Potato late blight caused by *Phytophthora infestans*: from molecular interactions to integrated management strategies[1]

DONG Suo-meng[1], ZHOU Shao-qun[2]

[1]Key Laboratory of Integrated Management of Crop Disease and Pests, Ministry of Education, Department of Plant Pathology and Key Laboratory of Plant Immunity, Nanjing Agricultural University, Nanjing 210095, P.R.China

[2] Shenzhen Branch, Guangdong Laboratory of Lingnan Modern Agriculture, Genome Analysis Laboratory of the Ministry of Agriculture and Rural Affairs, Agricultural Genomics Institute at Shenzhen, Chinese Academy of Agricultural Sciences, Shenzhen, P.R.China

Abstract

Over 170 years after the infamous Irish Potato Famine, potato late blight (PLB) caused by *Phytophthora infestans* remains the single most devastating disease of global potato production, causing up to 10 billion USD in yield loss and management costs. Through decades of research, growers and agronomists in the field as well as laboratory scientists have made significant progress in understanding the molecular pathogenesis process of this critical patho-system and effective management strategies to control PLB. Yet, the need to feed an ever-increasing global population under changing climate demands continued improvement in efficient and sustainable PLB management schemes that can be implemented across a broad economic spectrum. In this review, we briefly summarize the current understanding of the molecular interaction between *P. infestans* and its host plants, highlight the current integrated pest management strategy to control PLB on local and continental scales, and discuss the potential of further improvement of sustainable PLB control through genetic enhancement of crop resistance and emerging crop protection technologies.

Keywords: potato late blight, phytophthora infestans, integrated pest management

[1] *Correspondence DONG Suo-meng, E-mail: smdong@njau.edu.cn; ZHOU Shao-qun, E-mail: zhoushaoqun@caas.cn

Introduction

Potato Late Blight (PLB) caused by the oomycete plant pathogen *Phytophthora infestans* is a devastating disease worldwide and led to the infamous Irish potato famine in 1845-1852 (Bourke 1964, Savary *et al*. 2017). Originated from central Mexico or South America, this disease has spread to almost all major potato-producing countries including the United States, Canada, China, and India (Fry *et al.* 2015; Fry *et al.* 2016). To this date, PLB remains the most important biotic constraint to potato production worldwide and presents a major threat to global food security, especially for under-developed areas that heavily depend on potato as the major source of food (Pennisi,2010; Andersson *et al.* 2015). Globally, yield loss and management cost for PLB can add up to 3-10 billion USD per annum (Haverkort *et al*. 2009； Kamoun *et al*. 2015). In developing countries where efficient chemical control is often cost-prohibitive, PLB routinely lead to over 60% yield loss (Copeland *et al*.1993). In these areas, insufficient control for PLB and other crop diseases is a major cause of the four-fold lower per unit potato yield compared to the developed countries (Hareau *et al*.2014). On the other hand, pesticide cost for PLB control could account for 10 to 25 percent of the market value of the potato harvest in developed countries (Haverkort *et al*. 2009; Kamoun *et al*. 2015). In some growth areas, up to eight pesticide applications per growth season is required for sufficient control, presenting both heavy economic and environmental costs associated with potato production (Naumann *et al.* 2020).

In the field, symptoms of PLB infection typically first emerge as dark grey to brown water-soaked spots on leaf tissues, surrounded by white mold-like growth around the perimeter (Gevens *et al*. 2013). Under high humidity (>90%) and low temperature (10-23 ^{o}C), infection will rapidly spread within and between plants through systematic filamentous growth and spread of infectious asexual sporangia through air and water splash, and could lead to total necrosis of infected plants in an entire field within 5-10 days (Aylor *et al*. 2003; Nowicki *et al.* 2012). Underground tubers could become infected through systematic spread of the infection and through wash-off of conidia-containing sporangia. Infection of tubers is usually initiated at physical weak spots such as the eyes, lenticels, and existing wounds. The filamentous growth of the pathogen within tuber leads to color change, and is often compounded with secondary infection by soft rot bacteria, rendering the tuber rotten and unfit for human and livestock consumption (Fig. 1).

In the last decades, growers and researchers have made impressive strides in implementing successful local epidemic forecasting systems and guided chemical pesticide management regimes for efficient PLB control in the field (Fall *et al*. 2015; Poudel *et al*. 2020). Meanwhile, detailed molecular and genomic research have greatly improved our understanding of the pathogenic interaction between *P. infestans* and host plants, shedding light on the development of next-generation environmental-friendly management strategy of PLB (Haas *et al*. 2009; Xu *et al*.2011; Jupe *et al*. 2013). Integrated pest management (IPM) is an emergent approach that balance the immediate effectiveness and long-term environmental and ecological costs of pest control in agricultural practices. This approach represents a more sustainable option compared to traditional pest management regimes that emphasize on comprehensive crop protection exclusively. Successful implementation of IPM requires in-depth knowledge of the pest life history and pest-host interaction mechanisms in order to set proper threshold for suitable intervention, such as pesticide application and adjustment in agronomic practices at the most effective timing. These informed management actions are designed to achieve sufficient protective effect with minimal intervention, such that the overall pest management costs can be lowered without compromising crop yield and quality. In this review, we provide a brief overview of current understanding of the molecular pathology of *P. infestans*, focus on the current PLB management strategy that integrates effective chemical pesticides and forecasting systems, and discuss the potential of improved PLB management with genetic enhancement of crop resistance and other emerging crop protections technologies in this field. Together, these approaches could constitute the next generation of integrated pest management strategies against PLB.

Molecular interactions between *Phytophthora infestans* and hosts

As a hemibiotrophic pathogen, *P. infestans* initiates its infection as a biotroph, deriving essential nutrients from living host cells (Glazebrook 2005; Kamoun *et al*. 2015; Botero *et al*. 2018). Specialized invasion organs (i.e., *ex planta* appressoria and penetration pegs) will form at the tips of germinating zoospore cysts to pierce through physical barriers at plant surface (Whisson *et al*. 2016; Kots *et al*. 2017). Infection vesicles would form within the initially penetrated plant epidermal cell, and support subsequent filamentous hyphae growth within plant tissue intercellularly (Grenville-Briggs *et al*. 2005; Avrova *et al*.2008; Whisson *et al*. 2016).

As the hyphae expand, digit-like haustoria will form to invade host cells along the way, residing between the cell walls and plasma membranes of plant cells for nutrient uptake (Avrova *et al*. 2008; Dou *et al*. 2008; Petre and Kamoun 2014; Whisson *et al*. 2016). Established biotrophic infection of *P. infestans* supports the pathogen's shift towards a necrotrophic lifestyle, obtaining nutrients from dead plant tissues, and later development of reproductive sporangiophores and sporangia on the abaxial leaf surface (Grenville-Briggs *et al*. 2005; Nowicki *et al.* 2012).

At each stage of *P. infestans* infection, host plants are known to mount an array of defense responses, and the molecular interplay between host defense and *P. infestans* pathogenesis mechanisms at various fronts play a determining role in the eventual disease/no-disease outcome (Kamoun *et al*. 1997; Halterman *et al*. 2010; King *et al*.2014; Gao *et al*. 2013; Turnbull *et al*. 2019). On the plant epidermis, the physical pressure exerted by the penetration peg, as well as recognition of apoplastic pathogen elicitin molecules by receptors on the plant cell membrane, could induce active microfilament rearrangement, localized callose deposition, and activation of reactive oxygen species-, salicylic acid-, and ethylene-mediated signaling pathways, which regulate the production of antimicrobial small molecules and proteins (Shibata *et al.* 2010; Oh *et al*. 2014). Within plant tissues, plant-produced peptidases and proteases are secreted into the apoplast to inhibit intercellular growth of *P. infestans* hyphae (Wang *et al.* 2020). Ultimately, specific recognition of *P. infestans* pathogenesis molecules within plant cells by intracellular nucleotide-binding domain and leucine-rich repeat domain-containing receptors (NLRs) encoded by plant Resistance (*R*) genes could lead to localized programed cell death to restrict further expansion of the pathogen at its early biotrophic phase, a process well known as the plant hypersensitive response (HR)(Jones and Dangl 2006; Feechan *et al*. 2015).

Despite of the diverse host defense mechanisms, a large number of pathogenesis-related molecules are produced and secreted by *P. infestans* to overcome host defense and facilitate successful invasion. These so-called effector molecules could function either within or outside of host plant cells, participating in diverse physiological processes such as nutrient uptake, plant cell wall degradation, and host defense signaling interference (Osman *et al.* 2001; McLeod *et al.* 2003; Yang *et al*. 2016; He *et al*. 2018; Du *et al.* 2021). Interestingly, genes encoding such effector molecules tend to reside on the repeat-rich regions of *P. infestans*

genome, which demonstrate higher rate of evolution, suggesting that rich arsenal of effectors of this pathogen may be a result of its enhanced genome plasticity (Dong *et al.* 2014; Dong *et al.* 2015). Indeed, the rapid emergence of novel *P. infestans* pathogenic strains (or races) that escape from the surveillance of main effect *R* genes has been a major challenge in producing crop cultivars with durable genetic resistance against PLB.

Recommended agronomic practices for late blight management

Successful PLB management starts with careful agronomic practices. Most recommended culturing practices for alleviated PLB occurrence focus on two principles: avoiding excessive moisture in the environment, and reducing initial inoculum load around the field. For the first principle, tilling and other practices that improve soil aeration and drainage are recommended to reduce soil moisture. Excessive irrigation is strongly discouraged. Proper spacing between plants and hilling are also helpful to reduce shading and potential contact of infectious *P. infestans* sporangia with the tubers. Reduction of infectious *P. infestans* spores and sporangia in the environment that may serve as the initial inoculum is also key to alleviate PLB prevalence. Selection of disease-free seed tuber is the first step in eliminating source of PLB inoculum. Cutting and wounding of seed tubers are also discouraged, and need to be supplemented by pesticide treatment if the physical damage is unavoidable. In some growing areas, cull piles and volunteer plants from previous growing seasons can be the primary source of initial inoculum, as the pathogen can only overwinter on living plant tissues (Kirk 2003). Similarly, control of weeds, especially those in the same nightshade family as potato and tomato, can help reduce the inoculum load. As infection of *P. infestans* are typically initiated on aerial organs by airborne spores and sporangia, elimination of aboveground tissues through either chemical desiccation or physical defoliation is also recommended prior to tuber harvest (Perez and Forbes 2010).

Late blight management with chemical pesticides

In most potato-producing areas around the globe, application of chemical pesticides remains the most effective mean to control PLB. Thirty-six fungicides and fungicidal mixtures are registered in Europe for late blight control (https://agro.au.dk/forskning/internationaleplatforme/euroblight/). Classified by their modes of actions, three types of commercial pesticides are commonly adopted for PLB control (Nowicki *et al*. 2012; Yao *et al*. 2016). Protectants are capable of preventing *P. infestans* infection by

interfering with spore germination and/or initial penetration of plant surface processes (Lamichhane *et al*. 2018). Therefore, protectant pesticides need to be present in or on plant tissues prior to the arrival and germination of *P. infestans* spores. Curative pesticides can stop the filamentous growth of *P. infestans* hyphae even after its initial penetration and localized colonization of plant tissues, but prior to the occurrence of visible lesions and the re-emergence of sporangiophores. Finally, anti-sporulants are applied to reduce formation of reproductive sporangiophores and sporangia. Alternatively, these chemical pesticides could also be categorized based their sites of activities. Contact pesticides remain on the surface of plant tissues after application, and are therefore prone to run-off by environmental factors such as wind and rain. Translaminar pesticides can be absorbed by plants and retained within locally-treated tissues, whereas systemic pesticides are transported throughout plants after the initial application and absorption. Though the mode of action and the mobility of pesticides are correlated to some extent (*e.g.* curative pesticides have to be absorbed by plant tissues), pesticides of different mobility could also carry out their functions through the same mode of action (*e.g.* contact and systemic protectants). As an relatively unfriendly environmental effect, an increasing number of insensitive strains have emerged (Randall *et al*. 2014; Saville *et al*. 2015). Therefore, the application of pesticides needs to be scientifically-guided to complement the advantage of each type of pesticides given the crop status and disease dynamics in each given field in order to tailor the most effective and cost-efficient strategy of chemical control of PLB.

Despite of its effectiveness in PLB control, the economic and environmental, risks associated with frequent chemical pesticide application has become increasingly alarming. In some potato-producing areas, up to twenty rounds of pesticide application are required per season for effective control, and it is hence not surprising that pesticide costs could account for 10 to 25 percent of the market value of potato crop in these regions (Naumann *et al.* 2020). Abuse of pesticides have been a major contributing factor to the emergence of various pesticide-resistant populations of *P. infestans* around the globe, lowering the efficacy of chemical control of PLB, and in turn, demanding higher dosage and frequency of pesticide application, resulting in a malicious cycle. Therefore, mixed usage of diverse pesticides with different mode of actions has been encouraged. Concerted efforts to evaluate the effectiveness of various combination of pesticides against PLB with scientific experimental

design under real world field conditions have resulted in semi-quantitative scoring different pesticide treatment regimes across diverse environmental spectra, and the data from these perennial collaborative field tests are publicly available (Hansen 2021). Since the 1980s, various statistic models have been developed to forecast the potential outbreak of local late blight epidemic by integrating critical environmental attributes. Improvement in such decision support systems have been a major progress in PLB management in the last decades.

Decision support system-guided control of potato late blight

As the most effective protectant pesticides need to be present on plants prior to heavy loads of *P. infestans* spores reaching the plant surface, accurate prediction of the timing of potential epidemic onset holds the key to guided preventative pesticide treatment, and hence maximize the efficiency of chemical control of PLB. Since the 1940s, early observational studies of the outbreaks of PLB have called attention to the linkage between conductive environments and subsequent epidemic onset (Cook 1949). These associations have given birth to the most primitive forms of PLB forecasting models such as the 90% humidity criteria (Smith 1956; Fry *et al*. 2016). Through decades of development, there are more than dozens of PLB forecasting decision support systems (DSS) that are often regionally organized to predict and monitor PLB epidemics on a near-continental scale (Raymundo *et al*. 2002; Apel *et al*. 2003; Henshall *et al*. 2006; Fall *et al*. 2015; Small et al. 2015). Current DSS integrates multi-dimensional environmental attributes collected through on-site sensors to quantitatively assess the probability of PLB onset, and calculates the residual efficiency of pesticide by considering the time and environmental conditions since the previous application. In addition to environmental data, quantitative detection methods of *P. infestans* from field-collected samples have evolved multiple generations from simple polymerase chain reaction protocols (Judelson and Tooley 2000), to more sophisticated molecular techniques such as loop-mediated isothermal amplification and recombinase polymerase amplification assays (Hansen *et al*. 2016; Lu *et al*. 2020; Ristaino *et al*. 2020). Furthermore, since most current resistant potato cultivars were bred by stacking major effect resistance (*R*) genes (as will be discussed below), the probability of successful genetic resistance against PLB can be estimated by knowing the *R* genes present in the crop and the corresponding avirulence (*Avr*) genes present in the local *P. infestans* population. Incorporation of these high-dimensional data into sophisticated predictive models have drastically improved the efficiency of chemical control of PLB as well as

promoting the durability of crop genetic resistance, further demonstrating the necessity of an integrated pest management strategy for successful and sustainable PLB control (Kessel *et al.* 2018; Narouei-Khandan *et al*. 2020; Cucak *et al*. 2021).

Genetic enhancement of potato resistance against late blight

Ever since the Irish potato famine, grower and breeders have engaged in producing genetically-resistant potato cultivars. Through centuries of research, it is now well-recognized that the genetic resistance against PLB can either be race-specific (i.e., vertical resistance) or race-non-specific (i.e., horizontal resistance), and these two classes of resistance are each associated with distinct modes of action. The specificity of race-specific resistance typically arises from the one-on-one recognition of particular pathogen effectors by host NLRs, which triggers HR to restrict initial *P. infestans* infection (Jones and Dangl 2006; Haverkort *et al*. 2009; Rodewald and Trognitz 2013; Feechan *et al*. 2015). Hence, the genes that convey race-specific resistance are exclusively *R* genes. Although quite some potato *R* genes mediated disese resistance have been break down by epidemic strains, long-term field observation suggest several genes in cluding *RB, Rpi-vnt1*, *Rpi-Smira2 (R8), Rpi-blb2* confer relatively broad-spectrum resistance to most of the *P. infestans* strains, by recognizing *ipiO1*, *Avrvnt1*, *Avr8* and *Avrblb2* effector genes or their gene family members. In contrast, race-non-specific resistance involves complex genetic architecture and diverse molecular mechanisms, ranging from signaling components of plant defense response to metabolic and regulatory genes of antimicrobial molecules *(*Kobayashi *et al.* 2012; Shi *et al.* 2012; Yogendra *et al.* 2015; Tian *et al.* 2015; Yogendra *et al.* 2017; Zhou *et al*. 2018; Yoshioka *et al.* 2019). Yet, perhaps the best examples of non-*R* gene-mediated PLB resistance are mostly reported in nonhost plant species of *P. infestans* such as *Arabidopsis thaliana* (Prince *et al.* 2017), *Nicotiana benthamiana* (Shibata *et al*. 2016), and *Capsicum annum* (Lee *et al*. 2017), which are impossible to introduce into the cultivated potato germplasm through traditional breeding methods. Therefore, from a practical perspective, *R* genes-mediated PLB resistance remains the most useful genetic resource for potato germplasm enhancement, though it would be quickly rendered ineffective under field conditions as novel *P. infestans* races emerge. Nevertheless, genetic stacking of multiple *R* genes has been proven to provide more effective and durable protection against PLB.

Traditionally, *R* genes have been identified through genetic mapping with populations derived from crosses between cultivated potatoes, their wild relatives. Through this way, more than a dozen of *R* genes have been cloned from various wild potato species such as *Solanum demissum*, *S. bulbocastanum and S. venturii* (Song *et al*. 2003; van der Vossen *et al*. 2003; Haverkort *et al*. 2009; Nowicki *et al*. 2012). Advance in sequencing technologies and accumulating genomics resources have drastically accelerated the process of *R* gene discovery across wide phylogenetic range. Resistance gene-enrichment with custom-designed biotin probes followed by short read sequencing (RenSeq) allowed specific detection of *R* genes, which were often masked in Illumina short read-based genomes due to high level of internal repeats (Jupe *et al.* 2013). Combination of RenSeq with third generation single-molecule real-time (SMRT) sequencing further enabled direct recovery of full-length *R* genes from species without a reference genome (Witek *et al.* 2016, Witek *et al.* 2021). This technology has been recently applied to clone *R* genes from wild wheat species (Arora *et al.* 2019), as well as genome-wide curation of *R* genes across 18 Solanum species (Seong *et al.* 2020) and diverse *A. thaliana* accessions (Van de Weyer *et al.* 2019). As the third generation long-read sequencing technology become increasingly accessible, direct bioinformatic prediction results from plant genomes produced on such technology platform will be more reliable. Hence, we expect that *R* gene discovery and functional association with resistance phenotype against specific *P. infestans* race to become a routine practice in the near future.

Unlike *R* genes-mediated resistance studies, genetic dissection of non-race-specific resistance is challenging due to its complex genetic architecture and relatively small effect size. Therefore, it is perhaps not surprising that current examples of non-race-specific resistance-related genes are typically characterized through a reverse genetic approach. In these studies, transient or stable genetic knockout mutants of the target genes were usually tested and demonstrated increased susceptibility (Kobayashi *et al.* 2012; Shi *et al.* 2012; Tian *et al*. 2015; Yogendra *et al.* 2015; Yogendra *et al.* 2017; Zhou *et al*. 2018; Yoshioka *et al.* 2019). Yet, as most of the genes tested were parts of conserved signaling and metabolic pathways, genetic perturbation at these targets likely would have complex pleotropic effects that would extend beyond the resistance phenotype examined/reported. Furthermore, there is little guarantee that overexpressing a gene that lowered resistance when knocked down (or out) would result in enhanced resistance. Therefore, it is fair to say that race-non-specific resistance of *P.*

infestans remains at an early stage of basic research, and is unlikely to produce any practical genetic elements that could be directly used for breeding.

Aside from the task of resistance gene discovery and validation, another major bottleneck in genetic enhancement of *P. infestans* resistance or any trait at all is the slow process of tetraploid potato breeding. Unlike diploid crop species, where a desirable trait/allele can be directly introgressed into an elite cultivar, attempt to introduce exogenous genes into tetraploid potatoes is hampered by high level of heterozygosity, insufficient target gene copy number, and self-incompatibility (Ye *et al*. 2018; Ghislain *et al*. 2019; Zhou *et al*. 2020). Furthermore, though accumulating effective *R* genes are being discovered in wild potato species, few of such species can be successfully crossed with the cultivate species to produce viable offspring, and hence obstructing introgression of these genes into the cultivated germplasm through traditional breeding(Ghislain *et al*. 2019). Though the transgenic approach has been proposed (and to some extent implemented) to solve this issue, the volatile political and public opinion landscape in transgenics regulation thus far have prevented broader application of *R* gene stacking to produce durable *P. infestans*-resistant potato cultivar through transgenic technology.

Emerging technologies in late blight management

Though tremendous efforts have been made to control *P. infestans* through a combination of chemical pesticide application, forecasting system development, and resistance gene discovery, the current status of global PLB prevalence clearly shows that more needs to be done. In addition to continuous improvement of existing PLB management means (as showcased in sections above), novel technologies have also emerged and sometimes successfully tested. Although such technologies have yet to been widely acknowledged as effective means of control around the world, they present promising leads in revolutionizing the current PLB management regime and may transform our understanding of *P. infestans* pathosystems.

Assorted commercially available phytochemicals have been tested as potential environmental-friendly bio-pesticides. Among them, eugenol, matrine, carvacrol and zeylenone have emerged as promising candidates (Zhang *et al*. 2020; He *et al*. 2021). For example, application of 0.3% eugenol had demonstrated comparable, if not superior level of protective effect on potato crop to mainstream chemical pesticides such as mancozeb (80% WP) in a

side-by-side field test, and resulted in higher yield (Tian *et al*. 2013). In our hand, eugenol also demonstrated significant *in vitro* growth inhibitory effect on *P. infestans* grown on oatmeal agar (Fig. 2; IC_{50}=63.9 mg L^{-1}). The protective effect of eugenol can be further enhanced by delivery with nano-material carriers (Wang *et al*. 2021). Zeylenone, which isolated from *Uvaria grandiflora*, affecting energy metabolism of Phytophthora and could be develop as a potential botanical fungicide (He *et al*. 2021).

Biological control of *P. infestans* with competitive microbes have also been postulated as a potential mean to enhance the current PLB management strategy. For example, a *Trichoderma* strain HNA14 could over-compete *P. infestans* growth *in vitro*, inhibit *P. infestans* growth through mycoparasitism and production of toxic metabolites, and significantly reduce PLB disease index in field application (Yao *et al*. 2016). *Myxococcus fulvus* B25-I-3 with antagonistic activity against *P. infestans* was isolated by rabbit fecal induction method, which had strong inhibitory effect on the asexual reproduction and sexual reproduction of *P. infestans*(Wu *et al*. 2021). Combining Different Potato-Associated Pseudomonas showed improving the biocontrol of *P. infestans* (De *et al*. 2018).In addition to direct inhibitory effect on *P. infestans*, some bio-control agent may also facilitate PLB control by promoting host plant defense (Di Francesco *et al*. 2017). With rapid development in the field of microbiome research, we expect that various functional assembly of synthetic microbial consortia may demonstrate superior bio-control performance than any single microbe strain, and the full potential of bio-control of PLB is far from fulfilled at the current stage.

RNA interference (RNAi) is yet another novel technology that has been recently introduced into the potential arsenal of PLB control. Originally discovered as a part of plant antiviral defense mechanism, RNAi is now believed to play an important role across diverse environmental adaptation processes in plants, including defense against arthropod herbivores and filamentous pathogens (Zhao *et al*. 2021). Recent studies have revealed that some Phytophthora effectors can inhibit the RNA-silencing pathway in plants (Qiao *et al*. 2013). Host-induced gene silencing in *P. infestans* by potato was first demonstrated in 2015 by Jahan *et al*. suggesting that required molecular machinery for cross kingdom RNAi is present in the potato-*Phytophthora* pathosystem. The more recent discovery of a *P. capasici* (a related Phytophthora species) effector that suppresses plant cross-kingdom RNAi mechanism further suggest that bi-directional small RNA trafficking and functionality probably present yet another

battleground between Phytophthora pathogens and their host plants (Hou *et al.* 2019). Therefore, it may be possible to develop non-transgenic small RNA spray-based method to control *P. infestans* in the near future.

Conclusion and future prospect

Since its infamous outbreak in the mid-1800s, significant advancement in PLB control has been achieved through better agronomic practices, improved detection and forecasting systems, and perhaps most importantly, widespread application of chemical pesticides. Though the current management strategies can effectively prevent catastrophic epidemics of PLB, the economic and environmental costs associated with pervasive pesticide use and abuse are becoming increasingly unaffordable with global climate change and the ever-growing demand for quality food supply. Hence, broader collaborations among laboratory scientists, field pathologists, product developers, and crop growers are required in the years ahead to translate scientific progress and technological development in PLB research to a new generation of an efficient integrated PLB management strategy for sustaible potato production around the globe.

Acknowledgements

We thank Prof. Weixing Shan and anonymous reviewers for insightful suggestions to improve this manuscript. The *P. infestans* photos are provided by Dr. Wang Luyao and Dr. Gao Chuyun. This work is supported by National Natural Science Foundation of China (32130088) and Guangdong Major Project of Basic and Applied Basic Research (2021B0301030004) to Dong S., and by the Agricultural Science and Technology Innovation Program of Chinese Academy of Agricultural Sciences to Zhou S.

References

Andersson M N, Löfstedt C, Newcomb R D. 2015. Insect olfaction and the evolution of receptor tuning. *Frontiers in Ecology and Evolution*, 3, 53.

Aylor DE. 2003. Spread of plant disease on a continental scale: role of aerial dispersal of pathogens. *Ecology*, 84, 1989–1997.

Apel H, Paudyal M, Richter O. 2003. Evaluation of treatment strategies of the late blight Phytophthora infestans in Nepal by population dynamics modelling. *Environmental Modelling and Software*, 18, 355–364.

Arora S, Steuernagel B, Gaurav K, Chandramohan S, Long Y, Matny O, Johnson R, Enk J, Periyannan S, Singh N, Hatta MAM, Athiyannan N, Cheema J, Yu G, Kangara N, Ghosh S, Szabo L, Poland J, Bariana H, Jones JDG, Bentley A, Ayliffe M, Olson E, Xu S, Steffenson BJ, Ladugah E, Wulff BBH. 2019. Resistance gene cloning from a wild crop relative by sequence capture and association genetics. *Nature Biotechnology*, 37, 139-143.

Avrova AO, Boevink PC, Young V, Grenville-Briggs LJ, van West P, Birch PR, Whisson SC. 2008. A novel Phytophthora infestans haustorium-specific membrane protein is required for infection of potato. *Cellular Microbiology*, 10, 2271–2284.

Botero D, Valdés I, Rodríguez MJ, Henao D, Danies G, González AF, Restrepo S. 2018. A genome-scale metabolic reconstruction of Phytophthora infestans with the integration of transcriptional data reveals the key metabolic patterns involved in the interaction of its host. *Frontiers in Genetics*, 10, 244.

Bourke PMA. 1964. Emergence of potato blight, 1843-46. *Nature*, 203, 805-808.

Cook HT. 1949. Forecasting late blight epiphytotics of potatoes and tomatoes. *Journal of Agricultural Research*, 78, 554-563.

Copeland R, Dowley L, Moore J. 1993. Vulnerability of the Irish potato industry to harmful 669 organisms. *In Proceedings of Royal Irish Academy Seminar*, 95–106.

Cucak M, Moral RA, Fealy R, Lambkin K, Kildea S. 2021. Opportunities for an improved potato late blight management in the Republic of Ireland: Field evaluation of the modified Irish Rules crop disease risk prediction model. *Phytopathology*, 13.

De VM, Germanier F, Vuille N, Weisskopf L. 2018. Combining Different Potato-Associated *Pseudomonas* Strains for Improved Biocontrol of *Phytophthora infestans*. *Frontiers in Microbiology*, 9, 2573.

Di Francesco A, Milella F, Mari M, Roberti R. 2017. A preliminary investigation into *Aureobasidium pullulans* as a potential biocontrol agent against *Phytophthora infestans* of tomato. *Biological Control*, 114, 144-149.

Dong S, Raffaele S, Kamoun S. 2015. The two-speed genomes of filamentous pathogens: waltz with plants. *Current Opinion in Genetics and Development*, 35, 57-65.

Dong S, Stam R, Cano LM, Song J, Sklenar J, Yoshida K, Bozkurt TO, Oliva R, Liu Z, Tian M, Win J, Banfield MJ, Jones AME, ven der Hoorn RAL, Kamoun S. 2014. Effector specialization in a lineage of the Irish potato famine pathogen. *Science*, 343, 552-555.

Dou D, Kale SD, Wang X, Jiang RH, Bruce NA, Arredondo FD, Zhang X, Tyler BM. 2008. RXLR-mediated entry of Phytophthora sojae effector Avr1b into soybean cells does not require pathogen-encoded machinery. *Plant Cell*, 20, 1930–1947.

Du Y, Chen X, Guo Y, Zhang X, Zhang H, Li F, Huang G, Meng Y, Shan W. 2021. Phytophthora infestans RXLR effector PITG20303 targets a potato MKK1 protein to suppress plant immunity. *New Phytologist*, 229, 501-515.

Fall M, Van der Heyden H, Brodeur L, Leclerc Y, Moreau G, Carisse O. 2015. Spatiotemporal variation in airborne sporangia of Phytophthora infestans: Characterization and initiatives towards improving potato late blight risk estimation. *Plant Pathology*, 64, 178–190.

Feechan A, Turnbull D, Stevens LJ, Engelhardt S, Birch PRJ, Hein I, Gilroy EM. 2015. The hypersensitive response in PAMP and effector triggered immune responses. *In AN Gunawardena, PF McCabe, eds, Plant Programmed Cell Death. Springer Publishing* pp, 235–268.

Fry WE. 2016. Phytophthora infestans: New Tools (and Old Ones) Lead to New Understanding and Precision Management. *Annual Review of Phytopathology*, 54, 529-47.

Fry WE, Birch PR, Judelson HS, Grunwald NJ, Danies G, Everts KL, Gevens AJ, Gugino BK, Johnson DA, Johnson SB, McGrath MT, Myers KL, Ristaino JB, Roberts PD, Secor G, Smart CD. 2015. Five Reasons to Consider Phytophthora infestans a Reemerging Pathogen. *Phytopathology*, 105, 966-981.

Gao LL, Zheng JT, Millett BP, Bradeen JM. 2013. Insights into organ-specific pathogen defense responses in plants: RNA-seq analysis of potato tuber-Phytophthora infestans interactions. *BMC Genomics*, 14, 340.

Gevens AJ, Seidl AC. 2013. First Report of Late Blight Caused by Phytophthora infestans Clonal Lineage US-22 on Tomato and Potato in Wisconsin. *Plant Disease*, 97, 423.

Ghislain M, Byarugaba AA, Magembe E, Njoroge A, Rivera C, Román ML, Tovar JC, Gamboa S, Forbes GA, Kreuze JF, Barekye A, Kiggundu A. 2019. Stacking three late blight resistance genes from wild species directly into African highland potato varieties confers complete field resistance to local blight races. *Plant Biotechnology Journal*, 17, 1119-1129.

Glazebrook J. 2005. Contrasting mechanisms of defense against biotrophic and necrotrophic pathogens. *Annual Reviewof Phytopathol*, 43, 205–227.

Grenville-Briggs LJ, Avrova AO, Bruce CR, Williams A, Whisson SC, Birch PR, van West P. 2005. Elevated amino acid biosynthesis in Phytophthora infestans during appressorium formation and potato infection. *Fungal Genetics Biology*, 42, 244–256.

Haas BJ, Kamoun S, Zody MC, Jiang RHY, Handsaker RE, Cano LM, Grabherr M, Kodira CD, Raffaele S, Torto-Alalibo T, Bozkurt TO, Ah-Fong AM, Alvarado L, Anderson VL, Armstrong MR, Avrova A, Baxter L, Beynon J, Boevink PC, Bollmann SR, Bos JI, Bulone V, Cai G, Cakir C, Carrington JC, Chawner M, Conti L, Costanzo S, Ewan R, Fahlgren N, Fischbach MA, Fugelstad J, Gilroy EM, Gnerre S, Green PJ, Grenville-Briggs LJ, Griffith J, Grünwald NJ, Horn K, Horner NR, Hu CH, Huitema E, Jeong DH, Jones AM, Jones JD, Jones RW, Karlsson EK, Kunjeti SG, Lamour K, Liu Z, Ma L, Maclean D, Chibucos MC, McDonald H, McWalters J, Meijer HJ, Morgan W, Morris PF, Munro CA, O'Neill K, Ospina-Giraldo M, Pinzón A, Pritchard L, Ramsahoye B, Ren Q, Restrepo S, Roy S, Sadanandom A, Savidor A, Schornack S, Schwartz DC, Schumann UD, Schwessinger B, Seyer L, Sharpe T, Silvar C, Song J, Studholme DJ, Sykes S, Thines M, van de Vondervoort PJ, Phuntumart V, Wawra S, Weide R, Win J, Young C, Zhou S, Fry W, Meyers BC, van West P, Ristaino J, Govers F, Birch PR, Whisson SC,

Judelson HS, Nusbaum C. 2009. Genome sequence and analysis of the Irish potato famine pathogen Phytophthora infestans. *Nature*, 461, 393–398.

Halterman DA, Chen Y, Sopee J, Berduo-Sandoval J, Sánchez-Pérez A. 2010. Competition between Phytophthora infestans effectors leads to increased aggressiveness on plants containing broad-spectrum late blight resistance. *Plos ONE*, 5, e10536.

Hansen JG. 2021. Late blight fungicide table. *EuroBlight: a potato late blight network for Europe.* Retrieved from https://agro.au.dk/forskning/internationale-platforme/euroblight/control-strategies/late-blight-fungicide-table/

Hansen ZR, Knaus BJ, Tabima JF, Press CM, Judelson HS, Grunwald NJ, Smart CD. 2016. Loop-mediated isothermal amplification for detection of the tomato and potato late blight pathogen, *Phytophthora infestans*. *Journal of Applied Microbiology*, 120, 1010-1020.

Hareau G , Kleinwechter U, Pradel W, Suarez V, Okello J, Vikraman S. 2014. Strategic assessment of research priorities for potato. Lima (Peru) CGIAR Research Program on Roots, Tubers and Bananas (RTB) RTB Working Paper 2014‐8. Available online at: www.rtb.cgiar.org

Haverkort AJ, Struik PC, Visser RGF, Jacobsen E. 2009. Applied biotechnology to combat late blight in potato caused by Phytophthora infestans . *Potato Research*, 52, 249–264.

He J, Dou M, Xie J, Hou S, Liu Q, Hu Z, Zhang B, Zheng S, Yin F, Zhang M, Xie C, Lu D, Ding X, Zhu C, Sun R. 2021. Discovery of zeylenone from Uvaria grandiflora as a potential botanical fungicide. *Pest Management Sciense*, 27.

He Q, Naqvi S, McLellan H, Boevink PC, Champouret N, Hein I, Birch PRJ. 2018. Plant pathogen effector utilizes host susceptibility factor NRL1 to degrade the immune regulator SWAP70. *Proceedings of the National Academy of Sciences of the United States of America*, 115, E7834-E7843.

Henshall W, Shtienberg D, Beresford R. 2006. A new potato late blight disease prediction model and its comparison with two previous models. *New Zaeland Plant Protection*, 59, 150–154.

Hou Y, Zhai Y, Feng L, Karimi HZ, Rutter BD, Zeng L, Choi DS, Zhang B, Gu W, Chen X, Ye W, Innes RW, Zhai J, Ma W. 2019. A Phytophthora Effector Suppresses Trans-Kingdom RNAi to Promote Disease Susceptibility. *Cell Host Microbe*, 25, 153-165 e155.

Jones JD, Dangl JL. 2006. The plant immune system. *Nature*, 444, 323–329.

Judelson HS, Tooley PW. 2000. Enhanced polymerase chain reaction methods for detecting and quantifying *Phytophthora infestans* in plants. *Phytopathology*, 90, 1112-1119.

Jupe F, Witek K, Verweij W, Sliwka J, Pritchard L, Etherington GJ, Maclean D, Cock PJ, Leggett RM, Bryan GJ, Cardle L, Hein I, Jones JD. 2013. Resistance gene enrichment sequencing (RenSeq) enables reannotation of the NB-LRR gene family from sequenced plant genomes and rapid mapping of resistance loci in segregating populations. *Plant Journal*, 76, 530-544.

Kamoun S, Furzer O, Jones JD, Judelson HS, Ali GS, Dalio RJ, Roy SG, Schena L, Zambounis A, Panabières F, Cahill D, Ruocco M, Figueiredo A, Chen XR, Hulvey J, Stam R, Lamour K, Gijzen M, Tyler BM, Grünwald NJ, Mukhtar MS, Tomé DF, Tör M, Van Den Ackerveken G, McDowell J, Daayf F, Fry WE, Lindqvist-Kreuze H, Meijer HJ, Petre B, Ristaino J, Yoshida K, Birch PR, Govers F. 2015. The Top 10 oomycete pathogens in molecular plant pathology. *Molecular Plant Pathology*, 16, 413-34.

Kamoun S, Lindqvist H and Govers F. 1997. A novel class of elicitin-like genes from Phytophthora infestans. *Molecular Plant-Microbe Interactions*, 10, 1028–1030.

Kessel GJT, Mullins E, Evenhuis A, Stellingwerf J, Cortes VO, Phelan S, van den Bosch T, Forch MG, Goedhart P, van der Voet H, Lotz LAP. 2018. Development and validation of IPM strategies for the cultivation of cisgenically modified late blight resistant potato. *European Journal of Agronomy*, 96, 146-155.

King SRF, McLellan H, Boevink PC, Armstrong MR, Bukharova T, Sukarta O, Win J, Kamoun S, Birch PRJ, Banfield MJ. 2014. Phytophthora infestans RXLR effector PexRD2 interacts with host MAPKKKε to suppress plant immune signaling. *Plant Cell*, 26, 1345–1359.

Kirk WW. 2003. Thermal properties of overwintered piles of cull potatoes. *American Journal of Potato Reseach*, 80, 145-149.

Kobayashi M, Yoshioka M, Asai S, Nomura H, Kuchimura K, Mori H, Doke N, Yoshioka H. 2012. StCDPK5 confers resistance to late blight pathogen but increases susceptibility to early blight pathogen in potato via reactive oxygen species burst. *New Phytologist*, 196, 223-237.

Kots K, Meijer HJ, Bouwmeester K, Govers F, Ketelaar T. 2017. Filamentous actin accumulates during plant cell penetration and cell wall plug formation in Phytophthora infestans. *Cellular and Molecular Life Sciense*, 74, 909–920.

Lamichhane JR, Osdaghi E, Behlau F, Köhl J, Jones JB, Aubertot JN. 2018. Thirteen decades of antimicrobial copper com- pounds applied in agriculture. A review. *Agronomy for Sustainable Development,* 38, 28.

Lee HA, Kim S, Kim S, Choi D. 2017. Expansion of sesquiterpene biosynthetic gene clusters in pepper confers nonhost resistance to the Irish potato famine pathogen. *New Phytologist*, 215, 1132-1143.

Lu X, Zheng Y, Zhang F, Yu J, Dai T, Wang R, Tian Y, Xu H, Shen D, Dou D. 2020. A rapid, equipment-free method for detecting *Phytophthora infestans* in the field using a lateral flow strip-based recombinase polymerase amplification assay. *Plant Disease*, 104, 2774-2778.

McLeod A, Smart CD, Fry WE. 2003. Characterization of 1,3-beta-glucanase and 1,3;1,4-beta-glucanase genes from Phytophthora infestans. *Fungal Genetics Biology*, 38, 250-263.

Naumann M, Koch M, Thiel H, Gransee A, Pawelzik E. 2020. The Importance of Nutrient Management for Potato Production Part II: Plant Nutrition and Tuber Quality. *Potato Research*, 63, 121-137.

Narouei-Khandan HA, Shakya SK, Garrett KA, Goss EM, Dufault NS, Andrade-Piedra JL, Asseng S, Wallach D, Bruggen AHCV. 2020. BLIGHTSIM: A New Potato Late Blight Model Simulating the Response of *Phytophthora infestans* to Diurnal Temperature and Humidity Fluctuations in Relation to Climate Change. *Pathogens*, 9, 659.

Nowicki M, Foolad MR, Nowakowska M, Kozik EU. 2012. Potato and Tomato Late Blight Caused by Phytophthora infestans: An Overview of Pathology and Resistance Breeding. *Plant Disease*, 96, 4-17.

Oh SK, Kwon SY, Choi D. 2014. Rpi-blb2-Mediated Hypersensitive Cell Death Caused by Phytophthora infestans AVRblb2 Requires SGT1, but not EDS1, NDR1, Salicylic Acid-, Jasmonic Acid-, or Ethylene-Mediated Signaling. *The Plant Pathology Journal*, 30, 254-60.

Osman H, Mikes V, Milat ML, Ponchet M, Marion D, Prange T, Maume BF, Vauthrin S, Blein JP. 2001. Fatty acids bind to the fungal elicitor cryptogein and compete with sterols. *FEBS Letters*, 489, 55-58.

Pennisi E. 2010. Armed and dangerous. *Science*, 327, 804-805.
Perez W, Forbes GA. 2010. Potato late blight - technical manual. International Potato Center Collection.
Petre B and Kamoun S. 2014. How do filamentous pathogens deliver effector proteins into plant cells? *PLoS Biology*, 12, e1001801.
Poudel A, Pandey M, Shah K, Acharya B, Shrestha J. 2020. Evaluation of fungicides for management of late blight (Phytophthora infestans) of potato. *Agrica*, 9, 10–17.
Prince DC, Rallapalli G, Xu D, Schoonbeek HJ, Cevik V, Asai S, Kemen E, Cruz-Mireles N, Kemen A, Belhaj K, Schornack S, Kamoun S, Holub EB, Halkier BA, Jones JD. 2017. Albugo-imposed changes to tryptophan-derived antimicrobial metabolite biosynthesis may contribute to suppression of non-host resistance to Phytophthora infestans in Arabidopsis thaliana. *BMC Biology*, 15, 20.
Qiao Y, Liu L, Xiong Q, Flores C, Wong J, Shi J, Wang X, Liu X, Xiang Q, Jiang S. Zhang F, Wang Y, Judelson HS, Chen X, Ma W. 2013. Oomycete pathogens encode RNA silencing sup- pressors. *Nature Genetics*, 45, 330–333.
Randall E, Young V, Sierotzki H, Scalliet G, Birch PRJ, Cooke DEL, Csukai M, Whisson SC. 2014. Sequence diversity in the large subunit of RNA poly- merase I contributes to Mefenoxam insensitivity in Phytophthora infestans. *Molecular Plant Pathology*, 15, 664–676.
Raymundo R, Andrade-Piedra J, Juárez H, Forbes G, Hijmans RJ. 2002. Towards an integrated and universal cropdisease model for potato late blight. In Late Blight: Managing the Global Threat, Proceedings of Global Initiative on Late Blight (GILB) Conference, Hamburg, Germany, 11–13 July 2002; Lizárraga, C., Ed.; International Potato Center (CIP): Lima, Peru, 2002; pp. 77–82.
Ristaino JB, Saville AC, Paul R, Cooper DC, Wei Q. 2020. Detection of *Phytophthora infestans* by loop-mediated osthermal amplification, real-time LAMP, and droplet digital PCR. *Plant Disease*, 104, 708-716.
Rodewald J, Trognitz B. 2013. Solanum resistance genes against Phytophthora infestans and their corresponding avirulence genes. *Molecular Plant Pathology*, 14, 740–757.
Savary S, Bregaglio S, Willocquet L, Gustafson D, D'Croz DM, Sparks A, Castilla N, Djurle A, Allinne C, Sharma M, Rossi V, Amorim L, Bergamin A, Yuen J, Esker P, McRoberts N, Avelino J, Duveiller E, Koo J, Garrett K. 2017. Crop health and its global impacts on the components of food security. *Food Security*, 9, 311– 327.
Saville A, Graham K, Grünwald NJ, Myers K, Fry WE, Ristaino JB. 2015. Fungicide sensitivity of U.S. genotypes of Phytophthora infestans to six oomycete-targeted compounds. *Plant Disease*, 99, 659–666.
Seong K, Seo E, Witek K, Li M, Staskawicz B. 2020. Evolution of NLR resistance genes with noncanonical N-terminal domains in wild tomato species. *New Phytologist*, 227, 1530-1543.
Shi X, Tian Z, Liu J, van der Vossen EA, Xie C. 2012. A potato pathogenesis-related protein gene, StPRp27, contributes to race-nonspecific resistance against *Phytophthora infestans*. *Molecular Biology Reports,* 39, 1909-1916.
Shibata Y, Kawakita K, Takemoto D. 2010. Age-related resistance of Nicotiana benthamiana against hemibiotrophic pathogen Phytophthora infestans requires both ethylene- and salicylic acid-mediated signaling pathways. *Molecular Plant-Microbe Interactions*, 23, 1130-1142.

Shibata Y, Ojika M, Sugiyama A, Yazaki K, Jones DA, Kawakita K, Takemoto D. 2016. The full-size ABCG transporters Nb-ABCG1 and Nb-ABCG2 function in pre- and postinvasion defense against *Phytophthora infestans* in *Nicotiana benthamiana*. *Plant Cell*, 28, 1163-1181.

Small IM, Joseph L, Fry WE. 2015. Development and implementation of the BlightPro decision support system for potato and tomato late blight management. *Computers and Electronics in Agriculture*, 115, 57–65.

Smith LP. 1956. Potato blight forecasting by 90% humidity criteria. *Plant Pathology*, 5, 83-87.

Song JQ, Bradeen JM, Naess SK, Raasch JA, Wielgus SM, Haberlach GT, Liu J, Kuang HH, Austin-Phillips S, Buell CR, Helgeson JP, Jiang JM. 2003. Gene RB cloned from Solanum bulbocastanum confers broad spectrum resistance to potato late blight. *Proceedings of the National Academy of Sciences of the United States of America*, 100, 9128–9133.

Tian H, Shen Y, Xiao C, Gao j, Zhang Y. 2013. A new fungicide for potato late blight control – eugenol. *Zhong guo ma ling shu*(in Chinses), 27, 162-165.

Tian Z, He Q, Wang H, Liu Y, Zhang Y, Shao F, Xie C. 2015. The Potato ERF Transcription Factor StERF3 Negatively Regulates Resistance to Phytophthora infestans and Salt Tolerance in Potato. *Plant and Cell Physiology*, 56, 992-1005.

Turnbull D, Wang H, Breen S, Malec M, Naqvi S, Yang L, Welsh L, Hemsley P, Zhendong T, Brunner F, Gilroy EM, Birch PRJ. 2019. AVR2 Targets BSL Family Members, Which Act as Susceptibility Factors to Suppress Host Immunity. *Plant Physiology*, 180, 571-581.

Van de Weyer AL, Monteiro F, Furzer OJ, Nishimura MT, Cevik V, Witek K, Jones JDG, Dangl JL, Weigel D, Bemm F. 2019. A Species-Wide Inventory of NLR Genes and Alleles in Arabidopsis thaliana. *Cell*, 178, 1260-1272 e1214.

van der Vossen E, Sikkema A, Hekkert BTL, Gros J, Stevens P, Muskens M, Wouters D, Pereira A, Stiekema W, Allefs S. 2003. An ancient R gene from the wild potato species Solanum bulbocastanum confers broad-spectrum resistance to Phytophthora infestans in cultivated potato and tomato. *Plant Journal,* 36, 867–882.

Wang X, Zheng K, Cheng W, Li J, Liang X, Shen J, Dou D, Yin M, Yan S. 2021. Field application of star polymer-delivered chitosan to amplify plant defense against potato late blight. *Chemical Enginnering Journal*, 417, 129327.

Wang Y, Wang Y, Wang Y. 2020. Apoplastic Proteases: Powerful Weapons against Pathogen Infection in Plants. *Plant Communications,* 1, 100085.

Whisson SC, Boevink PC, Wang S, Birch PR. 2016. The cell biology of late blight disease. *Current Opinion in Microbiology*, 34, 127-135.

Witek K, Jupe F, Witek AI, Baker D, Clark MD, Jones JD. 2016. Accelerated cloning of a potato late blight-resistance gene using RenSeq and SMRT sequencing. *Nature Biotechnology*, 34, 656-660.

Witek K, Lin X, Karki HS, Jupe F, Witek AI, Steuernagel B, Stam R, van Oosterhout C, Fairhead S, Heal R, Cocker JM, Bhanvadia S, Barrett W, Wu CH, Adachi H, Song T, Kamoun S, Vleeshouwers VGAA, Tomlinson L, Wulff BBH, Jones JDG. 2021. A complex resistance locus in Solanum americanum recognizes a conserved Phytophthora effector. *Nature Plants,* 7, 198-208.

Wu ZH, Ma Q, Sun ZN, Cui HC, Liu HR. 2021. Biocontrol mechanism of Myxococcus fulvus B25-I-3 against Phytophthora infestans and its control efficiency on potato late blight. *Folia Microbiologica*, 66, 555-567.

Xu X, Pan SK, Cheng SF, Zhang B, Mu DS, Ni PX, Zhang GY, Yang S, Li RQ, Wang J, Orjeda G, Guzman F, Torres M, Lozano R, Ponce O, Martinez D, De la Cruz G, Chakrabarti SK, Patil VU, Skryabin KG, Kuznetsov BB, Ravin NV, Kolganova TV, Beletsky AV, Mardanov AV, Di Genova A, Bolser DM, Martin DM, Li G, Yang Y, Kuang H, Hu Q, Xiong X, Bishop GJ, Sagredo B, Mejía N, Zagorski W, Gromadka R, Gawor J, Szczesny P, Huang S, Zhang Z, Liang C, He J, Li Y, He Y, Xu J, Zhang Y, Xie B, Du Y, Qu D, Bonierbale M, Ghislain M, Herrera Mdel R, Giuliano G, Pietrella M, Perrotta G, Facella P, O'Brien K, Feingold SE, Barreiro LE, Massa GA, Diambra L, Whitty BR, Vaillancourt B, Lin H, Massa AN, Geoffroy M, Lundback S, DellaPenna D, Buell CR, Sharma SK, Marshall DF, Waugh R, Bryan GJ, Destefanis M, Nagy I, Milbourne D, Thomson SJ, Fiers M, Jacobs JM, Nielsen KL, Sønderkær M, Iovene M, Torres GA, Jiang J, Veilleux RE, Bachem CW, de Boer J, Borm T, Kloosterman B, van Eck H, Datema E, Hekkert Bt, Goverse A, van Ham RC, Visser RG. 2011. Genome sequence and analysis of the tuber crop potato. *Nature*, 475, 189–195.

Yang L, McLellan H, Naqvi S, He Q, Boevink PC, Armstrong M, Giuliani LM, Zhang W, Tian Z, Zhan J, Gilroy EM, Birch PR. 2016. Potato NPH3/RPT2-Like Protein StNRL1, Targeted by a Phytophthora infestans RXLR Effector, Is a Susceptibility Factor. *Plant Physiology*, 171, 645-57.

Yao Y, Li Y, Chen Z, Zheng B, Zhang L, Niu B, Meng J, Li A, Zhang J, Wang Q. 2016. Biological control of potato late blight using isolats of *Trichoderma. American Journal of Potato Reseach*, 93, 33-42.

Ye M, Peng Z, Tang D, Yang Z, Li D, Xu Y, Zhang C, Huang S. 2018. Generation of self-compatible diploid potato by knockout of S-RNase. *Nature Plants*, 4, 651-654.

Yogendra KN, Dhokane D, Kushalappa AC, Sarmiento F, Rodriguez E, Mosquera T. 2017. StWRKY8 transcription factor regulates benzylisoquinoline alkaloid pathway in potato conferring resistance to late blight. *Plant Sciense*, 256, 208-216.

Yogendra KN, Kumar A, Sarkar K, Li Y, Pushpa D, Mosa KA, Duggavathi R, Kushalappa AC. 2015. Transcription factor StWRKY1 regulates phenylpropanoid metabolites conferring late blight resistance in potato. *Journal of Experimental Botany*, 66, 7377-7389.

Yoshioka M, Adachi A, Sato Y, Doke N, Kondo T, Yoshioka H. 2019. RNAi of the sesquiterpene cyclase gene for phytoalexin production impairs pre- and post-invasive resistance to potato blight pathogens. *Molecular Plant Pathology*, 20, 907-922.

Zhang X, Song W, Chen H, Qian Z, Zeng J, Dong S. 2021. Status and prospects of chemical prevention and control of potato late blight. *China Plant Protection* (in Chinese), 41, 33-39.

Zhao JH, Zhang T, Liu QY, Guo HS. 2021. Trans-kingdom RNAs and their fates in recipient cells: advances, utilization, and perspectives. *Plant Communications,* 2, 100167.

Zhou Q, Tang D, Huang W, Yang Z, Zhang Y, Hamilton JP, Visser RGF, Bachem CWB, Robin Buell C, Zhang Z, Zhang C, Huang S. 2020. Haplotype-resolved genome analyses of a heterozygous diploid potato. *Nature Genetics*, 52, 1018-1023.

Zhou XT, Jia LJ, Wang HY, Zhao P, Wang WY, Liu N, Song SW, Wu Y, Su L, Zhang J, Zhong NQ, Xia GX. 2018. The potato transcription factor StbZIP61 regulates dynamic biosynthesis of salicylic acid in defense against Phytophthora infestans infection. *Plant Journal*, 95, 1055-1068.

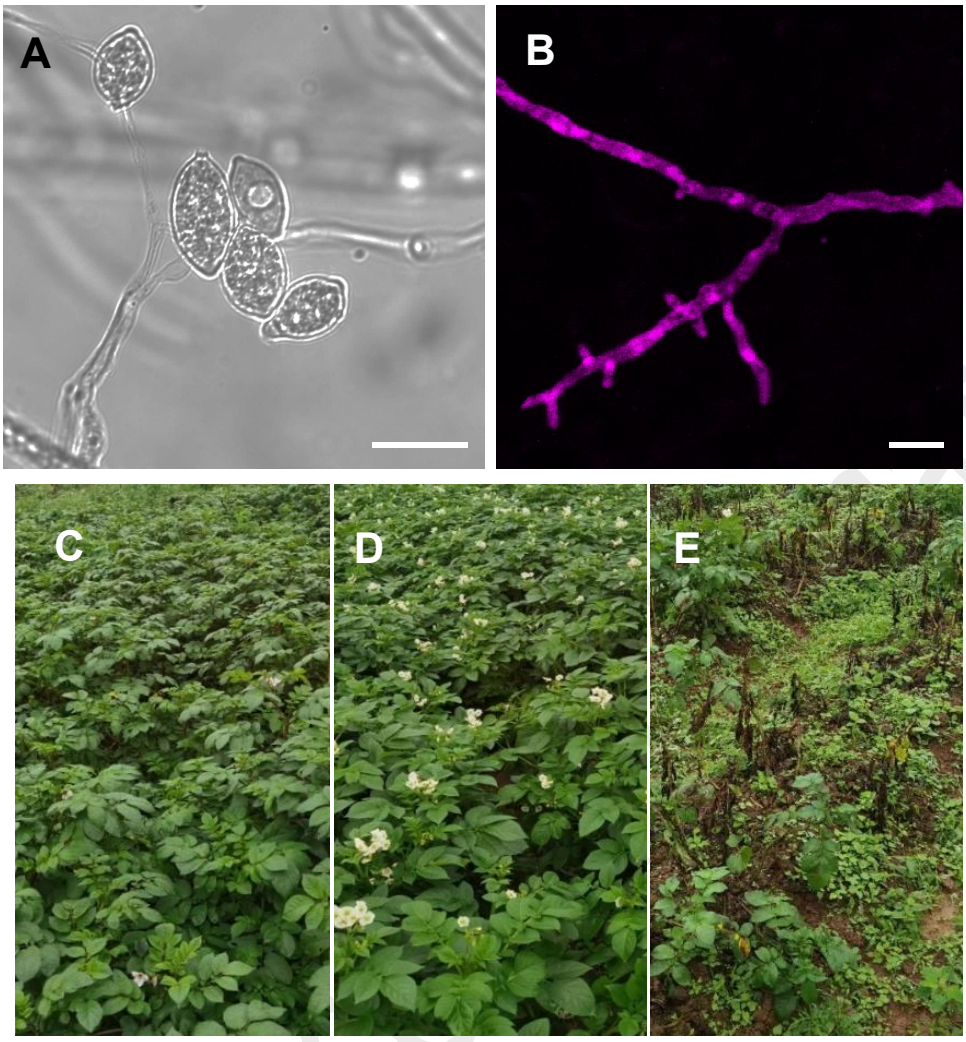

Fig. 1 *Phytophthora infestans*. A, the sporangia of *P. infestans* (bar=200 μM). Courtesy of Dr. Luyao Wang. B, the RFP labeled *P. infestans* mycelium in plant tissue (bar=30 μM). Courtesy of Dr. Chuyun Gao. C, the potato cultivar Qingshu 9 is resistant to PLB in field. D, the potato cultivar Yunshu 505 is resistant to PLB in field. E, the potato cultivar Favorita are susceptible in field. All these photograph are taken in Guizhou, China.

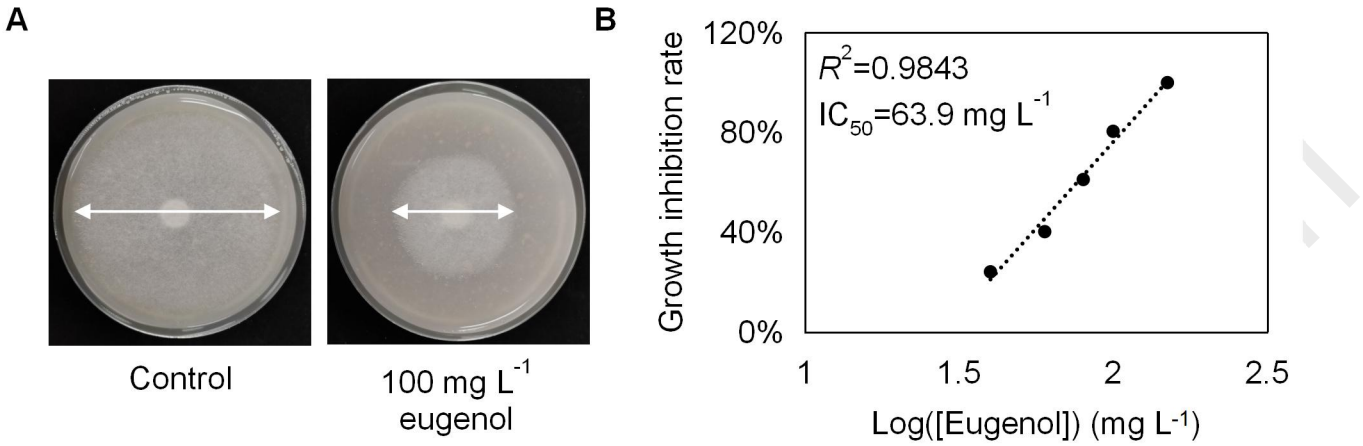

Fig. 2 *In vitro* growth inhibition of *Phytophthora infestans* by supplemented eugenol. *P. infestans* T30-1 culture was inoculated onto eugenol-supplemented oatmeal agar plates (*n*=8 at each concentration tested) with hyphae plugs (diameter=7 mm). Control plates (*n*=5) contained equal volume of DMSO supplement. Radial growth was quantified by diameters of hyphae out-growth at fifth day post-inoculation, and the inhibition rates were calculated. A, example *P. infestans* culture on control and 100 mg L^{-1} eugenol-supplemented plates with the diameters of filamentous growth marked by double arrows. B, dosage curve of *P. infestans* growth inhibition rate.