

French Polytech network form for PhD Research Grants from the China Scholarship Council

This document describes one of the PhD subjects proposed by the French Polytech network. The network is composed of engineering schools/universities. The document also provides information about the supervisor.

Supervisor information	
Family name	Giraud
First name	Sandrine
Email	sandrine.giraud@univ-angers.fr
Web reference	https://eng-irhs.angers-nantes.hub.inrae.fr/research/seed-borne-fungal-pathogens
Lab name	IRHS (Research Institute of Horticulture and Seeds), UMR1345 INRAE, Université d'Angers, L'institut Agro
Lab web site	https://irhs.angers-nantes.hub.inrae.fr/recherche
Polytech name	Polytech Angers
University name	Angers University
Country	France

PhD information	
Title	New molecular factors involved in fungal pathogenicity
Main topics regards to CSC list (3 topics at maximum)	Continuous assessment of the diseases of the plants and elimination of harmful insects Functional genome and proteinomist

	Animal and plant new transgenic techniques
Required skills in science and engineering	Molecular biology, mycology, plant biology

Subject description (two pages maximum including biblio)

Plant pathogenic fungi cause devastating diseases in crops, leading to enormous yield losses, reduced production quality [1,2] and threats to global food security [3–5]. The control of fungal diseases primarily relies on fungicides and resistant crops varieties. However, fungi evolve rapidly and circumvent these strategies [6]. Achieving sustainable control therefore requires a deeper understanding of fungal development and the mechanisms underlying plant infection.

The FungiSem team mainly studies seed-borne *Alternaria* species that are pathogenic to Brassicaceae crops (such as cabbage, radish, rapeseed) and wild species (included *Arabidopsis thaliana*), and Apiaceae crops (such as carrot). One of the team's research axes focuses on identifying pathogenicity factors, particularly those involved in fungal adaptation to environmental (chemical and physical) stresses, including those associated with the host plant microhabitat.

Brassicaceae crops as many other plants naturally use a defense system based on antimicrobial compounds, such as phytoanticipins and phytoalexins.

The accumulation of phytoalexins in the infection zone triggers the activation of protective mechanisms in phytopathogenic fungi. To counteract phytoalexins, these fungi employ two main strategies: (1) detoxification, either through enzymatic metabolism or active efflux via specific transporters [7,8]; and (2) compensation for the induced stress by activating signaling pathways that promote the expression of defense-related genes [9,10]. Previous studies performed on *A. brassicicola* on our team demonstrated that the three principal signaling pathways involved are the Cell Wall Integrity (CWI) pathway [9,10], the High-Osmolarity Glycerol (HOG) pathway [9,10], and the Unfolded Protein Response (UPR) pathway [9–11]. Work within our team has enabled us to identify natural, synthetic or semi-synthetic compounds capable of disrupting metabolic pathways that protect fungi against plant defenses. For airborne diseases, we have shown that exposure to this type of inhibitor has a synergistic effect, increasing the sensitivity of fungi to defensive compounds and reducing the overall level of disease [12].

In this functional genomics study conducted on *Alternaria* species, we aim to investigate two additional protective mechanisms:

- The analysis of metabolic pathways involved in detoxification, with a particular focus on fission pathways;
- The role of effectors in the pathogenicity

1. Fission pathways and *Alternaria brassicicola* pathogenicity

Filamentous fungi are ubiquitous organisms and key contributors to the degradation of aromatic compounds in the environment. Some species possess several aerobic metabolic pathways for the catabolism compounds, which converge on a limited number of conserved pathways responsible for opening of the aromatic ring via dioxygenases. These are referred to as central intermediate degradation pathways or “fission pathways” [13–16]. The diversity of these pathways is largely determined by ring-cleaving dioxygenases, which are key enzymes in this catabolic process. To date, three main central intermediate pathways have been identified and characterized to varying degrees in fungi: the 3-oxoadipate (or β -ketoadipate) pathway, divided into three branches based on the central intermediate (protocatechuate, catechol or hydroxyquinol) and involving intradiol dioxygenases, the gentisate pathway and the homogentisate pathway, both of which rely on extradiol dioxygenase.

In the literature, a link has been suggested between hydrocarbon catabolism and fungal pathogenicity. For instance, Martins *et al.* [17] colleagues demonstrated that the pathogenic potential of fungal communities increases upon exposure to a chlorinated aromatic compound. Moreover, the degradation of aromatic molecules by fungi such as *Botrytis cinerea* or *Fusarium oxysporum* has been shown to be essential for virulence in phytopathogenic contexts [18,19]. Catechol

dioxygenase also play a role in the detoxification of inducible class of plant defense compounds, such as stilbenoids (e.g. astringin) and flavonoid (e.g. flavan-3-ol catechin) [20].

2. The role of effectors in *Alternaria* sp pathogenicity

Effectors are typically defined as small, cysteine-rich, secreted proteins employed by pathogens to manipulate host cellular responses, thereby facilitating disease establishment and progression. While effectors from biotrophic and hemitrophic fungi have been extensively studied and are well documented [21], those from necrotrophic fungi have only been recently begun to receive attention [22,23]. Advances in bioinformatics and functional genomics have revealed that necrotrophic effectors can subvert and hijack plant physiological processes, including the programmed cell death, to promote infection [23]. Investigating the mechanisms by which necrotrophic effectors operate is essential for identifying genetics targets and strategies that could enhance plant resistance to these pathogens. To date, these factors have not been studied in *Alternaria* species.

To investigate these potential pathogenic mechanisms, we plan to use functional genomic approaches by generating mutants (that are deficient for key players or producing fluorescently labelled proteins) and compare their behaviour to those of the wild-type strain.

Bibliography

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