss attributable specifically to early blight has proved more difficult than is often assumed, because losses depend on the interaction between disease severity, crop maturity class, soil type and prevailing weather during the critical tuber bulking period, and because many field trials confound early blight control with the simultaneous suppression of other foliar pathogens by the same fungicide programme. A decade-long series of field trials conducted in Sweden across eighteen starch potato trials and six ware potato trials found that fungicide-treated starch potato yields exceeded untreated yields by an average of 11.9 percent, ranging from 1.9 to 29.9 percent across individual trials, with the calculated potential yield loss reaching 14.3 percent on average once minor residual infection in the treated plots was accounted for, while no significant yield loss attributable to early blight was detected in the ware potato trials (Liljeroth et al., 2025). The same study reported a positive correlation between average seasonal air temperature and infection rate in untreated plots, consistent with the weather relationships summarised in Section 4, and highlighted that the large range of variation observed among individual trial years and sites reflects complex interactions among the factors influencing both infection rate and final yield (Liljeroth et al., 2025).

This variability contrasts with the frequently cited figure of 40 to 50 percent yield loss reported from severely affected, largely uncontrolled production systems in parts of Asia, a figure that reflects worst-case conditions of high disease pressure and susceptible cultivars rather than a representative average across well-managed commercial production (Li et al., 2024). The divergence between the modest, single-digit-to-low-double-digit losses recorded in well-managed European trials and the much larger figures reported from less intensively managed systems elsewhere underscores that early blight is best understood not as an inherently catastrophic disease but as one whose economic impact is strongly mediated by the effectiveness of the management programme in place, reinforcing the case for the integrated approaches discussed in Section 7 rather than reliance on any single control tactic.

9. Future Directions

Several research priorities emerge from the evidence reviewed above. First, further work is needed to resolve the species composition of the early blight complex across a wider range of production regions, since the co-occurrence of *A. solani* with related large-spored and small-spored *Alternaria* taxa complicates the interpretation of both epidemiological monitoring and fungicide efficacy trials that do not molecularly confirm the causal agent; regional surveys that have consistently detected multiple co-occurring species on the same host tissue suggest that disease aetiology may depend on local crop organisation and the proximity of alternative *Alternaria* hosts, a factor that could usefully inform future management guidance (Ivanović et al., 2022). Second, the genomic diversity and recombination potential documented within European *A. solani* populations argue for sustained, geographically broad surveillance of fungicide sensitivity, ideally integrating whole-genome and targeted mutation screening approaches so that resistance can be detected and managed proactively rather than

reactively (Einspanier et al., 2022). Third, the transcriptomic identification of candidate defence pathways and hub genes associated with partial resistance provides a foundation for developing molecular markers that could accelerate breeding for maturity-independent resistance, provided that these candidate genes are validated across diverse genetic backgrounds and environments (Li et al., 2025). Fourth, the rapid progress achieved in deep learning-based image classification of early blight symptoms, including approaches incorporating explainable artificial intelligence to improve model transparency, suggests considerable potential for low-cost, farmer-accessible diagnostic tools, provided that future work addresses the current reliance on relatively controlled training image datasets and validates model performance under the full range of field lighting, background and canopy conditions encountered in commercial production (Dame et al., 2025). Finally, further regional calibration and cross-validation of weather-based and phenology-integrated forecasting models remain necessary before such tools can be recommended with confidence outside the specific climatic zones in which they were originally developed and tested.

10. Conclusions

Early blight caused by *Alternaria solani* is a globally distributed and economically significant constraint on potato production whose management continues to rely predominantly on fungicide application despite growing evidence of resistance to key chemistries. The disease is governed by a well-characterised, though not fully uniform, set of weather relationships in which temperature, leaf wetness duration and relative humidity interact with crop phenology to determine both the timing of epidemic onset and the rate of subsequent disease progress. Forecasting models built around these relationships, most notably adaptations of the tomato forecaster framework, offer a validated means of reducing fungicide input while maintaining control, but require regional calibration and benefit substantially from integration with plant developmental stage. Diagnostic capacity has expanded considerably beyond conventional visual scoring to include molecular assays capable of detecting latent infection and computational image analysis tools capable of rapid, scalable severity assessment, although neither has yet fully displaced visual assessment as the practical standard in commercial fields. Genetic resistance remains partial and polygenic, complicated by an unfavourable association with late maturity, but recent quantitative trait locus mapping and transcriptomic studies have begun to identify resistance mechanisms and candidate loci that are independent of maturity and therefore potentially more useful for breeding. Taken together, the evidence indicates that sustainable long-term management of early blight will depend on the coordinated integration of weather- and phenology-informed fungicide timing, deliberate resistance-management rotation, progressively improved host genetic resistance, and biological and cultural tactics, rather than on any single intervention applied in isolation.

11. Limitations

This review is subject to several limitations that should be considered when interpreting its conclusions. The narrative synthesis approach, while appropriate for integrating heterogeneous evidence across epidemiological, molecular and computational domains, does not provide a pooled quantitative estimate of effect sizes and remains susceptible to selection bias in the choice and interpretation of included studies, despite the explicit search and eligibility criteria applied. The literature search was restricted to English-language publications, which may have excluded relevant regional studies published in other languages, particularly from major potato-producing countries where research is not always disseminated in English-language journals. The evidence base on weather relations and forecasting models is geographically concentrated in a relatively small number of production regions, notably north-western Spain and parts of South Asia, and the numerical thresholds reported in these studies may not transfer directly to other climatic zones without local recalibration. Similarly, much of the genomic and transcriptomic evidence on resistance and fungicide sensitivity derives from a limited number of research groups and geographic origins, principally Europe, which may not capture the full extent of pathogen genetic diversity present globally. Finally, because early blight frequently co-occurs with other foliar and soil-borne pathogens under field conditions, and because many management trials evaluate fungicide programmes that simultaneously target multiple diseases, the yield loss and efficacy figures reported in the reviewed literature should be interpreted as indicative rather than universally generalisable estimates of the specific contribution of early blight in isolation.

Declaration of AI Use

This manuscript was prepared through the combined contributions of all author(s), including contributions to the study design, data, content development, results, interpretation, and related scholarly work. The author(s) acknowledge the use of Grammarly and ChatGPT to assist with grammar checking, language refinement, reference formatting. These AI-assisted tools were not used as authors and did not replace the intellectual contributions or scholarly judgment of the author(s). All AI-assisted outputs, including content, references, and interpretations, were carefully reviewed, revised, verified, and approved by the author(s). The author(s) accept full responsibility for the accuracy, integrity, and final content of the manuscript.

Competing Interests

Authors have declared that they have no known competing financial interests OR non-financial interests OR personal relationships that could have appeared to influence the work reported in this paper.

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