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Predicting Future *Phytophthora* Outbreaks: New Tools to Identify Emerging Lineages and Track Spread

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Abstract

The risk of the introduction of pathogens into the USA with trade requires continued surveillance and improved diagnostic capabilities at our borders. *Phytophthora infestans*, the causal agent of potato late blight, was responsible for the Irish potato famine and is still a threat to food security globally. A disease surveillance and mapping system called USABlight.org has been operative in the USA since 2011 to report disease presence and to alert stakeholders of the presence of blight. USABlight has now been transitioned into the Plant Aid Database (PaDB). An SSR genotyping querying system has been developed to identify emerging lineages, and sequence-based approaches have been used to track the spread of modern and historic lineages of the pathogen. A complete T-BAS phylogeny of *Phytophthora* has been released as a community tool for identification of new emergent *Phytophthora* species and for phylogenetic tracking of specific SSR lineages of *P. infestans*. We have also developed LAMP assays that can be deployed on smart phones for rapid in-field detection of specific lineages of *Phytophthora infestans.* Targeted amplicon sequencing is underway to monitor the emergence of specific lineages and changes in fungicide resistance and virulence phenotypes of the pathogen. All these tools will help us respond to and mitigate outbreaks, improve the deployment of host resistance, and inform policy.

Keywords Detection · Disease surveillance · *Phytophthora infestans* · Potato late blight

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Introduction

Management of new pests, pathogens, and invasive plants is a major challenge for global agricultural and forest ecosystems (Ristaino et al. 2021). Emerging diseases are on the rise in many parts of the world. *Phytophthora* species are responsible for diseases on a wide range of host crops, natural vegetation, and forestry worldwide, and represent a significant and emerging food security threat (Brasier 2008). *Phytophthora infestans* exemplifies this threat; it was the first species in the genus described and left a path of devastation on potato in its wake in the USA, Ireland, and mainland Europe in the nineteenth century (Berkeley 1846; Bourke 1964). Movement of infected potatoes led to the potato famine epidemics of the nineteenth century that resulted in widespread human hunger, disease, and ultimately the death of one million people in Ireland and the emigration of another million people (Bourke 1964; Ristaino et al. 2020a). The pathogen still causes a destructive foliar blight and infects potato and tomato globally (Fry et al. 2015; Ristaino et al. 2020a).

Late blight is considered the most important biotic constraint to potato production worldwide (Anderson et al. 2004). Under favourable weather conditions, tomato and potato crops can be destroyed within hours if fungicides are not used (Fig. 1A) (Ristaino et al. 2020b). Yield losses caused by late blight and the cost of control measures have been estimated to exceed 6.7 billion dollars annually (Haverkort et al. 2008). Socio-economic hardships are still caused by late blight, as evidenced by the severe epidemics that occurred in Russia in the 1990s, in the northeastern USA in 2009, and annually in Egypt, sub-Saharan Africa, and the Andean region where subsistence farmers grow potatoes (Hu et al. 2012; Fry et al. 2015; Ristaino et al. 2020b). Fungicides are limited in many areas of the developing world, and blight can become severe. US and European potato growers use 15–20 fungicide applications per growing season to keep the disease at bay and can lose millions of dollars annually to late blight if timely applications are not done.

Phytophthora infestans is considered a reemerging disease for several reasons. First, the pathogen has a polycyclic life cycle and sporangia can be dispersed over long distances of many kilometres and thus easily spread (Fry et al. 2015). The pathogen can also move in infected tubers, tomato fruit, or transplants (Hu et al. 2012). In fact, the spread of the pathogen in infected potato tubers has resulted in the movement and spread of aggressive lineages over long distances (Chowdappa et al. 2013; Cooke et al. 2012; Saville and Ristaino 2021). Fungicide-resistant strains of the pathogen emerged shortly after the release of mefenoxam in the 1980s and mefenoxam resistance still occurs (Davidse et al. 1988; Saville et al. 2015). Monoculture of highly susceptible potato varieties has also exacerbated disease. R-gene-based resistance in potato has been short-lived since the pathogen's genome plasticity has enabled it to evade host plant R gene-mediated resistance (Armstrong et al. 2005; Birch et al. 2008; Bos et al. 2010; Coomber et al. 2024; Gilroy et al. 2011; Haas et al. 2009; Vleeshouwers et al. 2011).

The ability of *P. infestans* to infect and remain latent in potato tubers or the fruits of tomato plants has enabled it to spread through national and international trade. The widespread dissemination of the US-22 clonal lineage in tomato transplants in

Fig. 1 Surveillance of *Phytophthora infestans*. **A** A research potato field with late blight from Stephen Kildea, Teasagc, Co. Carlow, Ireland. **B** A map of potato late blight data from 2011 to present from Plant-Aid.org. The system is managed by Chris Jones, the Center for Geospatial Analytics at NC State University

the USA in 2009 provides an example of the speed at which a specific lineage of *P. infestans* can be spread in plant material (Fry et al. 2013; Hu et al. 2012). In the case of potatoes, tubers destined for either food or seed are considered a risk for pathogen spread, and despite plant biosecurity protocols, the spread of *P. infestans* via tubers occurs (Chowdappa et al. 2013; Ristaino 2021a).

There is an urgent need to develop more real-time disease surveillance tools including web-based mapping and risk systems, genomic surveillance, and in-field diagnostics so stakeholders can identify the pathogen in imported transplants or tubers, identify emerging lineages and novel *Phytophthora* species, and manage them appropriately. We live in a global community and *Phytophthora infestans* is a community disease that does not recognize country borders. The following is a summary of a research presentation given by the senior author entitled "Predicting Future *Phytophthora* Outbreaks: New tools to Identify Emerging Lineages and Track Spread" given by the author at the EuroBlight 2024 meetings held in Lunteren, The Netherlands, May 13–17, 2027.

Biosurveillance of Late Blight—USABlight

We developed a disease mapping and surveillance system named USABlight in 2011 and began active surveillance, tracking, and genotyping of *P. infestans* after severe late blight outbreaks occurred throughout the eastern USA from infected tomato transplants in 2009 (Fry et al. 2013). The USABlight surveillance system was initially funded by a USDA NIFA grant and then a USDA IPM cap grant. In 2018, we received funds from the NSF Predictive Intelligence for Pandemic Preparedness (PIPP) programme to develop real-time surveillance capabilities. The data from the USABlight system is now part of Plant-aid.org and is housed at NC State University. This system now contains 15 years of data on late blight disease occurrences on tomato and potato in the USA. Disease occurrence data is submitted by growers, researchers, and homeowners. The submitted reports are viewed by research and extension validators to confirm diagnosis and ensure accurate mapping occurs. Outbreaks are recorded via a web GIS system and validators are notified via email (Fig. 1B). Once confirmed, the reporter is contacted and the outbreak is reported to the public site at the county level. Samples from disease reports are submitted and are genotyped using microsatellite simple sequence repeats (SSR) using 12-plex microsatellite markers (Li et al. 2013). Samples in the past were genotyped in the Fry, Smart, and Hansen labs at Cornell University, the Ristaino lab at NC State and are now genotyped in the Restrepo Lab at Cornell

USABlight data has recently been migrated to the Plant Aid Database, a larger database that also monitors outbreaks of cucurbit downy mildews and *Phytophthora ramorum*. First late blight disease reports usually occur in Florida each year, and disease occurs later in increasingly northern states as the season progresses. A clear change in pathogen genotypes has emerged over time (Fig. 2). Initially, the US-8 and US-11 lineages were predominantly on the west coast on potato. The US-22 lineage emerged in 2009 on tomato and increased over time and was subsequently displaced by US-23 around 2012. The US-23, which infects both tomato and potato, has increased in occurrence over time. The US-24 lineage occurred in limited areas of the Midwest in seed producing states, and the US-25 lineage has only been reported in New York. US-23 remains the dominant lineage on both tomato and potato in the USA.

The mefenoxam-resistant lineage US-8 was common in early years and has since declined in potato. It has been displaced by the mefenoxam-sensitive US-23 lineage on both potato and tomato, enabling growers to once again use this compound in the field (Hu et al. 2012; Saville et al. 2015). In 2015, fungicide sensitivity baseline data to a range of oomycete-targeted fungicides was collected on all recent US lineages of *P. infestans*. The US-8 and US-11 lineages were mefenoxam resistant (Fig. 3A) while the rest of the lineages were sensitive to mefenoxam (Fig. 3B) (Saville et al.

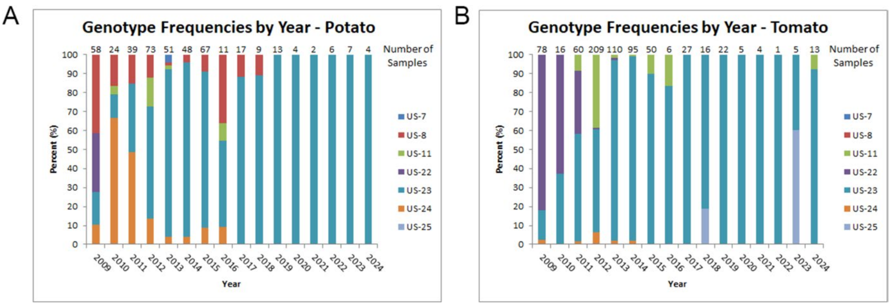

Fig. 2 Lineages of *Phytophthora infestans* reported from USABlight on **A** potato and **B** tomato found in the USA from 2011 to 2024. Isolates were collected by USABlight team collaborators and genotyped by microsatellite genotyping (SSR) at either Cornell University (Fry/Smart lab) or NC State (Ristaino lab)

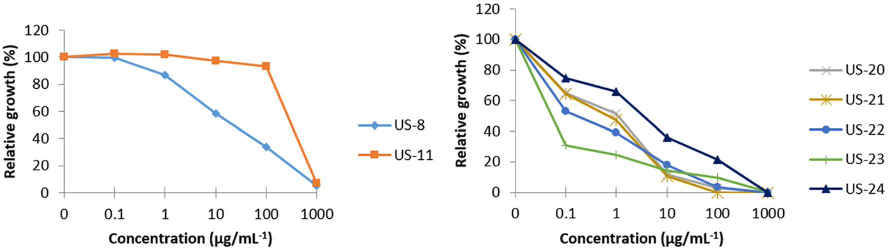

Fig. 3 Lineages of *Phytophthora infestans* that differ in resistance to mefenoxam 2009–2023. US-8 and US-11 (left) are resistant to mefenoxam while US-20, US-21, US-22, US-23, and US-24 (right) are sensitive to mefenoxam

2015). Other compounds tested in the study included fluopicolide, cyazofamid, etridiazole, azoxystrobin, cymoxanil, and mandipropamid (Saville et al. 2015). US lineages remained sensitive to all compounds but mefenoxam in the 2015 study. Recently, novel fungicide-resistant lineages of *P. infestans* with resistance to mandipropamid (EU-43), oxathiapiprolin (OSBPI) (EU-43 and EU-46), and fluazinam (EU-37) have been reported in the UK, Denmark, and Sweden (Abuley et al. 2023; EuroBlight 2023; Ericsson 2024; Lynott et al. 2023; Mboup, 2016). Studies have not been done with recent US lineages to test for resistance to these compounds since the original baseline study of 2015 (Saville et al. 2015). It is important for growers to remain vigilant and to rotate fungicides with different modes of action when spraying fungicides for control of late blight to prevent resistance development.

The USABlight surveillance system is useful since growers can also check the map and determine the appropriate time to begin fungicide applications if late blight is reported nearby and weather is conducive. The web statistics on the use of USABlight show that the outbreak map is the most frequently viewed page after the home page. In fact, 42% of all the sessions on USABlight include viewing the outbreak map. Growers not only view the map but can sign up for email alerts. During the 2017 season, over 7595 alerts were sent to users covering 363 geographic locations.

One important goal of USABlight was to improve fungicide use efficiency and reduce the number of fungicide applications for control of late blight. The USAlight disease alert system and the Blight Pro decision support tools have helped growers target when to use fungicides, reduce application on a wider scale, and deploy resistant varieties that require fewer fungicide applications (Small et al. 2015). We evaluated the benefits of using weather-based disease forecasting systems for tomato late blight and found a significant reduction in the number of sprays and significant economic value to tomato growers (Liu et al. 2018). Late blight researchers in the USA in various states continue to collect, monitor, and send samples for genotyping and alert growers of disease outbreaks and lineages nearby so they can better deploy timely fungicide applications to manage the disease (Ristaino et al. 2020b). Fungicide forecasting systems are used in many potato growing regions in the USA and in other parts of the world to predict late blight (Cucak et al. 2021; Narouei-Khandan et al. 2020; Wilbur 2024).

We have seen an increase in warm temperature *Phytophthora* species causing disease on potato and tomato since 2017 in wet fields flooded by storms. Foliar blight on potatoes from *P. nicotianae* can occur under warm, wet conditions and can be easily mistaken for foliar leaf infections caused by the late blight pathogen *P. infestans*, because the symptoms are similar (Saville et al. 2023). *Phytophthora nicotianae* can be splash-dispersed from soil to foliage during heavy rain. The pathogen can survive in soil at temperatures up to 32 °C and has caused outbreaks in the southern and eastern USA on potato and tomato in recent years. All *P. nicotianae* isolates tested were mefenoxam sensitive. Since *P. nicotianae* can sexually reproduce and survive as oospores in soil, we continue to monitor its occurrence (Saville et al.,al 2023). Since *P. nicotianae* is soilborne, crop rotation is a useful management strategy to avoid planting in fields with a history of the pathogen.

Tracking Outbreak Strains and Genotyping

It has been long known that *Phytophthora* species have a remarkably flexible genetic system (Brasier 1992). This flexibility in *P. infestans* is now known to be combined with a large repeat-rich genome and repertoire of effector genes (Haas et al. 2009), which supports its pathogenicity and adaptability. Genetic variation is also illustrated by elevated ploidy within *P. infestans* (Hamed & Gisi 2013), SSRs (Cooke et al. 2012), and genomic SNPs analysis (Coomber et al. 2024; Martin et al. 2015). Sexual reproduction enables the pathogen to generate new pathogenic variants, and asexual reproduction with a high reproductive rate allows the fittest and most aggressive forms to spread rapidly at spatial scales from region to continent (Cooke et al. 2012; Saville and Ristaino, 2020a). *Phytophthora infestans* does not reproduce sexually in the US, but sexual reproduction is well documented in Mexico, the Netherlands, and Scandinavia (Goodwin et al. 1994; Drenth et al. 1994; Yuen and Andersson 2013). Examples of such clonal spread include the US-8, US-22, and US-23 clonal lineages in the USA (Fry and Goodwin 1997; Hu et al. 2012; Saville et al. 2015) and the 13_A2 lineage in Europe and India (Cooke et al., 2012a; Dey et al. 2017). The US-23 and 13_A2 clonal lineages attained regional domination within a few growing seasons. While US lineages have changed over time, they are not as genetically diverse as lineages found in some European countries where the pathogen reproduces sexually.

Many different *Phytophthora* species can infect potato and tomato. To track the emerging *Phytophthora* species, we developed an interactive T-BAS tool and phylogenetic framework for *Phytophthora* using multilocus genotyping (Carbone et al. 2017, 2019; Coomber et al. 2023). The *Phytophthora* T-BAS tool uses multilocus sequences from eight nuclear loci and one mitochondrial locus and includes 192 species of *Phytophthora*. The phylogenetic tree was inferred using the RAxML maximum likelihood programme. The T-BAS tool provides a visualization framework allowing users to place unknown isolates on a curated phylogeny of all *Phytophthora* species (https://guide-tbas.cifr.ncsu.edu/tbas). Critically, the tree can be updated in real-time as new species are described and submitted for inclusion. The tool contains metadata including clade, host species, substrate, sexual characteristics, distribution, and reference literature, which can be visualized on the tree and downloaded for other uses. A search engine was also developed to identify microsatellite (SSR) genotypes of *P. infestans* based on genetic distance to known lineages (Fig. 4). The SSR T-BAS tree contains all the known SSR genotypes and allows the user to identify a new *P. infestans* lineage and place it in the tree if it has not been reported previously. In the future, we plan to incorporate population genomics into forecasting systems to track the spread of specific lineages of *P. infestans* more rapidly and understand hotspots of evolution and monitor the spread of problematic lineages over space and time. The SSR T-BAS tool allows users to query the database and track SSR genotypes by host, year, and genotype. The tree is hosted within the DeCIFR platform at the Center for Integrated Fungal Research (https://decifr.cifr.ncsu.edu/) and is freely available to registered users through T-BAS (https://tbas.cifr.ncsu.edu/).

We have made significant strides in our understanding of the evolution and origins of *P. infestans*. *Phytophthora infestans* has several closely related sister species present in Mexico (*P. ipomoeae*, *P. mirabilis*) and the Andes of Peru, Ecuador, and Colombia (*P. andina*, *P. betacei*, and *P. urerae*). We examined the evolutionary history of *Phytophthora infestans* and its close relatives in the 1c clade (Coomber et al. 2025a). We compared modern aggressive lineages of *P. infestans* from the USA, South America, and Mexico with historic lineages from nineteenth-century outbreaks to examine the pathogen's global spread and determine evolutionary relatedness (Coomber et al. 2025a). We used whole genome sequence data from 69 isolates of *Phytophthora* species in the 1c clade, including *P. infestans*, and conducted a range of genomic analyses. We consistently identified distinct and later divergence of the two Mexican *Phytophthora* species, *P. mirabilis* and *P. ipomoeae*, from the *P. infestans*, *P. andina*, and *P. betacei* complex (Fig. 5A). *P. andina*, *P. betacei*, and *P. infestans* formed a species complex with indistinct species boundaries, hybridizations between the species, and short times to common ancestry. Historic nineteenth-century *P. infestans* exhibited more recent divergence (0.65 kiloyears (KYR) or 0.65 thousand years) than other 1c clade species of *Phytophthora* (*P. infestans*, *P. betacei*, *P. andina*) from South America, which diverged 5.0 thousand years ago. All modern populations were derived from historic *P. infestans* famine lineages (Fig. 5B). US-1,

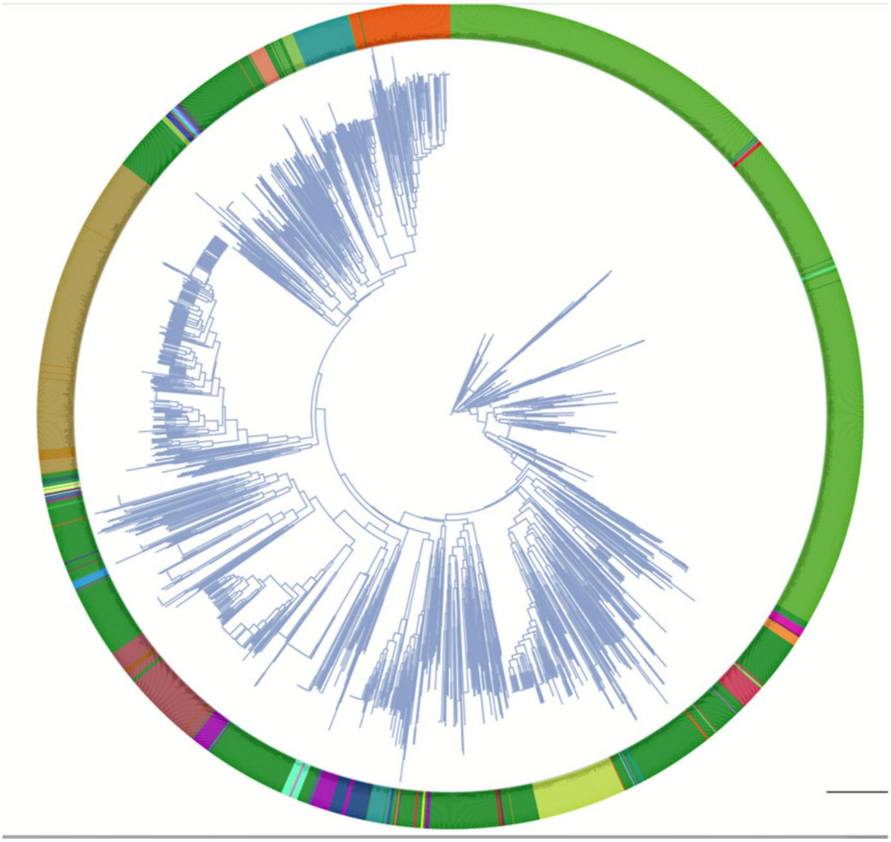

Fig. 4 *Phytophthora infestans* SSR T-BAS tree **A** showing all known global SSR lineages of *Phytophthora infestans*. Lineage names are shown in legend with US and EU lineages country name first. The microsatellite T-BAS tree can be found at T-BAS V2.3 on the DICIFR website at https://guide-tbas.cifr.ncsu.edu/tbas

South American, and Mexican populations diverged later (Fig. 5B). Speciation in the 1c clade and evolution of *P*. *infestans* occurred in the Andes. Based on the time of divergence of *P*. *infestans* from its closest relatives, *P*. *andina* and *P*. *betacei* in the Andean region, we consider the Andes to be the centre of origin of *P*. *infestans*, with modern globalization contributing to admixture between *P*. *infestans* populations today from Mexico, the Andes, and Europe (Coomber et al. 2025a).

The US-23 clonal lineage is widespread in the USA and sensitive to mefenoxam. However, we know that isolates of US-23 differ in virulence on tomato and that some are more aggressive than others. In addition, host resistance breaking strains that can overcome both *Ph2* and *Ph3* resistance (R) genes in tomato have been observed in North Carolina populations (Coomber et al. 2025b). A new genotyping platform for *P. infestans* is needed to track the short-term evolution of US-23. Currently, we have evaluated the potential utility of the known cloned effectors documented in the

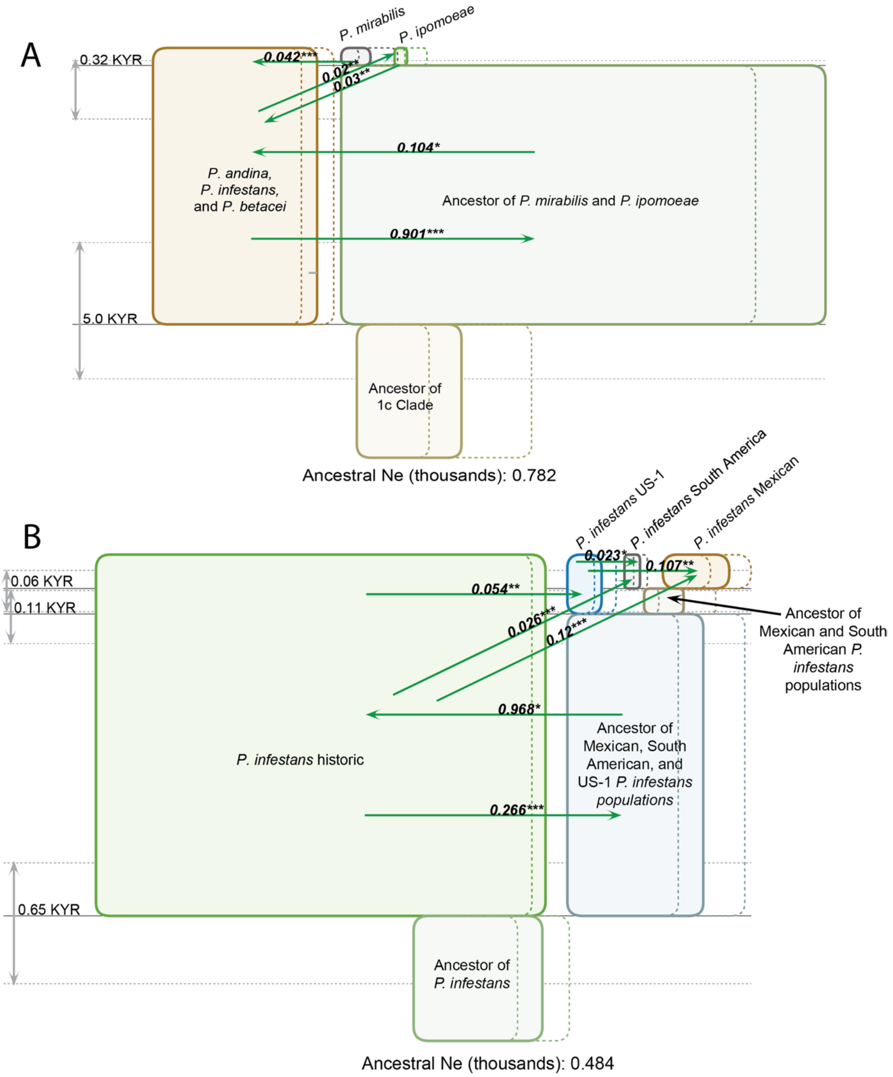

Fig. 5 Genealogy of **A** *P. mirabilis*, *P. ipomoeae*, and the *P. andina*-*P. infestans*-*P. betacei* species complex inferred with IMa3 and visualized with the IMfig programme. The phylogeny is depicted as a series of boxes organized hierarchically, with ancestor boxes positioned in between the corresponding descendants, and the width of boxes proportional to estimated N_e (effective population size). **B** Estimation of migration rates, time of divergence, and ancestral population size between five subpopulations of *P. infestans* (Historic, US-1, South American (SA), and Mexican) inferred with IMA3 and visualized with IMFig. More gene flow is observed into and out of the Andes. Image reproduced from Coomber et al. (2025a).

literature using representatives from recent US genotypes (US-8, US-11, US-22, US-23, US-24) as well as 13_A2 and noted historic lineages (US-1, FAM-1). We are exploring a platform based on the MARPLE system (Radhakrishnan et al. 2019)

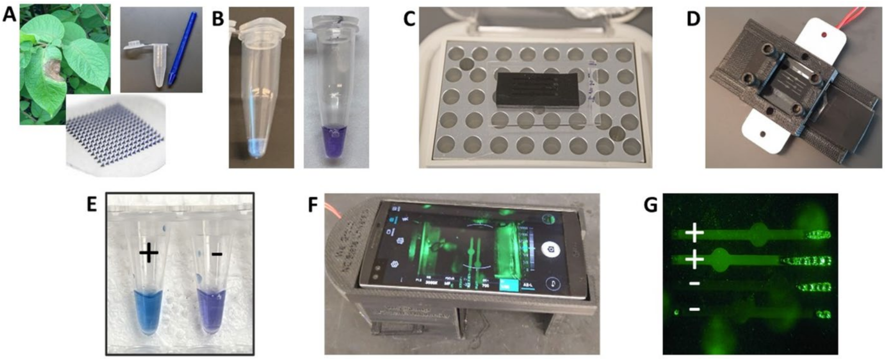

Fig. 6 Workflow of *Phytophthora infestans* LAMP assay. **A** DNA is extracted from tissue using either a microneedle (MN) or fast NaOH extraction. **B** Lyophilized master mix (lyoBeads) rehydrated with extracted DNA and buffer. LAMP assay is heated on either **C** a microfluidic chip on AgDia heat block or **D** a microfluidic chip on a hot slide or **E** in tubes on an AgDia heat block. Colour change from violet (negative) to light blue indicates a positive reaction, and **F** LAMP reactions can be visualized from Eva-Green fluorescence on a smartphone platform. **G** Positive reactions fluoresce bright green and negative reactions do not fluoresce. Image modified from Mainello-Land et al. (2025).

using targeted amplicon sequencing of specific effectors (e.g. *Avr3a*, *AVR1*, *AVR-vnt1*) to monitor emerging traits of new lineages and effector changes within the US-23 lineage. Sequences will be compared using principal component analysis and maximum likelihood analysis to determine if differences can be observed. PCR is run on a mini thermocycler that is field ready. The genotyping is run on a MinION sequencer. We plan to monitor mitochondrial DNA haplotype and fungicide sensitivity using markers for mandipropamid (CesA3) resistance (Blum et al. 2010) and oxathiapiprolin (OSBP) resistance (Mboup et al. 2022) to look for changes in US-23 to these fungicides. Genotype by sequencing data has confirmed that US-23 lineages show genetic variation (Hansen et al. 2016), but association of these differences with phenotypic traits of interest to growers like fungicide resistance or virulence will be needed.

Disease Detection

Deployment of rapid diagnostic assays can reduce the spread of plant diseases. We have developed and tested rapid field detection methods using LAMP assays for the detection of *Phytophthora infestans*, *P. ramorum*, and *P. kernoviae* (Ristaino et al. 2020b; Mainello-Land et al. 2020b). We have also developed an "all *Phytophthora*" LAMP assay that detects the major *Phytophthora* species on potato and tomato. The workflow includes using microneedle patches (MN) to quickly extract DNA from an infected potato leaf (Paul et al. 2020, 2021) (Fig. 6). Then, DNA is eluted off the MN into a buffer, and this solution is used to rehydrate a LyoBead, which contains all the reagents and primers needed to detect *P. infestans* and run the LAMP assay (Ristaino et al. 2020a). We have also developed LAMP assays to detect other common tomato diseases, including early blight (*Alternaria* spp.), bacterial spot (*Xanthomonas perforans*), and tomato spotted wilt virus (TSWV) (Shymanovich et al. 2024a). We developed a CRISPR/Cas12a cassette that can be used in combination with LAMP to detect the California resistance-breaking strain of TSWV in tomato (Shymanovich et al. 2024b). These CRISPR detection assays allow highly specific detection of mutations within genes of interest in the target pathogens and could be used to rapidly detect fungicide resistant strains in the future.

We have also developed two prototype volatile organic compound (VOC) sensors, including a colorimetric sensor and a wearable plant sensor that can detect pathogen volatiles released from *P. infestans*–infected tomato (Li et al. 2019, 2021; Lee et al. 2023). While this work is still in progress, it holds promise for rapid and continuous detection of plant stress by both abiotic (water and temperature stress) and biotic stress (*P. infestans* and *P. ramorum* infection). Further work is needed to make these sensors more robust for field use or continuous monitoring where wind, water, and fungicides can interfere with plant volatile release and sensor readings.

Data Integration and New Analytic Tools for Management

In a recent perspective piece written by the author and a team of scientists, we suggested the need for more active surveillance of plant diseases using web-based platforms such as USABlight or EuroBlight (Ristaino et al. 2021). Disease surveillance data can be visualized using geospatial analytics to track the movement of outbreak strains on the Plant-Aid.org (Fig. 7). The Plant Aid platform includes the late blight mapping system. Data from disease surveillance efforts can be incorporated into the Pest and Pathogen Spread (PoPs) pathogen risk model to predict and forecast spread based on weather parameters such as temperature and rainfall and host presence (Jones et al. 2021). Disease detection reports can be input from assays such as LAMP assays. Genomic surveillance of *P. infestans* SSR genotypes is also mapped (Fig. 7). Phylogenomics of specific strains is also integrated into the platform via the T-BAS tool. Big data predictors include transportation and trade networks, geography, weather and climate parameters, disease detection from DNA sequence data, pathogen detection sensors, text mining of historical and social media data, citizen science data, and identification apps. Advances in earth observations via satellite and remote sensing are revolutionizing our ability to see plant disease on the ground at larger spatial scales. Plans are underway to expand this type of disease surveillance for *P. infestans* and other foliar pathogens. At the field level, by deploying sensors for early pathogen detection, we may be able to prevent outbreaks before they become epidemics.

We can also learn from historical outbreak data as well. Advances in data mining and text analytics have allowed us to recreate plant disease outbreak maps from nineteenth century late blight location data (Saeffer et al. 2024). Social media reports can also enable us to determine where pests and pathogens are being “talked” about in social media. Phylogenomic surveillance by using SSR genotyping, single nucleotide polymorphisms (SNPs), or pathogen population genomics is now allowing us

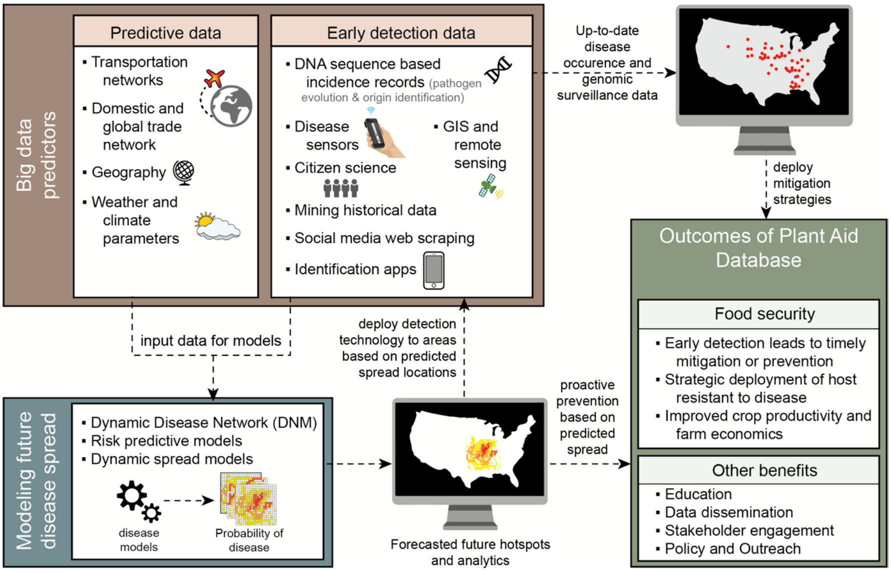

Fig. 7 Critical components and data analytics are integrated into the Plant Aid Database. Big data predictors include transportation and trade networks, geography, weather and climate parameters, disease detection from DNA sequence data, pathogen detection sensors, text mining of historical and social media data, citizen science data, and identification apps. These data can be used to model disease spread and create outbreak maps and predict future spread, understand pathogen evolution, and identify origin locations. Enhanced monitoring and proactive mitigation strategies can be deployed in forecasted future hotspots. Image reproduced from Ristaino et al. (2021).

to monitor the spread of specific lineages of *P. infestans* or specific phenotypic traits such as fungicide resistance or the ability to overcome a particular R gene. The *P. infestans* LAMP detection results can be fed into the Plant Aid Database to quickly confirm pathogen detection in samples from the field so data on outbreak occurrence can be quickly mapped. Once other phenotypic trait markers are developed such as information on fungicide sensitivity or virulence phenotype, these data could also be included in PADB.

Timely digital delivery of information to stakeholders can help growers choose when and what fungicide to spray based on real time information from *Phytophthora* outbreaks. Adaptive management and stakeholder input are vital to improve and expand disease surveillance systems like Plant-Aid.org and other novel tool sets needed to manage late blight.

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Author Contribution JBR conceived, analyzed, and wrote this review paper.

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Data Availability All data presented in this review article is available from the cited publications by the corresponding author.

Declarations

Competing Interests The author declares no competing interests.

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