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REVIEW ARTICLE

Advancements and Emerging Molecular Technologies in Plant-Pathogen Interaction Studies

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Abstract. Pathogens employ various strategies and produce multiple virulence factors to successfully infect plant hosts and complete their life cycle. Conversely, plant hosts are equipped with a range of immune responses to defend against these attackers. This interplay between plant and pathogen results in dynamic interactions involving the activation of biological processes and the production of molecular signals at the cellular level. Significant progress has been made with recent technologies, advancing our understanding of the molecular mechanisms underlying these interactions. In this review, we explore the current knowledge of the biology of foliar plant pathogen infections and host immunity. We emphasize the molecular technologies, including genetic manipulation techniques and omics approaches, that are currently available and applied in the study of plant-microbe interactions, addressing multiple aspects of this expanding field.

Keywords: Foliar Pathogen, Plant Immunity, Plant Disease, Virulence Factors

1. Introduction

The impact of climate change has triggered several environmental shifts, including threatening global agriculture and food security. Several plant pathogens are rising with newly equipped strategies to invade the plant hosts, consequently leading to crop yield reduction. In a successful disease cycle, plant pathogens employ many virulence strategies to invade or suppress plant immunity and obtain essential nutrients and food sources from the host plants (Melotto and Kunkel, 2013; Pfeilmeier et al., 2016). These strategies include toxin secretion and the delivery of virulence-associated molecules. For the plant pathogenic bacteria, the most notable foliar pathogen is *Pseudomonas syringae*, which infects a wide range of plant species (Mansfield et al., 2012). *P. syringae* is one of the most common plant pathogens, with over 60 pathovars identified in this species that infect a distinctive group of host plants, including many economically significant crops. Some strains of this pathogen can infect a model plant *Arabidopsis*, providing an excellent pathosystem for understanding the molecular insights of plant-microbe interactions.

Foliar pathogen, such as *P. syringae*, exhibits two interconnected phases of growth, epiphytic and endophytic phases. Upon arrival on the leaf surface, many strains of *P. syringae*, can survive and multiply to establish the epiphytic population. For example, *P. syringae* pv. *syringae* B728a can achieve a large epiphytic population on the leaf surface and is often used widely for epiphytic studies (Monier and Lindow, 2004). They later enter inside the leaf interior through natural openings, such as stomata, hydathodes, or wounds, and proliferate inside leaf tissues (Melotto et al., 2008). This results in the appearance of disease symptoms, starting with water-soaked patches, followed by extensive necrosis. The previous transcriptomic study of *P. syringae* revealed that the model pathogen has distinct adaptation mechanisms for different leaf habitats (Yu et al., 2013). The pathogens favor flagellar motility, biosurfactant production, and chemotaxis on the leaf surface, whereas the endophytic bacteria favor the mechanisms that help attenuate the plant immune responses, such as the degradation of certain amino acids associated with plant defense mechanism and the production of bacterial secondary metabolites, such as phytotoxins (Yu et al., 2013).

Owing to the advancements of molecular techniques, sequencing technologies, and multi-omics data analysis for the past years, we have gained more knowledge of the molecular mechanisms underlying pathogen pathogenicity. This knowledge helps us to better understand the life cycle of plant pathogens and how they can successfully infect healthy plants, as well as the mechanisms of plant immune responses against these invaders. In this review, we begin by introducing the strategies and virulent factors that are important for plant pathogen survival in plant hosts. We mainly focus on foliar pathogenic bacteria as they have a well-studied model system. We then delve into plant immunity and how pathogens exploit it as their targets. In the final section, we discuss the progress in the emerging molecular technologies used in plant-pathogen interaction studies.

2. Strategies and Virulence Factors for Plant Pathogen Survival

2.1 Quorum sensing (QS): the language of bacterial communication

To achieve colonizing success, bacteria normally coordinate their behaviors and operate synchronously among multiple cells rather than acting individually. They rely on quorum sensing, which is the system that allows cell-to-cell communication through the detection and response to diffusible small molecules that are directly proportional to the density of bacterial populations (Joshi et al., 2021). These QS signals are commonly small (less than 1,000 Da) organic molecules or peptides with 5-20 amino acids, for example, N-acyl homoserine lactones (AHLs), 2-alkyl-4-quinolones (AQs), long-chain fatty acids, and furanones (Williams, 2007). Most gram-negative bacteria produce AHLs as QS signal molecules. AHL-mediated QS are well characterized and are known to regulate the expression of virulence-related genes of several phytopathogenic bacteria. In fact, six of the top 10 plant pathogenic bacteria, as ranked by their scientific and economic importance, rely on AHL-mediated QS systems (Mansfield et al., 2012). Thus, in this section, we focus on the QS that is mediated by AHLs.

AHLs are synthesized via AHL synthases, which are generally homologous to LuxI protein of Vibrio fischeri, the organism in which QS was first described. These LuxI homologs catalyze the formation of AHLs by forming an amide bond between a fatty acyl chain and a precursor, S-adenosylmethionine (SAM) (Fuqua et al., 2001). AHLs are generally produced at a basal level when low numbers of bacterial cells are present. As population cell density increases, AHLs are highly accumulated until the threshold concentration is reached. AHLs diffuse across the bacterial cells and directly bind to a cytoplasmic transcriptional regulator, LuxR. LuxR is comprised of two domains, an N-terminal region that binds to its cognate AHL and a C-terminus that is a DNA-binding site. The binding of AHL to LuxR receptor results in the alteration of protein conformation, inducing the LuxR-AHL complex to function as a positive or negative regulator to activate or suppress the expression of target genes, including AHL synthase activation (Figure 1). In *P. syringae*, AHL-mediated QS networks have been identified and characterized in many pathovars. For example, the AHL-mediated QS in *P. syringae* B728a has been shown to link with epiphytic fitness, exopolysaccharide production, and motility (Quiñones et al., 2005). The transcriptomic study of *P. syringae* pv. tabaci 11528 also indicated the involvement of AHL in bacterial motility and pathogenesis (Cheng et al., 2017).

2.2 Exopolysaccharides

Several pathogens must survive the plant surface environment before they can invade inside the leaf tissue. The leaf surface is a challenging habitat as it provides spatially

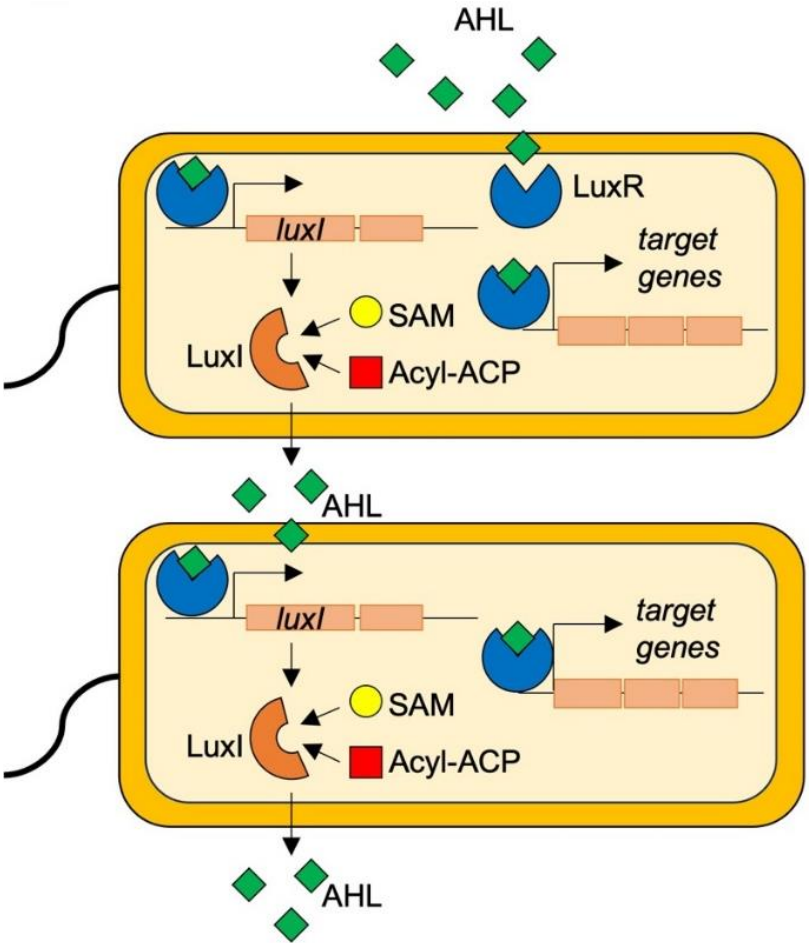

Figure 1. LuxI/LuxR regulatory system. AHLs are synthesized via LuxI synthase by forming an amide bond between a fatty acyl chain, from acyl-acyl carrier protein (Acyl-ACP), and a precursor, S-adenosylmethionine (SAM). At high cell density, AHLs are highly accumulated until the threshold concentration is reached. AHLs diffuse across the bacterial cell and bind to LuxR regulator. LuxR-AHL complex functions as a positive or negative regulator to activate or suppress the expression of target genes, including LuxI-AHL synthase activation.

heterogeneous and limited nutrient availability for pathogens (Lindow and Brandl, 2003). They also need to survive the abiotic stresses on leaves, including damaging UV radiation, desiccation, and oxidative stress (Beattie, 2011). Thus, many pathogens have their own strategies to cope with this harsh environment on plant surface. Exopolysaccharide molecules are carbohydrate polymers secreted by bacteria to facilitate their survival and pathogenesis during phyllosphere colonization. The bacterial cells generally reside in exopolysaccharides, which help maintain a hydrated layer surrounding bacteria, provide protection from hydrophobic and toxic compounds, and promote bacterial virulence (Killiny et al., 2013).

2.3 Bacterial secretion systems

Bacteria rely on secretion systems for the transportation of proteins from their cytoplasm to different cellular compartments, the surrounding environment, and other prokaryotic or eukaryotic cells (Green and Mecsas, 2016). There are several types of secretion systems, including, general secretion (Sec), twin arginine translocation (Tat), and eight types of secretion systems (T1SS-T7SS, T9SS), each designated for the transport of specific protein subsets (Pena et al., 2019). Among these, T3SS particularly plays a significant role in the bacterial virulence of many pathogenic bacteria as it enables them to deliver effector proteins into the cytoplasm of the host cells by the needlelike apparatuses called pilus (Figure 2). Type III effectors typically function within the plant cells to modulate various cellular activities, such as suppressing plant immunity, interfering with plant hormone synthesis and signaling, and regulating plant transcription.

2.4 Toxins

Many plant pathogens secrete small, low-molecular-weight toxins as part of their virulence, each with distinct modes of action (Figure 2). Lipodepsipeptide toxins, such as syringomycins and syringopeptins, are produced by various *Pseudomonas* spp., including, *P. syringae*, *P. fuscovaginae*, and *P. cichorii*, and are known to directly damage plant cells to induce tissue necrosis in infected plants (Coraiola et al., 2008; Melotto and Kunkel, 2013; Huang et al., 2015). With their amphipathic structure, these toxins can insert into the lipid bilayers of plant cell membranes, leading to the formation of pores and subsequently the induction of electrolyte leakage (Girard et al., 2020). A genome-wide fitness profiling of *P. syringae* pv. *syringae* B728a has also highlighted a greater contribution of syringomycin to bacterial fitness in the leaf apoplast than that of syringopeptin (Helmann et al., 2019).

Some other toxins can induce plant chlorosis and necrosis by interfering with the host metabolisms. For example, phaseolotoxin, mangotoxin, and tabtoxin are modified peptide toxins produced by various pathovars of *P. syringae*. These toxins inhibit enzymes involved in amino acid biosynthesis, resulting in amino acid deficiencies and the accumulation of nitrogen-containing intermediates that can be used as a food source for pathogens (Arrebola et al., 2011). Phaseolotoxin is generally active by releasing the toxic moiety, octicidine, via hydrolysis once inside the plant cells, which subsequently induces plant chlorosis. Tabtoxin also functions through similar mechanisms, which is hydrolyzed to release its toxic moiety, tabtoxinine-ß-lactam, leading to severe chlorosis in symptomatic tissue (Langston-Unkefer et al., 1987).

The polyketide phytotoxin, coronatine, is very well-studied and a good example of bacterial toxins that can interfere with plant hormone signaling. Coronatine is also a phytohormone mimic, which became known after its discovery as a toxin. Many *P. syringae* strains produce coronatine, which is a non-host specific toxin that contributes to bacterial virulence via several mechanisms. Coronatine is a structural and functional analog of jasmonoyl-L-isoleucine (JA-Ile), which is recognized by the plant COI1/JAZ receptor complex and activates the JA-Ile signaling pathway.This activation subsequently promotes plant susceptibility through the antagonistic regulatory crosstalk between JA and SA signaling (Geng et al., 2014). Coronatine is essential during both the early and late stages of infection, including the suppression of stomatal immunity, promoting apoplastic proliferation, and inducing plant necrosis and chlorosis (Mecey et al., 2011).

3. Plant Immunity

Upon pathogen infection, plants elicit two layered innate immunity. The first layer is activated upon the recognition of microbe-associated molecular patterns (MAMPs) through surface-localized pattern-recognition receptors (PRRs), leading to pattern-triggered immunity (PTI). To promote invasion and maintain an endophytic population, many pathogens deliver virulence-associated molecules, such as effectors, into the apoplast or the plant cells to manipulate and suppress host defense mechanisms (Wang et al., 2022). As a counter-defense strategy, plants use intracellular nucleotide-binding leucine-rich repeat (NLR) receptors to detect the pathogen effectors and activate the second layer of plant immunity known as effector-triggered immunity (ETI) (Peng et al., 2018). Despite the difference in receptor recognition, PTI and ETI share many similar downstream responses with distinct amplitudes and dynamics (Yuan et al., 2021). Some defense mechanisms elicited by PTI and/or ETI, including, apoplast alkalinization, reactive oxygen species (ROS) burst, calcium flux, and activation of phytohormone signaling (Figure 2). These activities lead to plant resistance against pathogens in the apoplast, where the invaders likely experience cellular stresses

4. Molecular Technologies in Plant-Pathogen Interaction Studies

4.1 Genetic manipulative techniques

Modification of genetic materials has proved successful in studying the functions of genes involved in several biological processes for many decades. Homologous recombination is perhaps one of the most classical approaches used for genome editing. This approach relies on the exchanges of DNA sequences between two similar strands of DNA. By generating the DNA sequences that are similar to the portion of the targeted location on the genome, the precise gene or targeted DNA sequences can be manipulated. To date, this technique is used regularly to delete targeted genes in plants and phytopathogens to study the biological processes underlying plant-pathogen interactions. CRISPR gene editing is another tool that is widely used in recent years. CRISPR/Cas9, in particular, allows genome manipulation at a precise location by using synthetic guide RNA that complements to the targeted genes, and Cas9, an enzyme nuclease that can cut the DNA and randomly replace it with other nucleotides. These genetic manipulative techniques enable the creation of different types of genetic modification, including gene knockout, gene deletion, gene insertion and point mutation.

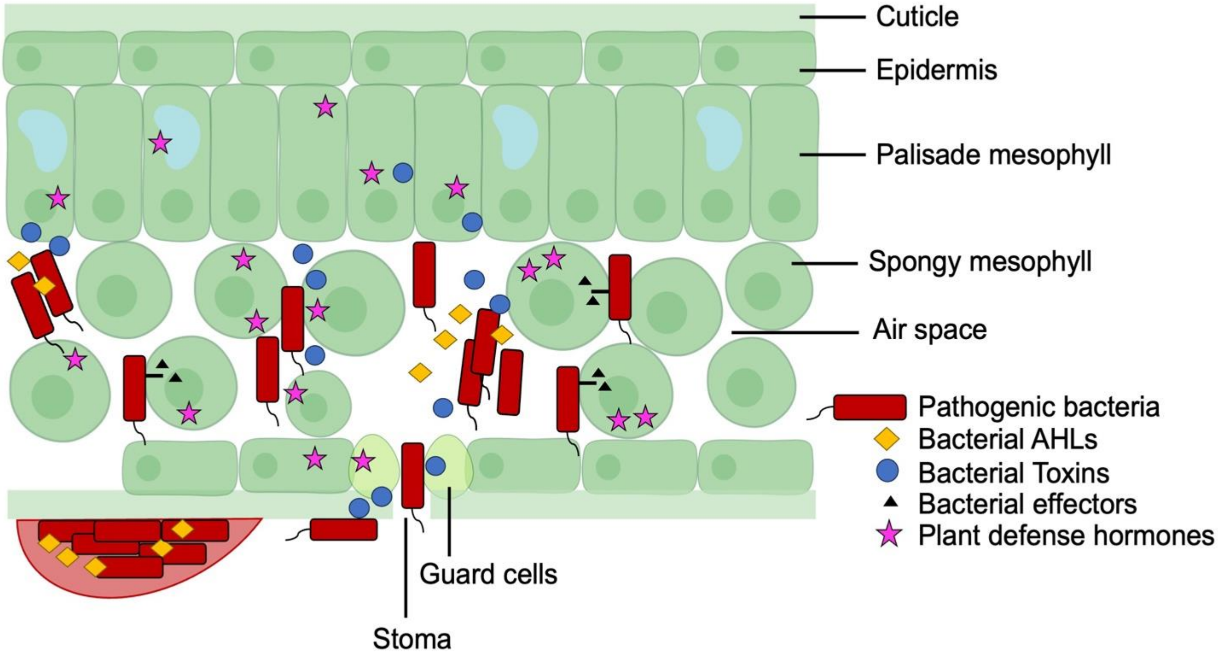

Figure 2. Virulent factors produced by foliar pathogens during plant infection. Epiphytic bacteria often form aggregates to survive on the leaf surface, and they produce exopolysaccharides regulated by N-acyl homoserine lactone (AHL)-mediated quorum sensing, providing protection against the harsh leaf environment. AHLs also control the flagellar-driven motility of bacteria as they navigate the environment. Toxins are produced and released to facilitate the bacterial colonization of leaves by suppressing stomatal immunity, promoting endophytic proliferation, and inducing plant necrosis. They can also deliver bacterial effectors directly into the plant cells to manipulate various plant cellular metabolisms, especially targeting plant hormone-mediated defense networks.

4.2 Transcriptomics

Utilizing next-generation sequencing, RNA molecules from experimental samples can be relatively detected and quantified in a short period of time. This technology contributes to the massive production of gene expression profiling under different conditions, such as the comparison between wild type and mutant samples, regulatory alterations of pathogens under different environments, differentially expressed genes (DEGs) of plant pathogens at each stage of their infection cycle. Several previous studies have utilized RNA-sequencing as a tool to gain insight in the molecular mechanisms of pathogen virulence, disease symptoms, and plant immune responses (Table 1). These gene expression profiles can also serve as a database for selecting potential molecular markers for breeding crops with disease tolerance.

4.3 Proteomics

The study of identification, function, structures, and interactions of proteins is another key approach to understanding the molecular mechanisms of plant-microbe interactions. Proteins play crucial roles in the regulation of specific signaling pathways to establish the relationships between plants and other organisms, whether they are pathogens or beneficial symbionts. These pathways include, for example, microbial recognition, biotic stress-related responses, plant defense responses and the induction of plant resistance (Jain et al., 2021). Current proteomics approaches that are available include the gel-based and non-gel based methods. Gel-based methods, such as two-dimensional gel electrophoresis (2DE) and differential gel electrophoresis (DIGE), allow for the separation, identification, and quantification of proteins. (Jain et al., 2024). Non-gel based methods include the use of liquid chromatography to separate peptides after sequence-specific digestion, which has become a core tool for large-scale proteomics, such as multidimensional protein identification technology (MudPIT) and isobaric tag for relative and absolute quantification (iTRAQ). A detailed overview on the application of proteomics in plant-microbe studies is reviewed extensively by Jayaraman et al., 2012; Jain et al., 2021; Jain et al., 2024. Proteomics techniques used in selected plant-pathogen interaction studies can be found in Table 1.

4.4 Metabolomics

Plant and pathogen metabolites play crucial roles in several metabolic processes during plant-microbe interactions. For example, some metabolites serve as signaling molecules to regulate pathogen virulence or the initiation of plant defense mechanism, whereas some metabolites can play a direct role as antimicrobial molecules. Current metabolomic research primarily relies on mass spectrometry for detection and quantification of compounds. Approaches can include targeted metabolomics, where a list of metabolites is set for analysis, or it can be untargeted metabolomics, which includes other undefined metabolites and provides the metabolomic profiles of the samples. Detected metabolites are typically carbohydrates, amino acids and peptides, organic acids, lipids, and nucleic acids. However, specific extraction protocols can be developed to detect other specialized molecules such as polyphenols. The application of metabolomics has provided insight into small molecules generated as part of metabolic pathways activated during the interaction between plants and microbial organisms. Although several metabolome databases for specific organisms are available, there is still no specific database for plant-microbe studies (Castro-Moretti et al., 2020). Some of the selected work that applied metabolomics in the investigation of plant-microbe studies are listed in Table 1.

Table 1. Selected works representing the use of current molecular technologies in plant-pathogen interaction studies.

Molecular Tool	Plant/Pathogen	Main Finding	Contribution	Reference
Transcriptomics (RNA- seq technology)	Peanut/ *Cercospora arachidicola* (Hori)	Identified DEGs involved in disease resistance, NLR in particular, from resistant and susceptible peanuts against early leaf spot disease caused by *C. arachidicola* (Hori)	Molecular mechanisms of plant defense responses	Gong et al., 2020
Transcriptomics (RNA- seq technology)	Canola/ *Sclerotinia sclerotiorum*	Identified DEGs from the pathogen *S. sclerotiorum* involved in the suppression of host defense. Highlight the key role of peroxisome metabolism in *S. sclerotiorum* pathogenesis.	Molecular mechanisms underlying pathogen virulence and infection stages	Chittem et al., 2020
Transcriptomics (RNA- seq technology)	Rice/ *Xanthomonas oryzae* pv. *oryzae* (*Xoo*)	Identified candidate genes of resistant rice genotype that are important during combined biotic (disease) and abiotic (drought) stress.	Molecular markers and targeted genes for improving resistant cultivars	Pal et al., 2022
Transcriptomics (RNA- seq technology)	*Pectobacterium carotovorum*	Demonstrated a spatiotemporal expression of *P. carotovorum*. Highlight the significant roles of pectolytic enzymes from the pathogen and the lowered plant defensive mechanism in maceration.	Molecular mechanisms underlying pathogen virulence and disease symptoms	Fan et al., 2020
Metatranscriptomics (RNA- seq technology)	*Arabidopsis*/ *Fusarium oxysporum*	Revealed the expression of plant genes that responded differently to endophyte and pathogen	Mechanisms of plant transcriptome reprogramming to regulate response against beneficial and pathogenic fungi.	Guo et al., 2021
Proteomics (iTRAQ)	*Nicotiana benthamiana/* Tobacco mosaic virus (TMV)	Identified plant proteins involved in cross-protection against TMV	Molecular mechanisms underlying cross-protection	Das et al., 2019
Proteomics (iTRAQ)	Potato/ *Phytophthora infestans*	Identified common and cultivar specific proteins associated with defense mechanisms against late blight disease	Molecular mechanisms of plant defense responses	Xiao et al., 2020
Metabolomics (GC-TOF-MS)	Tomato/ *Salmonella enterica*	Provided evidence that plant surface metabolites contribute to the growth and colonization success of *S. enterica* in pyllosphere	Molecular mechanisms underlying bacterial colonization in plants	Han and Micallef, 2016
Metabolomics (TOF-MS)	Tomato/ *Alternaria solani, Alternaria alternata*	Identified PTI-associated metabolites such as trigonelline	Molecular mechanisms of plant defense responses	Munoz Hoyos et al., 2024

5. Conclusion

To ensure successful plant colonization, pathogens employ several strategies to overcome plant immunity, including the production of signaling molecules, toxins, and effector proteins. By incorporating multiple virulence pathways, pathogens can damage plant cells, interfere with plant metabolism, suppress immune responses, and more. On the other hand, plants defend themselves by employing immune networks, such as Pattern-Triggered Immunity (PTI) and Effector-Triggered Immunity (ETI), to orchestrate appropriate immune responses. Recent research has made significant progress in uncovering the molecular mechanisms underlying plant-pathogen interactions throughout the course of infection. However, many discoveries still await exploration. Molecular technologies such as CRISPR/Cas9, transcriptomics, proteomics, and metabolomics have proven to be essential in advancing our knowledge and contributing to rapid progress in the study of plant-microbe interactions. The authors strongly believe that technological advancements will accelerate even further in the near future, providing more powerful tools to deepen our understanding and develop more effective strategies for managing plant diseases.

References

Arrebola E, Cazorla FM, Perez-Garcia A, de Vicente A (2011) Chemical and metabolic aspects of antimetabolite toxins produced by *Pseudomonas syringae* pathovars. Toxins (Basel) 3:1089-110

Beattie GA (2011) Water relations in the interaction of foliar bacterial pathogens with plants. Annu Rev Phytopathol 49:533-55

Coraiola M, Paletti R, Fiore A, Fogliano V, Dalla SM (2008) Fuscopeptins, antimicrobial lipodepsipeptides from Pseudomonas fuscovaginae, are channel forming peptides active on biological and model membranes. J Pept Sci 14: 496-502

Cheng F, Ma A, Luo J, Zhuang X, Zhuang G (2017) N-acylhomoserine lactone-regulation of genes mediating motility and pathogenicity in Pseudomonas syringae pathovar tabaci 11528. Microbiologyopen 6

Chittem K, Yajima WR, Goswami RS, Del Rio Mendoza LE (2020) Transcriptome analysis of the plant pathogen Sclerotinia sclerotiorum interaction with resistant and susceptible canola (Brassica napus) lines. PLoS One 15, e0229844

Das PP, Chua GM, Lin Q, Wong SM (2019) iTRAQ-based analysis of leaf proteome identifies important proteins in secondary metabolite biosynthesis and defence pathways crucial to cross-protection against TMV. J Proteomics 196: 42-56

Fan J, Ma L, Zhao C, Yan J, Che S, Zhou Z, Wang H, Yang L, Hu B (2020) Transcriptome of Pectobacterium carotovorum subsp. carotovorum PccS1 infected in calla plants in vivo highlights a spatiotemporal expression pattern of genes related to virulence, adaptation, and host response. Mol Plant Pathol 21: 871-891

Fuqua C, Parsek MR, Greenberg EP (2001) Regulation of gene expression by cell-to-cell communication: acyl-homoserine lactone quorum sensing. Annu Rev Genet 35: 439-68

Geng X, Jin L, Shimada M, Kim MG, Mackey D (2014) The phytotoxin coronatine is a multifunctional component of the virulence armament of *Pseudomonas syringae*. Planta 240: 1149-65

Gong L, Han S, Yuan M, Ma X, Hagan A, He G (2020) Transcriptomic analyses reveal the expression and regulation of genes associated with resistance to early leaf spot in peanut. BMC Res Notes 13: 381

Green ER, & Mecsas J (2016) Bacterial secretion systems: an overview. Virulence mechanisms of bacterial pathogens, 4: 213-239

Girard L, Hofte M, De Mot R (2020) Lipopeptide families at the interface between pathogenic and beneficial

Pseudomonas-plant interactions. Crit Rev Microbiol 46: 397-419

Guo L, Yu H, Wang B, Vescio K, DeIulio GA, Yang H, Berg A, Zhang L, Edel-Hermann V, Steinberg C, Kistler HC, Ma LJ (2021) Metatranscriptomic Comparison of Endophytic and Pathogenic Fusarium-Arabidopsis Interactions Reveals Plant Transcriptional Plasticity. Mol Plant Microbe Interact 34: 1071-1083

Han S, & Micallef SA (2016) Environmental Metabolomics of the Tomato Plant Surface Provides Insights on Salmonella enterica Colonization. Appl Environ Microbiol 82: 3131-3142

Helmann TC, Deutschbauer AM, Lindow SE (2019) Genome-wide identification of *Pseudomonas syringae* genes required for fitness during colonization of the leaf surface and apoplast. Proc Natl Acad Sci U S A 116: 18900-18910

Huang CJ, Pauwelyn E, Ongena M, Debois D, Leclere V, Jacques P, Bleyaert P, Hofte M (2015) Characterization of Cichopeptins, New Phytotoxic Cyclic Lipodepsipeptides Produced by Pseudomonas cichorii SF1-54 and Their Role in Bacterial Midrib Rot Disease of Lettuce. Mol Plant Microbe Interact 28: 1009-22

Jain A, Singh HB, Das S (2021) Deciphering plant-microbe crosstalk through proteomics studies. Microbiol Res 242, 126590

Joshi JR, Khazanov N, Charkowski A, Faigenboim A, Senderowitz H, Yedidia I (2021) Interkingdom Signaling Interference: The Effect of Plant-Derived Small Molecules on Quorum Sensing in Plant-Pathogenic Bacteria. Annu Rev Phytopathol 59: 153-190

Langston-Unkefer PJ, Robinson AC, Knight TJ, Durbin RD (1987) Inactivation of pea seed glutamine synthetase by the toxin, tabtoxinine-beta-lactam. Journal of Biological Chemistry, 262(4) pp.1608-1613

Lindow SE, & Brandl MT (2003) Microbiology of the phyllosphere. Appl Environ Microbiol 69: 1875-83

Mansfield J, Genin S, Magori S, Citovsky V, Sriariyanum M, Ronald P, Dow M, Verdier V, Beer SV, Machado MA, Toth I, Salmond G, Foster GD (2012) Top 10 plant pathogenic bacteria in molecular plant pathology. Mol Plant Pathol 13: 614-29

Mecey C, Hauck P, Trapp M, Pumplin N, Plovanich A, Yao J, He SY (2011) A critical role of STAYGREEN/ Mendel's I locus in controlling disease symptom development during *Pseudomonas syringae* pv tomato infection of Arabidopsis. Plant Physiol 157: 1965-74

Melotto M, Underwood W, He SY (2008) Role of stomata in plant innate immunity and foliar bacterial diseases. Annu Rev Phytopathol 46: 101-22

Melotto M, & Kunkel BN (2013) Virulence strategies of plant pathogenic bacteria. In E Rosenberg, E Stackebrand, EF DeLong, F Thompson, S Lory, eds, The Prokaryotes: Prokaryotic Physiology and Biochemistry, Ed 4. Springer-Verlag, Berlin, pp 61–82

Monier JM, & Lindow SE (2004) Frequency, size, and localization of bacterial aggregates on bean leaf surfaces. Appl Environ Microbiol 70: 346-55

Munoz Hoyos L, Anisha WP, Meng C, Kleigrewe K, Dawid C, Huckelhoven R, Stam R (2024) Untargeted metabolomics reveals PTI-associated metabolites. Plant Cell Environ 47: 1224-1237

Pal G, Bakade R, Deshpande S, Sureshkumar V, Patil SS, Dawane A, Agarwal S, Niranjan V, PrasannaKumar MK, Vemanna RS (2022) Transcriptomic responses under combined bacterial blight and drought stress in rice reveal potential genes to improve multi-stress tolerance. BMC Plant Biol 22: 349

Pena RT, Blasco L, Ambroa A, Gonzalez-Pedrajo B, Fernandez-Garcia L, Lopez M, Bleriot I, Bou G, Garcia-Contreras R, Wood TK, Tomas M (2019)

Relationship Between Quorum Sensing and Secretion Systems. Front Microbiol 10: 1100

Peng Y, van Wersch R, Zhang Y (2018) Convergent and Divergent Signaling in PAMP-Triggered Immunity and Effector-Triggered Immunity. Mol Plant Microbe Interact 31: 403-409

Pfeilmeier S, Caly DL, Malone JG (2016) Bacterial pathogenesis of plants: future challenges from a microbial perspective: Challenges in Bacterial Molecular Plant Pathology. Mol Plant Pathol 17: 1298-313

Quinones B, Dulla G, Lindow SE (2005) Quorum sensing regulates exopolysaccharide production, motility, and virulence in *Pseudomonas syringae*. Mol Plant Microbe Interact 18: 682-93

Wang Y, Pruitt RN, Nurnberger T, Wang Y (2022) Evasion of plant immunity by microbial pathogens. Nat Rev Microbiol 20: 449-464

Williams P (2007) Quorum sensing, communication and cross-kingdom signalling in the bacterial world. Microbiology (Reading) 153: 3923-3938

Xiao C, Huang M, Gao J, Wang Z, Zhang D, Zhang Y, Yan L, Yu X, Li B, Shen Y (2020) Comparative proteomics of three Chinese potato cultivars to improve understanding of potato molecular response to late blight disease. BMC Genomics 21: 880

Yu X, Lund SP, Scott RA, Greenwald JW, Records AH, Nettleton D, Lindow SE, Gross DC, Beattie GA (2013) Transcriptional responses of *Pseudomonas syringae* to growth in epiphytic versus apoplastic leaf sites. Proc Natl Acad Sci U S A 110, E425-34

Yuan M, Ngou BPM, Ding P, Xin XF (2021) PTI-ETI crosstalk: an integrative view of plant immunity. Curr Opin Plant Biol 62:102030