REVIEW ARTICLE
doi: 10.2306/scienceasia1513-1874.2025.034

ScienceAsia 51 (2): 2025: ID 2025034: **1–9**

The crucial role of lipid biosynthesis in fungal pathogenesis of rice

Kalaivani Nadarajah

School of Biological Sciences and Biotechnology, Faculty of Science and Technology, Universiti Kebangsaan Malaysia, 43600 UKM Bangi, Malaysia

e-mail: vani@ukm.edu.my

Received 18 Nov 2024, Accepted 13 Feb 2025
Available online 1 May 2025

ABSTRACT: Lipid biosynthesis plays a critical role in the pathogenicity and virulence of fungal pathogens affecting rice, particularly in *Magnaporthe oryzae*, *Rhizoctonia solani*, and *Fusarium* species. Glycerol, a key product of lipid metabolism, is essential for maintaining turgor pressure, which is crucial for processes such as conidiogenesis and host penetration. This review explores the intricate lipid biosynthesis pathways and their associated genes, emphasizing the significance of fatty acid biosynthesis in supporting fungal growth and pathogenicity. Additionally, the differing strategies employed by biotrophic and necrotrophic fungi are examined, highlighting how biotrophic fungi rely on living host tissues for sustenance while necrotrophic fungi actively kill host cells to obtain nutrients. This distinction underscores the varied metabolic adaptations and lipid utilization mechanisms these fungi deploy in their pathogenic lifestyles. Recent insights into the roles of key genes involved in lipid metabolism reveal potential targets for biocontrol strategies and highlight the importance of understanding lipid biosynthesis as a crucial component of fungal virulence in rice pathogens.

KEYWORDS: lipid biosynthesis, fungal virulence and pathogenicity in rice, biotroph, necrotroph

INTRODUCTION

Rice, a staple food for more than half of the world's population, is crucial for global food security, especially in Asia, where it is the primary crop cultivated. However, rice production is frequently challenged by various fungal pathogens, which can cause severe yield losses and threaten global food supplies. Among these pathogens, *Magnaporthe oryzae*, the causative agent of rice blast disease, stands out due to its destructive impact, with annual losses sufficient to feed 60 million people [1]. This pathogen's ability to go undetected during its initial biotrophic phase makes it particularly challenging to manage, and often leads to significant crop devastation.

The infection cycle of *M. oryzae* begins with the dispersal of its spores, which, germinates and forms appressorium. This specialized structure generates the turgor pressure necessary to breach the plant's defenses, a process heavily reliant on lipid biosynthesis [2]. The critical role of lipids extends beyond mere penetration, contributing to the pathogen's overall virulence by supporting metabolic processes essential for its survival and proliferation within the host [3]. In addition to *M. oryzae*, other fungal pathogens such as *Rhizoctonia solani*, *Fusarium* species, *Curvularia* species, and *Alternaria* species also present significant threats to rice cultivation. *R. solani*, the agent of sheath blight, targets the leaves and stems of rice plants, leading to reduced photosynthetic capacity and lower yield [4–6]. Like *M. oryzae*, *R. solani* depends on lipid metabolism for its pathogenicity. The energy derived from lipid breakdown fuels the formation of infection structures, while lipid-derived signaling molecules regulate virulence and adaptation to the host environment [7].

Fusarium species, responsible for diseases like bakanae and seedling blight, also exploits lipid biosynthesis to enhance their virulence. These pathogens produce mycotoxins such as fumonisins and trichothecenes, which disrupt host cell membrane and interferes with physiological processes, facilitating the invasion and colonization of plant tissues [8]. The production of these mycotoxins, along with other virulence factors, is closely linked to lipid metabolism, making it a key target for managing these pathogens [9]. *Curvularia* and *Alternaria* species, which cause leaf spot and leaf blight, respectively, also rely on lipid reserves to support their growth and pathogenicity. These pathogens utilize lipid-derived signaling molecules to regulate germination, colonization, and other aspects of their infection processes [10]. The dependence of these diverse fungal pathogens on lipid metabolism underscores the potential of targeting lipid biosynthesis in the development of novel strategies for disease management in rice.

Understanding how these pathogens exploit lipid metabolism and biosynthesis to enhance their virulence can lead to innovative approaches, including the development of targeted fungicides or genetic interventions. These strategies could significantly improve rice resistance to fungal diseases, thereby bolstering

global food security and sustaining rice production in the face of increasing biotic pressures.

GENOMIC INSIGHTS AND SECRETOME PROFILES OF KEY RICE PATHOGENS

The draft genome of *M. oryzae*, was sequenced and the analyzed of the generated data showed the gene expression profiles across various growth stages and environmental stresses [1]. As a model organism for fungal plant pathogens, *M. oryzae* exhibits features like appressorium development and invasive hyphae that are crucial for its interaction into plant cell membranes and shares similarities with other plant pathogens [2]. The availability of its genome has significantly advanced research into rice blast disease, particularly in understanding lipid metabolism and its role in pathogenicity.

The secretome of *M. oryzae* includes approximately 1,546 predicted proteins, many of which are homologous to those found in saprophytic fungi such as *Neurospora crassa*, *Aspergillus nidulans*, *Chaetomium globosum*, and *Trichoderma reesei*. Among these secreted proteins are those involved in lipid biosynthesis and metabolism. These pathways are involved in the synthesis of key lipid molecules that contribute to the structural integrity and functionality of appresorium [11]. Lipid metabolism in *M. oryzae* is intertwined with secondary metabolism and pathogenicity. The synthesis and deposition of dihydroxynaphthalene (DHN)-melanin into the appresorium's cell wall is essential for the infection process. DHN-melanin, a type of dark pigment, protects the fungus from host plant defenses and environmental stresses. Pyriculol and its analogs, which are secondary metabolites involved in redox reactions, further enhances fungal survival and pathogenicity [12]. Disruptions in lipid biosynthesis pathways can lead to altered secondary metabolite production and pathogenicity, as demonstrated by the deletion of *PoYPD1* and *OSM1* in *M. oryzae* [13].

In addition to *M. oryzae*, other rice pathogens like *R. solani* and *Fusarium* sp. also exhibit complex lipid metabolic pathways. For example, *F. graminearum*, which causes head blight, produces trichothecenes that are crucial for its virulence [14]. Lipid biosynthesis and metabolism in *Fusarium* sp. contribute to the production of these virulence factors, influencing fungal morphogenesis and pathogenicity. The cAMP signaling pathway, involving adenylate cyclase, is pivotal for fungal morphogenesis and pathogenicity in *M. oryzae*. This pathway influences appressorium formation and penetration, linking lipid metabolism to the overall pathogenic processes [2]. The interplay between lipid metabolism, secondary metabolite production, and signaling pathways is integral to the pathogenicity of most of the above-mentioned rice fungal pathogens.

REGULATORY PATHWAYS OF LIPID BIOSYNTHESIS IN FUNGI

MAPK signaling pathways

Mitogen-Activated Protein Kinase (MAPK) pathways are critical for environmental signal transduction and transcriptional regulation, involving MAPK, MAP kinase kinase (MAPKK), and MAP kinase kinase kinase (MAPKKK) [22, 23]. In *M. oryzae*, these cascades regulate appressorium formation, tissue colonization, invasive growth, osmoregulation, and stress responses [15]. Key MAPK genes, including *PMK1*, *MPS1*, and *OSM1*, are essential for the pathogenesis of fungal pathogens. *PMK1*, in particular, plays a pivotal role in regulating appressorium formation. This gene functions similarly to the yeast kinases *FUS3* and *KSS1*, which are involved in cell signaling processes. *PMK1* operates downstream of cAMP (cyclic adenosine monophosphate)-mediated signals, which are critical for appressorium morphogenesis, the process by which the fungus differentiates into structure capable of penetrating the plant surface. Without this pathway, the pathogen's ability to infect and cause disease in host plants is significantly impaired [24]. In *R. solani* and *Fusarium* sp., MAPK pathways play a critical role in regulating stress responses, growth, and virulence. Key genes involved in these processes include *MAPK1*, *MAPK2*, *FgK1*, and *FgK2*, which are essential for the pathogenicity of these fungi [25]. *MAPK1* is crucial for managing osmotic stress and maintaining fungal cell wall integrity, while *MAPK2* regulates cell cycle processes and hyphal development, which are essential for the invasion of host plants. In *Fusarium* sp., *FgK1* and *FgK2* play significant roles in fungal development and pathogenicity. *FgK1* is involved in spore formation and plant invasion, whereas *FgK2* controls mycotoxin production, a key virulence factor [26]. One *Fusarium* sp., *F. verticillioides* utilizes MAPK signaling not only for the production of mycotoxins, but also in growth and stress adaptation of the fungi.

cAMP signaling pathways

cAMP functions as a crucial secondary messenger in eukaryotic cells, activating protein kinase A (PKA). In *M. oryzae*, cAMP-dependent protein kinase is critical for pathogenesis, particularly in the formation of the appressorium [27]. High concentrations of external cAMP can induce appressorium formation, and the cAMP signaling pathway plays an important role in sensing the host surface and promoting infection structure development [28]. Mutants lacking *PKA1* in *M. oryzae* and *Fusarium* sp. exhibit defects in the development of infection structures and show significantly reduced virulence [27]. In addition to cAMP signaling, autophagy-related genes, such as *ATG8*, are important for degrading lipids to provide energy during the infection process, particularly when external nutrients are limited. This ATG8-mediated autophagy is vital

Table 1 Secretome proteins of fungal pathogens and their roles in pathogenicity.

Pathogen	Secretome protein	Function	Ref.
M. oryzae	MoCDIP4	Induces cell death in rice cells	[15]
M. oryzae	MoCDIP1	Induces plant cell death and enhances pathogenicity	[15]
M. oryzae	MoHEG2	Hemicellulose-degrading enzyme	[16]
M. oryzae	MoAsp1	Aspartic protease involved in host colonization	[15]
R. solani	RsPG1	Pectin-degrading enzyme contributing to plant cell wall degradation	[17]
R. solani	RsRlpA	Necrosis-inducing protein	[18]
F. fujikuroi	FfLip1	Lipase involved in lipid metabolism and pathogenicity	[19]
F. oxysporum	Fow1	Fungal necrosis-inducing factor	[20]
F. oxysporum	SIX1	Effector protein that modulates host immune responses	[21]

for maintaining energy homeostasis and sustaining infection in pathogens like *M. oryzae* and *R. solani* [29]. Moreover, the cAMP pathways are also crucial in *R. solani* and *Fusarium* sp., including *F. graminearum* and *F. oxysporum*, where they regulate processes like conidiation, stress responses, and pathogenicity [30]. Another important gene, *CAP1*, in *M. oryzae* influences actin cytoskeleton dynamics, which is critical during hyphal penetration into the host. Mutations in cAMP-related genes, including those affecting *CAP1*, can significantly impair fungal virulence and infection capability [23, 31].

Lipid metabolism

Lipids, including fatty acids, glycerolipids, and sterol lipids, are vital for cellular functions and energy storage in fungi [7]. In *M. oryzae*, fatty acids and lipids are crucial for appressorium formation and turgor pressure [32]. *R. solani* depends on lipid metabolism for hyphal growth and stress responses, while *Fusarium* sp. rely on it for conidiation and pathogenicity [33, 34]. Lipids also play a role in mycotoxin production by *Fusarium* sp., highlighting their importance in fungal physiology and virulence [20].

Glyoxylate cycle

In *M. oryzae*, the glyoxylate cycle plays a crucial role by converting fatty acids and C2 compounds (like acetate) into C4 precursors, which are necessary for biosynthetic processes such as gluconeogenesis. This cycle is essential for the fungus to generate glucose from non-carbohydrate sources, supporting energy production and growth during infection [35]. Key enzymes in this pathway, such as isocitrate lyase and malate synthase, are critical for these metabolic processes [35]. Similarly, *R. solani* utilizes the glyoxylate cycle to promote mycelial growth and the formation of sclerotia, which are resilient structures that help the fungus survive under adverse conditions. In *Fusarium* sp., the glyoxylate cycle enhances fatty acid metabolism, enabling more efficient utilization of lipids as an energy source, which in turn supports increased virulence [36]. Recent studies have further connected the glyoxylate cycle to mycotoxin production and stress adaptation in *Fusarium* sp., indicating its broader role in fungal survival and pathogenicity [11].

Glycerol and lipid biosynthesis pathway

In *M. oryzae*, lipid and glycogen reserves are rapidly broken-down during infection, a process regulated by the *CPKA*/*SUM1*-encoded protein kinase (PKA) holoenzyme, which is essential for generating turgor pressure in the appressorium. The breakdown of triacylglycerol (TAG) to produce glycerol is crucial for fungal pathogens like *M. oryzae*. This process is regulated by Protein Kinase A (PKA), which activates lipases that hydrolyze TAG into diacylglycerol (DAG), then into monoacylglycerol (MAG), and finally into free fatty acids and glycerol. Glycerol is essential for generating the high turgor pressure required for the fungus to penetrate the plant surface, particularly during appressorium development. Glycerol is also synthesized from intermediates like dihydroxyacetone phosphate (DHAP) in glycolysis, which is converted to glycerol-3-phosphate and then dephosphorylated to glycerol.This process is closely tied to the fungus's lipid metabolism and is influenced by environmental signals through cAMP signaling, which regulates PKA activity. The glycerol-derived turgor pressure is further supported by aquaporins and osmolytes, ensuring proper osmotic balance. These coordinated mechanisms enable efficient host invasion. Glycerol is also synthesized from pyruvate in the peroxisome through gluconeogenesis. Pyruvate is converted to oxaloacetate, then to phosphoenolpyruvate, and ultimately to dihydroxyacetone phosphate (DHAP). DHAP is reduced to glycerol-3-phosphate and then dephosphorylated to glycerol. This pathway serves as an alternative source of glycerol to aid in generating turgor pressure for host invasion [34, 37, 38]. Fatty acids produced through β-oxidation are of importance for appressorium formation and penetration into the host [4] (Fig. 1). Similarly, in *R. solani* and *Fusarium* sp., lipid and glycerol biosynthesis are critical for maintaining pathogenicity and supporting infection [34, 38].

Polyketide biosynthesis

Polyketide biosynthesis involves the conversion of acetyl-CoA into acyl groups through repetitive condensation reactions. This process is closely linked to other key pathways such as lipid biosynthesis, melanin production, and the glyoxylate cycle [11]. In *M. oryzae*, the melanin produced via polyketide biosynthesis is critical for the fungus to penetrate the host plant's leaves, as melanin helps generate the necessary turgor pressure in the appressorium [7]. Similarly, in *R. solani* and *Fusarium* sp., polyketides play important roles in enhancing virulence, providing stress tolerance, and contributing to the production of mycotoxins, which aid in infection and survival under adverse conditions [26] (Fig. 1).

LIPID CONTRIBUTIONS TO FUNGAL VIRULENCE MECHANISMS

Lipids, particularly triacylglycerols, phospholipids, and fatty acids, play a critical role in the virulence of key fungal pathogens affecting rice, including *M. oryzae*, *R. solani*, *Fusarium* sp., and *Alternaria* sp. These fungi rely on lipid biosynthesis to generate glycerol, a vital molecule for creating the turgor pressure required for penetrating plant tissues. In *M. oryzae*, pathogenicity is strongly linked to the utilization of storage lipids like triacylglycerols, which provide energy for the infection process from spore attachment to the development of penetration hyphae [7]. Lipid storage in vacuoles, primarily in the form of triacylglycerols and phospholipids, is critical for sustaining the growth of the germ tube and appressorium through their continuous degradation [15, 39].

The *PTH2* gene in *M. oryzae* encodes CAT2, a protein crucial for the transport of acetyl-CoA, which is necessary for fatty acid metabolism. Mutants lacking *PTH2* are unable to infect plants, emphasizing the importance of acetyl-CoA production in fungal virulence [27, 31]. Similarly, the *AGT1* gene is essential for lipid mobilization, conidial germination, and appressorium formation. Mutations in *AGT1* impair β-oxidation and the glyoxylate cycle, rendering the fungus non-pathogenic due to the inability to mobilize stored triacylglycerols [40]. Additionally, mutants deficient in intracellular triacylglycerol lipases, enzymes required for lipid breakdown, are unable to infect plants because of impaired acetyl-CoA generation, which is necessary for penetration [7, 41].

In *R. solani*, lipid metabolism, particularly the mobilization of triacylglycerols and phospholipids, is equally important for pathogenicity. Lipid bodies are broken down during infection to fuel hyphal growth and penetration into host tissues. Disruptions in lipid transport and storage severely affect the fungus's ability to colonize host tissues, reducing virulence [3, 41]. In *Fusarium* sp., such as *F. graminearum* and *F. oxysporum*, lipid derived molecules like oxylipins are involved in signaling pathways that regulate fungal development and pathogenicity [42]. Mutations in lipid biosynthesis enzymes impair mycotoxin production and reduce the pathogen's ability to infect host plants. The glyoxylate cycle, which relies on fatty acids, plays a critical role in adapting to the host environment, and its disruption in *Fusarium* sp. is linked to decreased virulence [42]. In *F. verticillioides*, altered lipid metabolism directly affects mycotoxin production and stress adaptation, further demonstrating the importance of lipids in fungal virulence [43].

Alternaria sp., particularly *A. alternata*, rely heavily on lipid metabolism, specifically the synthesis and breakdown of triacylglycerols and phospholipids, to produce secondary metabolites and toxins that are key to their virulence. Disruptions in lipid biosynthesis and mobilization reduces pathogenicity, impairing the fungi's ability to infect and damage host plants [44]. In *M. oryzae*, the Pmk1 MAP kinase signaling pathway is crucial for regulating the mobilization and degradation of lipid bodies within the appressorium, a process that depends on cAMP-dependent protein kinase A [40]. Mutations in the isocitrate lyase gene in *M. grisea* and *Fusarium* sp. result in defects in appressorium formation and mycotoxin production, leading to a significant reduction in pathogenicity [40]. This metabolic pathway is also vital for the virulence of other rice pathogens, such as *R. solani*, which depend on the glyoxylate cycle for effective host invasion [45] (Fig. 1).

COMPARATIVE ANALYSIS OF LIPID BIOSYNTHESIS IN BIOTROPHIC AND NECROTROPHIC FUNGI

Lipid biosynthesis in rice pathogens plays a crucial role in their ability to interact with host plants, with significant variation between biotrophic and necrotrophic fungi. Biotrophic pathogens, such as *Ustilago virens*, the causative agent of rice false smut, establish an intimate, parasitic relationship with living host cells. These pathogens manipulate lipid metabolism to maintain host cell integrity and ensure a continuous supply of nutrients without activating strong host defense responses [50]. *U. virens* forms specialized structures known as haustoria, which are used to extract nutrients directly from the host. Lipid biosynthesis in these biotrophs is critical for producing membrane components such as sterols and sphingolipids, which are essential for maintaining haustorium structure and function. The involvement of sterol biosynthesis genes in haustorium development has been well documented, highlighting their importance in sustaining biotrophic interactions [51]. Furthermore, biotrophs synthesize lipid-derived signaling molecules, such as oxylipins and jasmonates, which can modulate host immune responses to prevent premature host cell death and allow for prolonged infection [41].

In contrast, necrotrophic pathogens, such as

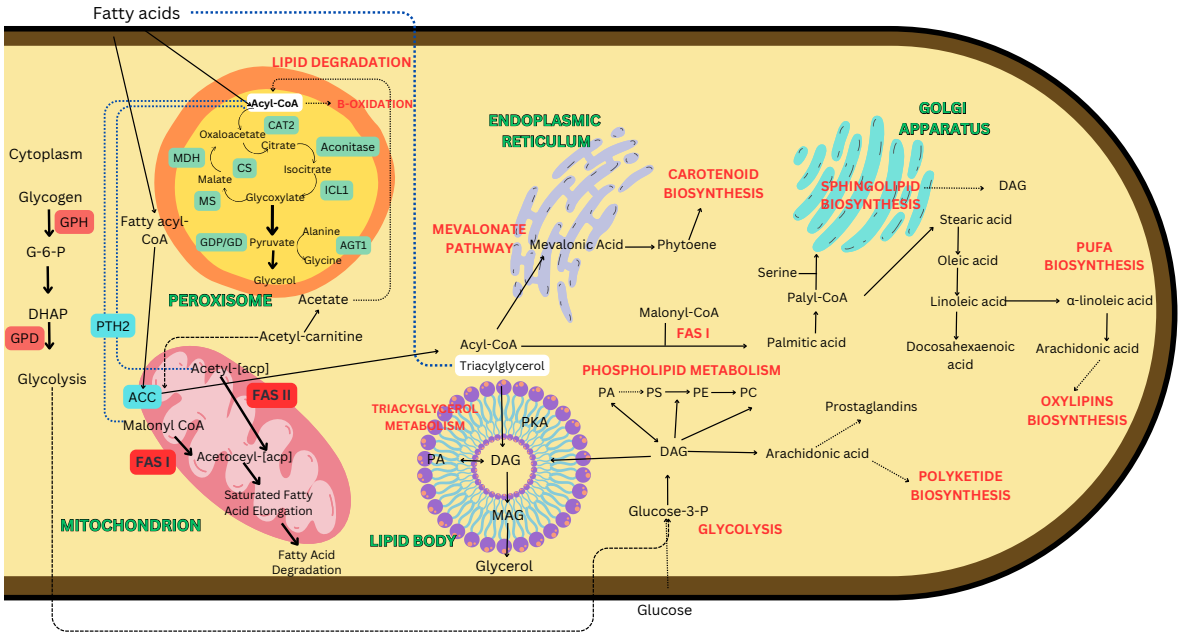

Fig. 1 This figure illustrates the interconnected pathways of lipid metabolism within a eukaryotic cell, highlighting the roles of various organelles. The peroxisome and mitochondrion facilitate fatty acid degradation and acetyl-CoA production, which support energy generation and lipid biosynthesis. The lipid body stores triacylglycerol (TAG) and diacylglycerol (DAG), while the endoplasmic reticulum (ER) synthesizes complex lipids like phospholipids, sphingolipids, and polyunsaturated fatty acids (PUFAs). The Golgi apparatus aids in sphingolipid biosynthesis, and glycolysis provides intermediates like glycerol-3-phosphate (G3P) for lipid synthesis. Specialized pathways, such as the mevalonate pathway, polyketide biosynthesis, and oxylipin production, branch from lipid precursors, reflecting the integration of lipid metabolism with energy, storage, and secondary metabolite production.

Table 2 Role of lipids in virulence of rice pathogens.

Pathogen	Lipid type	Role in virulence	Ref.
M. oryzae	Glycerol	Accumulates in appresorium to generate turgor pressure	[27]
M. oryzae	Sphingolipids	Involved in cell wall integrity and signal transduction	[46]
M. oryzae	Phospholipids	Involved in appresorium development and function	[47]
M. oryzae	Glycolipids	Facilitates cell wall adhesion and penetration	[26]
R. solani	Fatty Acids	Disrupts plant cell membranes to facilitate infection	[45]
R. solani	Phytotoxins (lipid-derived)	Induces necrosis in host tissues	[33]
F. fujikuroi	Lipase	Hydrolyzes host lipids, aiding in host penetration	[3]
F. oxysporum	Sterols	Stabilizes fungal membranes during infection	[48]
F. graminearum	Oxylipins	Modulates host immune response and enhances pathogenicity	[49]
F. verticillioides	Polyketides	Serves as toxins that inhibit host defense mechanisms	[43]

R. solani and *F. fujikuroi*, which cause sheath blight and bakanae disease in rice, respectively, exhibit a more aggressive lipid metabolism. These fungi actively kill host cells, exploiting the released nutrients to support their rapid growth and virulence. Necrotrophs upregulate pathways related to fatty acid biosynthesis and β-oxidation to generate energy and produce virulence factors, such as phytotoxins, which contribute to host cell death [45]. Lipid peroxidation and the production of reactive oxygen species (ROS) are critical mechanisms by which necrotrophic fungi induce oxidative stress in the host, leading to membrane disruption and tissue necrosis [52]. For instance, *Fusarium* species enhance lipid metabolism to produce mycotoxins like fumonisins and trichothecenes, which disrupt host cellular membranes and accelerate disease progression [53]. Additionally, genes involved in oxylipin biosynthesis play a central role in necrotrophic pathogenesis, as oxylipins can trigger programmed cell death in host tissues, further promoting pathogen spread [43]. These distinct lipid metabolic pathways underscore the divergent survival strategies of biotrophic and necrotrophic fungi. Biotrophs, like *U. virens*, regulate lipid profiles to sustain long-term colonization, while

necrotrophs rapidly mobilize lipids to drive virulence and host destruction. Understanding the molecular mechanisms behind lipid biosynthesis and utilization in these pathogens could provide new targets for controlling fungal diseases in rice. Targeting key enzymes involved in sterol and fatty acid synthesis, or disrupting lipid-derived signaling pathways, may offer innovative strategies for enhancing rice resistance to these economically important pathogens.

KEY GENES REGULATING LIPID BIOSYNTHESIS

Fatty acid synthase (FAS) subunits

The fatty acid synthase (FAS) complex is a critical enzyme system responsible for the *de novo* synthesis of long-chain fatty acids, which are essential for the construction of fungal cell membranes and energy storage molecules. The FAS complex consists of two subunits: α (FAS2) and β (FAS1), which work together to catalyze the repeated condensation of malonyl-CoA and acetyl-CoA to form long-chain fatty acids. Studies in *Saccharomyces cerevisiae* and other model yeasts have shown that the FAS complex contains six active catalytic centers, with distinct enzymatic activities required for fatty acid elongation, including acetyltransferase, enoyl reductase, and thioesterase [7, 54]. In *M. oryzae*, the lipid biosynthesis pathway driven by the *FAS1* and *FAS2* genes is directly linked to the formation of appresorium [55]. Disruption of either sub-unit can impair appressorium formation, reducing the pathogen's ability to infect and colonize rice tissues.

Acetyl-CoA carboxylase (ACC)

Acetyl-CoA carboxylase catalyzes the conversion of acetyl-CoA to malonyl-CoA, which is a crucial substrate for the fatty acid elongation cycle in the fatty acid biosynthesis pathway. ACC plays a pivotal role in both the anabolic and catabolic aspects of lipid metabolism, as malonyl-CoA is not only used for fatty acid biosynthesis but also regulates β-oxidation by inhibiting the carnitine shuttle, thus controlling the flow of fatty acids into mitochondria for degradation [41]. In fungal pathogens like *M. oryzae*, disruption of ACC significantly hampers lipid synthesis, leading to defects in appressorial turgor pressure generation, which is critical for breaching the plant epidermis. This results in a marked reduction in pathogenicity. ACC plays a similarly crucial role in necrotrophic pathogens like *R. solani* and *Fusarium* species, where its activity supports the synthesis of lipids required for membrane integrity, virulence factor production, and energy metabolism during host invasion [15].

Role of *PTH2*, *AGT1*, and *ICL1* in lipid metabolism

Several key genes involved in lipid metabolism, including *PTH2*, *AGT1*, and *ICL1*, have been identified as critical to the pathogenicity of *M. oryzae* and other phytopathogenic fungi. *PTH2* is involved in acetyl-CoA production, a central intermediate in the lipid biosynthesis pathway. Acetyl-CoA serves as a precursor for both fatty acid and sterol synthesis. Mutants lacking *PTH2* exhibit impaired lipid biosynthesis, reduced virulence, and a diminished ability to form appressoria, demonstrating the gene's importance in infection [56]. *AGT1* encodes alanine-glyoxylate aminotransferase, a key enzyme in the glyoxylate cycle that facilitates lipid mobilization and supports appressorial development by providing energy and carbon skeletons from stored lipids. Deletion of *AGT1* disrupts the glyoxylate cycle, leading to defective infection structures and attenuated virulence in *M. oryzae* [57]. *ICL1* encodes isocitrate lyase, another critical enzyme of the glyoxylate cycle, enabling fungi to utilize lipids as a carbon source, especially during the early stages of infection when nutrients are scarce. *ICL1* mutants show defects in lipid utilization, appressorium formation, and reduced virulence in both *M. oryzae* and *R. solani* [58]. This highlights the glyoxylate cycle's role in facilitating fungal adaptation to the host environment.

Lipase genes and peroxisomal β-oxidation

Lipases play an essential role in hydrolyzing triacylglycerols into free fatty acids, which are subsequently utilized for energy production or further processed into complex lipids required for membrane biosynthesis and signal transduction. In fungal pathogens like *M. oryzae* and *Fusarium* species, lipase activity, especially from genes such as *LIP1*, is crucial for degrading stored lipids to fuel the formation of appressoria. Appressorial development is energy-intensive, requiring high levels of lipid mobilization and β-oxidation to generate the turgor pressure necessary for host tissue penetration [59, 60]. Peroxisomal β-oxidation, mediated by enzymes encoded by genes like *MFE1* (multifunctional enzyme 1) and *SCAD* (short-chain acyl-CoA dehydrogenase), is responsible for the breakdown of fatty acids into acetyl-CoA within peroxisomes. This process is particularly important during the early stages of infection, where energy production must occur under nutrient-limited conditions. The acetyl-CoA generated through β-oxidation supports both energy metabolism and biosynthetic pathways, including the production of secondary metabolites such as toxins [61]. In *M. oryzae*, disruption of β-oxidation genes like *SCAD* results in reduced pathogenicity, underscoring the importance of lipid degradation in fungal virulence [62].

TARGETING LIPID BIOSYNTHESIS FOR EFFECTIVE DISEASE MANAGEMENT

Lipid biosynthesis is critical for fungal pathogenicity in rice, making it a promising target for disease control strategies. Lipid metabolism supports fungal cell structure, energy production, and key infection processes.

For instance, in *M. oryzae*, lipids are essential for appressorium formation and host penetration, where disruption of enzymes like fatty acid synthase and acyl-CoA desaturase can impede fungal growth and infection [7, 47, 58]. Targeting sphingolipid biosynthesis is particularly effective, as these lipids are vital for fungal membrane integrity. Inhibitors could weaken fungal cells, increasing their vulnerability to treatments [63]. Additionally, overlapping targets between herbicides and fungicides present opportunities for developing new fungicides that disrupt lipid biosynthesis in pathogens like *R. solani* [64].

In *Fusarium* sp., disrupting lipid-derived molecules like oxylipins, which regulate development and virulence, can reduce pathogenicity by impairing mycotoxin production. Targeting the glyoxylate cycle, crucial for survival in glucose-deficient environments, also shows promise where mutants in enzymes like ICL exhibit reduced virulence [26–65]. Practical applications include developing fungicides targeting lipid metabolism, utilizing biocontrol agents like *Trichoderma* and *Bacillus* spp., and genetic modifications in rice for enhanced resistance [66–68]. This approach integrates chemical treatments with biological strategies, offering a comprehensive method for managing rice fungal diseases.

CONCLUDING REMARKS

Lipid biosynthesis and metabolism play a central role in determining the pathogenicity and virulence of fungal pathogens in rice. These processes are essential for the formation of key infection structures, such as appresorium in biotrophic fungi, and for energy production, membrane integrity, and toxin synthesis in necrotrophic pathogens. Understanding the molecular mechanisms governing lipid metabolism in these pathogens opens new avenues for disease control. Targeting critical enzymes or pathways, such as fatty acid synthase, acetyl-CoA carboxylase, or β-oxidation, can disrupt the energy supply and structural components required for pathogen virulence. Furthermore, inhibiting lipid-derived signaling molecules that modulate host immune responses offers a promising strategy for reducing disease severity. In the future, this knowledge could be leveraged to develop more targeted fungicides, design resistant rice varieties, or employ gene-editing technologies to weaken pathogen virulence by altering key metabolic pathways, ultimately enhancing rice crop resilience against devastating fungal diseases [69].

Acknowledgements: I would like to thank the Ministry of Higher Education for the Fundamental Research Grant FRGS/1/2023/STG01/UKM/01/1 that was awarded enabling the publication of the manuscript. This is a publication under the Sustainable Crop Management and Improvement University Research Group.

REFERENCES

1. Fukagawa NK, Ziska LH (2019) Rice: Importance for global nutrition. *J Nutr Sci Vitaminol (Tokyo)* **65**(Supp), S2–S3.
2. Anjago WM, Zhou T, Zhang H, Shi M, Yang T, Zheng H, Wang Z (2018) Regulatory network of genes associated with stimuli sensing, signal transduction and physiological transformation of appressorium in *Magnaporthe oryzae*. *Mycol* **9**, 211–222.
3. van der Meer-Janssen YP, van Galen J, Batenburg JJ, Helms JB (2010) Lipids in host-pathogen interactions: pathogens exploit the complexity of the host cell lipidome. *Prog Lipid Res* **49**, 1–26.
4. Mat Razali N, Hisham SN, Kumar IS, Shukla RN, Lee M, Abu Bakar MF, Nadarajah K (2021) Comparative genomics: Insights on the pathogenicity and lifestyle of *Rhizoctonia solani*. *Int J Mol Sci* **22**, 2183.
5. Nadarajah K, Ali HZ, Muni NM (2014) The host pathogen interactions observed between *Fusarium* sp. F2 and rice. *Plant Omics* **8**, 572–580.
6. Krishnan HK, Mat Muni N, Sahruna NS, Nadarajah K (2014) Severity of rice disease caused by *Curvularia* spp in Malaysia. *J Adv Biol* **4**, 266–275.
7. Sangappillai V, Nadarajah K (2020) Fatty acid synthase beta dehydratase in the lipid biosynthesis pathway is required for conidiogenesis, pigmentation and appressorium formation in *Magnaporthe oryzae* S6. *Int J Mol Sci* **21**, 7224.
8. Shakeel Q, Mubeen M, Sohail MA, Ali S, Iftikhar Y, Tahir Bajwa R, Aqueel MA, Upadhyay SK, et al (2023) An explanation of the mystifying bakanae disease narrative for tomorrow's rice. *Front Microbiol* **14**, 1153437.
9. Stępień Ł, Lalak-Kańczugowska J, Witaszak N, Urbaniak M (2020) *Fusarium* secondary metabolism biosynthetic pathways: so close but so far away. In: Mérillon JM, Ramawat K (eds) *Co-Evolution of Secondary Metabolites*, Reference Series in Phytochemistry, Springer, Cham., pp 211–247.
10. Beccaccioli M, Reverberi M, Scala V (2019) Fungal lipids: biosynthesis and signalling during plant-pathogen interaction. *Front Biosci (Landmark Ed)* **24**, 168–181.
11. Liu N, Qi L, Huang M, Chen D, Yin C, Zhang Y, Wang X, Yuan G, et al (2022) Comparative secretome analysis of *Magnaporthe oryzae* identified proteins involved in virulence and cell wall integrity. *Genom Proteom Bioinform* **20**, 728–746.
12. Fan X, Zhang P, Batool W, Liu C, Hu Y, Wei Y, He Z, Zhang SH (2023) Contribution of the tyrosinase (MoTyr) to melanin synthesis, conidiogenesis, appressorium development, and pathogenicity in *Magnaporthe oryzae*. *J Fungi (Basel)* **9**, 311.
13. Motoyama T, Yun CS, Osada H (2021) Biosynthesis and biological function of secondary metabolites of the rice blast fungus *Pyricularia oryzae*. *J Ind Microbiol Biotechnol* **48**, kuab058.
14. Pusztahelyi T, Holb IJ, Pócsi I (2016) Plant-fungal interactions: special secondary metabolites of the biotrophic, necrotrophic, and other specific interactions. In: Mérillon JM, Ramawat K (eds) *Fungal Metabolites*, Reference Series in Phytochemistry, Springer, Cham., pp 1–58.
15. Wei YY, Liang S, Zhu XM, Liu XH, Lin FC (2023) Recent

advances in effector research of *Magnaporthe oryzae*. *Biomol* **13**, 1650.
16. Mogga V, Delventhal R, Weidenbach D, Langer S, Bertram PM, Andresen K, Thines E, Kroj T, et al (2016) *Magnaporthe oryzae* effectors MoHEG13 and MoHEG16 interfere with host infection and MoHEG13 counteracts cell death caused by Magnaporthe-NLPs in tobacco. *Plant Cell Rep* **35**, 1169–1185.
17. Chen X, Li L, He Z, Zhang J, Huang B, Chen Z, Zuo S, Xu J (2018) Molecular cloning and functional analysis of two novel polygalacturonase genes in *Rhizoctonia solani*. *Can J Plant Pathol* **40**, 39–47.
18. Charova SN, Dölfors F, Holmquist L, Moschou PN, Dixelius C, Tzelepis G (2020) The RsRlpA effector is a protease inhibitor promoting *Rhizoctonia solani* virulence through suppression of the hypersensitive response. *Int J Mol Sci* **21**, 8070.
19. Feng J, Liu G, Selvaraj G, Hughes GR, Wei Y (2005) A secreted lipase encoded by LIP1 is necessary for efficient use of saturated triglyceride lipids in *Fusarium graminearum*. *Microbiol* **151**, 3911–3921.
20. Achari SR, Edwards J, Mann RC, Kaur JK, Sawbridge T, Summeral BA (2021) Comparative transcriptomic analysis of races 1, 2, 5 and 6 of *Fusarium oxysporum* f.sp. *pisi* in a susceptible pea host identifies differential pathogenicity profiles. *BMC Genom* **22**, 734.
21. Jangir P, Mehra N, Sharma K, Singh N, Rani M, Kapoor R (2021) Secreted in xylem genes: drivers of host adaptation in *Fusarium oxysporum*. *Front Plant Sci* **12**, 628611.
22. Nadarajah KK (2020) ROS homeostasis in abiotic stress tolerance in plants. *Int J Mol Sci* **21**, 5208.
23. Abdul Malik NA, Kumar IS, Nadarajah K (2020) Elicitor and receptor molecules: orchestrators of plant defense and immunity. *Int J Mol Sci* **21**, 963.
24. Cruz-Mireles N, Osés-Ruiz M, Derbyshire P, Jégousse C, Ryder LS, Bautista MJA, Eseola A, Sklenar J, et al (2024) The phosphorylation landscape of infection-related development by the rice blast fungus. *Cell* **187**, 2557–2573.
25. Segorbe D, Pietro AD, Pérez-Nadales E, Turrà D (2017) Three *Fusarium oxysporum* mitogen-activated protein kinases (MAPKs) have distinct and complementary roles in stress adaptation and cross-kingdom pathogenicity. *Mol Plant Pathol* **18**, 912–924.
26. Perincherry L, Lalak-Kańczugowska J, Stępień Ł (2019) *Fusarium*-produced mycotoxins in plant-pathogen interactions. *Toxins (Basel)* **11**, 664.
27. Tan J, Zhao H, Li J, Gong Y, Li X (2023) The devastating rice blast airborne pathogen *Magnaporthe oryzae*: A review on genes studied with mutant analysis. *Pathogens* **12**, 379.
28. Sadat MA, Han JH, Kim S, Lee YH, Kim KS, Choi J (2021) The membrane-bound protein, MoAfo1, is involved in sensing diverse signals from different surfaces in the rice blast fungus. *Plant Pathol J* **37**, 87–98.
29. Xie X, Pei M, Liu S, Wang X, Gong S, Chen J, Zhang Y, Wang Z, et al (2024) Comprehensive analysis of autophagy-related genes in rice immunity against *Magnaporthe oryzae*. *Plants* **13**, 927.
30. Guo L, Breakspear A, Zhao G, Gao L, Kistler HC, Xu JR, Ma LJ (2016) Conservation and divergence of the cyclic adenosine monophosphate-protein kinase A (cAMP-PKA) pathway in two plant-pathogenic fungi: *Fusarium graminearum* and *F. verticillioides*. *Mol Plant Pathol* **17**, 196–209.
31. Gupta L, Vermani M, Ahluwalia SK, Vijayaraghavan P (2021) Molecular virulence determinants of *Magnaporthe oryzae*: disease pathogenesis and recent interventions for disease management in rice plant. *Mycol* **12**, 174–187.
32. Cao N, Zhu XM, Bao JD, Zhu LH, Liu H, Lin FC, Li L (2023) Acyl-coenzyme A binding protein MoAcb1 regulates conidiation and pathogenicity in *Magnaporthe oryzae*. *Front Microbiol* **14**, 1179536.
33. Liu N, Yun Y, Yin Y, Hahn M, Ma Z, Chen Y (2019) Lipid droplet biogenesis regulated by the FgNem1/Spo7-FgPah1 phosphatase cascade plays critical roles in fungal development and virulence in *Fusarium graminearum*. *New Phytol* **223**, 412–429.
34. Kuźniak E, Gajewska E (2024) Lipids and lipid-mediated signaling in plant-pathogen interactions. *Int J Mol Sci* **25**, 7255.
35. Dunn MF, Ramírez-Trujillo JA, Hernández-Lucas I (2009) Major roles of isocitrate lyase and malate synthase in bacterial and fungal pathogenesis. *Microbiol* **155**, 3166–3175.
36. Lee SH, Han YK, Yun SH, Lee YW (2009) Roles of the glyoxylate and methylcitrate cycles in sexual development and virulence in the cereal pathogen *Gibberella zeae*. *Eukaryot Cell* **8**, 1155–1164.
37. Huang Z, Cao H, Wang H, Huang P, Wang J, Cai YY, Wang Q, Li Y, et al (2023) The triglyceride catabolism regulated by a serine/threonine protein phosphatase, Smek1, is required for development and plant infection in *Magnaporthe oryzae*. *Mol Plant Pathol* **24**, 1256–1272.
38. Miguel-Rojas C, Cavinder B, Townsend JP, Trail F (2023) Comparative transcriptomics of *Fusarium graminearum* and *Magnaporthe oryzae* spore germination leading up to infection. *mBio* **14**, e0244222.
39. Pusztahelyi T, Holb IJ, Pócsi I (2016) Plant-fungal interactions: Special secondary metabolites of the biotrophic, necrotrophic, and other specific interactions. In: Mérillon JM, Ramawat K (eds) *Fungal Metabolites*, Reference Series in Phytochemistry, Springer, Cham., pp 1–58.
40. Falter C, Reumann S (2022) The essential role of fungal peroxisomes in plant infection. *Mol Plant Pathol* **23**, 781–794.
41. Wang X, Liu Y, Keyhani NO, Zhu S, Wang J, Wang J, Jin D, Fan Y (2022) A perilipin affects lipid droplet homeostasis and aerial hyphal growth, but has only small effects on virulence in the insect pathogenic fungus *Beauveria bassiana*. *J Fungi (Basel)* **8**, 634.
42. Beccaccioli M, Pucci N, Salustri M, Scortichini M, Zaccaria M, Momeni B, Loreti S, Reverberi M, et al (2022) Fungal and bacterial oxylipins are signals for intra- and inter-cellular communication within plant disease. *Front Plant Sci* **13**, 823233.
43. Beccaccioli M, Salustri M, Scala V, Ludovici M, Cacciotti A, D'Angeli S, Brown DW, Reverberi M (2021) The effect of *Fusarium verticillioides* fumonisins on fatty acids, sphingolipids, and oxylipins in maize germlings. *Int J Mol Sci* **22**, 2435.
44. Meena M, Gupta SK, Swapnil P, Zehra A, Dubey MK, Upadhyay RS (2017) Alternaria toxins: potential virulence factors and genes related to pathogenesis. *Front Microbiol* **8**, 1451.

45. Senapati M, Tiwari A, Sharma N, Chandra P, Bashyal BM, Ellur RK, Bhowmick PK, Bollinedi H, et al (2022) *Rhizoctonia solani* Kühn pathophysiology: status and prospects of sheath blight disease management in rice. *Front Plant Sci* **13**, 881116.
46. Wang L, Zhang X, Li L, Bao J, Lin F, Zhu X (2024) A key sphingolipid pathway gene, MoDES1, regulates conidiation, virulence and plasma membrane tension in *Magnaporthe oryzae*. *Microbiol Res* **279**, 127554.
47. Zhao J, Sun P, Sun Q, Li R, Qin Z, Sha G, Zhou Y, Bi R, et al (2022) The MoPah1 phosphatidate phosphatase is involved in lipid metabolism, development, and pathogenesis in *Magnaporthe oryzae*. *Mol Plant Pathol* **23**, 720–732.
48. Ibrahim SRM, Sirwi A, Eid BG, Mohamed SGA, Mohamed GA (2021) Bright side of *Fusarium oxysporum*: secondary metabolites bioactivities and industrial relevance in biotechnology and nanotechnology. *J Fungi* **7**, 943.
49. Wang Q, Sun Y, Wang F, Huang PC, Wang Y, Ruan X, Ma L, Xin L, et al (2021) Transcriptome and oxylipin profiling joint analysis reveals opposite roles of 9-oxylipins and jasmonic acid in maize resistance to gibberella stalk rot. *Front Plant Sci* **12**, 699146.
50. Qiu S, Fang A, Zheng X, Wang S, Wang J, Fan J, Sun Z, Gao H, et al (2022) *Ustilaginoidea virens* nuclear effector SCRE4 suppresses rice immunity via inhibiting expression of a positive immune regulator OsARF17. *Int J Mol Sci* **23**, 10527.
51. Mapuranga J, Zhang L, Zhang N, Yang W (2022) The haustorium: the root of biotrophic fungal pathogens. *Front Plant Sci* **13**, 963705.
52. Nadarajah KK (2023) Defensive strategies of ROS in plant-pathogen interactions. In: Verma PK, Mishra S, Srivastava V, Mehrotra S (eds) *Plant Pathogen Interaction*, Springer, Singapore, pp 163–183.
53. Perochon A, Doohan FM (2024) Trichothecenes and Fumonisins: Key players in *Fusarium*-cereal ecosystem interactions. *Toxins* **16**, 90.
54. Wang Z, Su C, Zhang Y, Shangguan S, Wang R, Su J (2024) Key enzymes involved in the utilization of fatty acids by *Saccharomyces cerevisiae*: A review. *Front Microbiol* **14**, 1294182.
55. Wang Q, Huang Z, Khan IA, Li Y, Wang J, Wang J, Liu XH, Lin F, et al (2024) Key transcription factors required for outburst of rice blast disease in *Magnaporthe oryzae*. *Phytopathol Res* **6**, 5.
56. Chen XL, Wang Z, Liu C (2016) Roles of peroxisomes in the rice blast fungus. *Biomed Res Int* **2016**, 9343417.
57. Bhadauria V, Banniza S, Vandenberg A, Selvaraj G, Wei Y (2012) Peroxisomal alanine: glyoxylate aminotransferase *AGT1* is indispensable for appressorium function of the rice blast pathogen, *Magnaporthe oryzae*. *PLoS One* **7**, e36266.
58. bin Yusof MT, Kershaw MJ, Soanes DM, Talbot NJ (2014) FAR1 and FAR2 regulate the expression of genes associated with lipid metabolism in the rice blast fungus *Magnaporthe oryzae*. *PLoS One* **9**, e99760.
59. Subramoni S, Suárez-Moreno ZR, Venturi V (2010) Lipases as pathogenicity factors of plant pathogens. In: Timmis KN (ed) *Handbook of Hydrocarbon and Lipid Microbiology*, Springer, Berlin, Heidelberg, pp 3269–3277.
60. Kim S, Lee J, Park J, Choi S, Bui DC, Kim JE, Shin J, Kim H, et al (2023) Genetic and transcriptional regulatory mechanisms of lipase activity in the plant pathogenic fungus *Fusarium graminearum*. *Microbiol Spectr* **11**, e0528522.
61. Matsuoka S, Saito T, Kuwayama H, Morita N, Ochiai H, Maeda M (2003) MFE1, a member of the peroxisomal hydroxyacyl coenzyme A dehydrogenase family, affects fatty acid metabolism necessary for morphogenesis in *Dictyostelium* spp. *Eukaryot Cell* **2**, 638–645.
62. Aliyu SR, Lin L, Chen X, Abdul W, Lin Y, Otieno FJ, Shabbir A, Batool W, et al (2019) Disruption of putative short-chain acyl-CoA dehydrogenases compromised free radical scavenging, conidiogenesis, and pathogenesis of *Magnaporthe oryzae*. *Fungal Genet Biol* **127**, 23–24.
63. Rollin-Pinheiro R, Singh A, Barreto-Bergter E, Del Poeta M (2016) Sphingolipids as targets for treatment of fungal infections. *Future Med Chem* **8**, 1469–1484.
64. Duke SO, Pan Z, Bajsa-Hirschel J, Tamang P, Hammerschmidt R, Lorsbach BA, Sparks TC (2023) Molecular targets of herbicides and fungicides — are there useful overlaps for fungicide discovery? *J Agric Food Chem* **71**, 20532–20548.
65. Ekwomadu TI, Akinola SA, Mwanza M (2021) *Fusarium mycotoxins*, their metabolites (free, emerging, and masked), food safety concerns, and health impacts. *Int J Environ Res Public Health* **18**, 11741.
66. Abbas A, Mubeen M, Zheng H, Sohail MA, Shakeel Q, Solanki MK, Iftikhar Y, Sharma S, et al (2022) *Trichoderma* spp. genes involved in the biocontrol activity against *Rhizoctonia solani*. *Front Microbiol* **13**, 884469.
67. Nadarajah K (2024) *Principles in Plant Microbe Interaction for Sustainable Agriculture*, Penerbit UKM.
68. Natthaphon K, Pisut Y, Patchanee A, Umaporn U, Vanicha TL, Chatsuda S (2024) Characterization of a multifunctional biocontrol strain, *Bacillus subtilis* CH6, and its antagonistic mechanism against *Pyricularia oryzae* causing rice blast disease. *ScienceAsia* **50**,2024096.
69. Abdul Hamid NW, Nadarajah K (2022) Microbe related chemical signalling and its application in agriculture. *Int J Mol Sci* **23**, 8998.