

## SELF FUNDED PHD OPPORTUNITY

### Role of small RNAs in *Arabidopsis*-downy mildew interaction

**Title:** Role of small RNAs in *Arabidopsis*-downy mildew interaction

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#### Background

Noncoding 20 to 30 nucleotide (nt)-long small RNAs (sRNAs) have been known to be involved in the regulation of gene expression and defence in eukaryotes [1, 2, 3]. Different types of RNAs such as double-stranded RNA (dsRNA) and small interfering RNA (siRNA) can trigger homologous RNA degradation or inhibit mRNA translation [4, 5]. This process is known as RNA silencing and plays a significant role in various biological processes including innate immunity [6, 7] and development [1, 8]. In plant-microbe interactions, plants and microbes can exchange RNA molecules, which then integrate into RNA silencing machinery in reciprocal recipient cells. Such cross-kingdom RNA transfer was first demonstrated between fungus and plants [9]. *Hyaloperonospora arabidopsidis* (*Hpa*) is an obligate biotrophic oomycete pathogen and causes downy mildew disease on *Arabidopsis thaliana*. The *Hpa*-*Arabidopsis* system has been used as a model to investigate pathogen effectors [10] and plant immunity [11]. This pathogen has both sexual and asexual reproduction.

#### Working hypothesis

*Arabidopsis*-*Hpa* system has been well established and the resources are available. Our group has been working on this system for a while and have the relevant expertise. We hypothesize that in addition to effectors and PAMPs, small RNAs are also involved in the interaction in this system. We want to investigate the role of small RNAs in this model system.

#### Brief research programme and methodology

- 1) Identify and validate small RNAs in *Arabidopsis*-*Hpa* system using RNA-seq.
- 2) Determine whether any of *Hpa* sRNAs involve in pathogenicity.
- 3) Identify *Arabidopsis* transcripts repressed during *Hpa* infection.
- 4) Use RNA silencing technology to reveal the role of these small RNAs.

Student will have research training in: Molecular biology, plant pathology, bioinformatics and plant transformation techniques and transcriptomics. Student will have opportunity to work with different groups and laboratories. Supervisors have extensive experience in supervising students, and collaborated and published joint papers before. Results obtained from this work will be published in internationally well-known journals and will be presented at international scientific meetings.

**References:** **1)** Qin *et al.*, 2017; *Plant Physiol.* 174,1067–1081; **2)** Chen *et al.*, 2018, *Plant Physiol.* 176, 2700-2719; **3)** Zhang *et al.*, 2018, *Plant Sci.* 278, 113–117; **4)** Huang *et al.*, 2016, *J. Integr.Plant Biol.* 58, 312–327;

**5)** Nejat and Mantri, 2018, *Critical Reviews in Biotechnology* 38, 93–105; **6)** Deng *et al.*, 2018, *PLoS Pathog* 14, e1006756–22; **7)** Brant and Budak, 2018, *Front. Plant Sci.* 9:1038; **8)** Li *et al.*, 2017, *Plant J.* 90, 654–670; **9)** Weiberg *et al.*, 2013, *Science* 342, 118–123. **10)** Woods-Tör *et al.*, 2018, *Frontiers in Plant Sci.* 9, 1957; **11)** Holub, 2007, *Curr. Opin. in Plant Biol.* 10, 415–424.