

**Project Title:** **Pathogen-Induced Transcriptional Re-programming in Host Defense Response**

**Project Number** **IMURA1025**

**Monash Main Supervisor**  
(Name, Email Id, Phone) Prof. Sureshkumar Balasubramanian,  
[mb.suresh@monash.edu](mailto:mb.suresh@monash.edu) *Full name, Email*

**Monash Co-supervisor(s)**  
(Name, Email Id, Phone) -

**Monash Head of Dept/Centre** (Name,Email) Prof. Craig White, [craig.white@monash.edu](mailto:craig.white@monash.edu) *Full name, email*

**Monash Department:** School of Biological Sciences, Faculty of Science

**Monash ADGR**  
(Name,Email) Prof Peter Betts, peter.betts@monash.edu *Full name, email*

**IITB Main Supervisor**  
(Name, Email Id, Phone) Prof. Rajesh Patkar  
[rajeshpatkar@iitb.ac.in](mailto:rajeshpatkar@iitb.ac.in) *Full name, Email*

**IITB Co-supervisor(s)**  
(Name, Email Id, Phone) - *Full name, Email*

**IITB Head of Dept**  
(Name, Email, Phone) Prof. Rohit Srivastava  
[head.bio@iitb.ac.in](mailto:head.bio@iitb.ac.in) *Full name, email*

**IITB Department:** Biosciences & Bioengineering (BSBE)

### Research Clusters:

### Research Themes:

Highlight which of the Academy's CLUSTERS this project will address? <i>(Please nominate JUST <u>one</u>. For more information, see <a href="http://www.iitbmonash.org">www.iitbmonash.org</a>)</i>		Highlight which of the Academy's Theme(s) this project will address? <i>(Feel free to nominate more than one. For more information, see <a href="http://www.iitbmonash.org">www.iitbmonash.org</a>)</i>	
1	Material Science/Engineering (including Nano, Metallurgy)	1	Artificial Intelligence and Advanced Computational Modelling
2	Energy, Green Chem, Chemistry, Catalysis, Reaction Eng	2	Circular Economy
3	Math, CFD, Modelling, Manufacturing	3	Clean Energy
4	CSE, IT, Optimisation, Data, Sensors, Systems, Signal Processing, Control	4	Health Sciences
5	Earth Sciences and Civil Engineering (Geo, Water, Climate)	5	Smart Materials
6	<b><u>Bio, Stem Cells, Bio Chem, Pharma, Food</u></b>	6	<b><u>Sustainable Societies</u></b>
7	Semi-Conductors, Optics, Photonics, Networks, Telecomm, Power Eng	7	Infrastructure
8	HSS, Design, Management		

## The research problem

Diseases caused by fungal pathogens in crops can cause 10-30% loss in yield annually (1). Coupled with the growing population of the world, and the warming climate, this poses a significant challenge to food security in various parts of the globe including countries such as India and Australia ([www.ipcc.ch](http://www.ipcc.ch)). There are global efforts to understand the molecular mechanisms through which pathogens evade host immune response and successfully cause diseases. Understanding the mechanisms would allow us to develop technologies and varieties that would aid in reducing crop losses due to fungal diseases and thereby increasing food security. *This project aims to dissect and elucidate the mechanisms on how pathogens may reprogram the transcriptional machinery in host plants.* Successful completion of this project has the potential to mitigate risks to food security.

The proposed project will use cereal blast disease caused by the ascomycete filamentous fungal pathogen *Magnaporthe oryzae* as a system of study (2). Prof Patkar at IITB is an expert in this area of research (3, 4). Cereal blast disease is an economically important disease on cultivated crops (rice, barley, wheat and millets) worldwide. The disease on rice plants alone is responsible for ~30% yield loss annually, which is equivalent to the amount required to feed ~60 million people each year (5). This is a well-established patho-system (6), where the efforts so far have been to understand two aspects: a) mechanisms and strategies used by the pathogen to escape/evade resistance mechanisms in host plants and b) strategies host uses to develop resistance. The findings thus far have revealed various proteins and small molecules in the blast fungus (7), which play essential roles in host-pathogen interaction. While certain cell-signalling proteins/enzymes are found to be involved in the specialised fungal development (appressorium formation) required for pathogenesis, several secretory effector proteins and small molecules that modify the host response have also been identified at the host-pathogen interface (7, 8). However, how pathogens either via these proteins or other mechanisms may reprogram the transcriptional response of the host plant is largely unknown. This project aims to address this knowledge gap using genomics and natural variation approach. Prof Balasubramanian from Monash University is an expert on genomics and natural variation in plants (9, 10, 11, 12).

This project will explore pathogen-induced transcriptional reprogramming in different host plants as a virulence strategy employed by the blast fungal pathogen. Further, we hope to understand the mechanism by which the blast fungal pathogen may have evolved to reprogram transcription in distinct ways in different host plants. This study will explore both transcriptional as well as post-transcriptional effects at the level of RNA splicing, using cutting-edge computational biology approaches together with solid functional assays using the well-established cereal blast patho-system.

### References (\*\* Papers from project supervisors)

1. Simón MR, Börner A and Struik PC (2021) Editorial: Fungal Wheat Diseases: Etiology, Breeding, and Integrated Management. **Front. Plant Sci.** 12:671060. doi: 10.3389/fpls.2021.671060
2. Asibi, AE., Chai, Q and Coulter, JA (2019) Rice Blast: A Disease with implication for global food security, **Agronomy**, 9(8):451.
3. \*\*\*Patkar R.N., Benke P., Qu Z., Constance C.Y., Fan Y., Swarup S. and Naqvi N.I (2015). A Fungal Monooxygenase-Derived Jasmonate Attenuates Host Innate Immunity. **Nature Chemical Biology** 11: 733-40.
4. \*\*\*Thaker, A., Mehta, K. & Patkar, R (2022) Feruloyl esterase *Fae1* is required specifically for host colonisation by the rice-blast fungus *Magnaporthe oryzae*. **Curr Genet** 68, 97–113. <https://doi.org/10.1007/s00294-021-01213-z>
5. Nalley, Lawton et al (2016) "Economic and Environmental Impact of Rice Blast Pathogen (*Magnaporthe oryzae*) Alleviation in the United States." **PLoS ONE** 11(12):e0167295. doi:10.1371/journal.pone.0167295
6. Wilson R and Talbot N (2009) Under Pressure: Investigating the Biology of Plant Infection by *Magnaporthe oryzae*. **Nature Reviews Microbiology** 7(3):185-95.
7. Jessie Fernandez, Kim Orth (2018) Rise of a Cereal Killer: The Biology of *Magnaporthe oryzae* Biotrophic Growth. **Trends in Microbiology** 26(7): 582-597.
8. \*\*\*Patkar RN and Naqvi NI (2017) Fungal manipulation of hormone-related plant defense. **PLoS Pathogens** 13(6):e1006334.
9. \*\*\*Dent, Cl., Singh, S., Mukherjee, S., Mishra, S., Sarwade, RS., Shamaya, N., Loo, KP., Harrison, P., Sureshkumar, S., Powell, D and Balasubramanian, S (2021) Quantifying splice site usage: a simple yet powerful approach to analyse splicing. **NAR-Genomics and Bioinformatics**,

- 3(2):1.
10. \*\*\*Eimer, H., Sureshkumar, S., Singh Yadav, A., Kraupner-Taylor, C., Bandaranayake, C., Seleznev, A., Thomason, T., Fletcher, S.J., Gordon, S.F., Carroll, B.J. and **Balasubramanian, S** (2018) RNA-dependent epigenetic silencing directs transcriptional downregulation caused by intronic repeat expansions. **Cell**, 174(5):1095-1105.
  11. \*\*\*Tasset, C., Singh Yadav, A., Sureshkumar, S., Singh, R., van der Woude, L., Nekrasov, M., Tremethick, D., van Zanten, M. and **Balasubramanian, S** (2018) *POWERDRESS*-mediated histone deacetylation is essential for thermomorphogenesis in *Arabidopsis thaliana*. **PLoS Genetics**, 14(3):e1007280.
  12. \*\*\*Sureshkumar, S., Dent, C., Seleznev, A., Tasset, C. and **Balasubramanian, S** (2016) Nonsense-mediated mRNA decay modulates FLM-dependent thermosensory flowering response in *Arabidopsis*. **Nature Plants**, 2(5):16055.

## Project aims

This project will test the hypothesis that pathogens can induce transcriptional reprogramming in the host to evade resistance. To test this hypothesis, the proposed project work involves the following objectives:

- 1) To set up infection assays using different host plants and the blast fungal pathogen *M. oryzae* and to extract total RNA thereafter at appropriate stages of the infection lifecycle.
- 2) To analyse the global transcriptome of the aforementioned stages, to assess pathogen-induced transcriptional changes.
- 3) To assess pathogen-induced post-transcriptional changes (i.e., changes in RNA splicing) using newly developed computational tool SpliSER.
- 4) To assess how these pathogen-induced changes have evolved in a host-specific manner.

## How skills/experience of the IITB and the Monash supervisor(s) support the proposed project

This work requires diverse expertise that is often not present in a single research group. This specific project requires expertise in the analysis of fungal-plant interactions, which involves handling of the culture of the fungal pathogen and its cereal host plants. In addition, it requires expertise in the area of computational biology. And both of these are nicely complemented by the supervisory team.

Dr. Patkar's lab at IITB [<https://www.bio.iitb.ac.in/people/faculty/patkar-r/>] is well-established to set up the infection assays and in studying molecular mechanisms underlying the host (plant)-pathogen interactions. On the other hand, Prof. Balasubramanian has the expertise in the area of analysis of genomics and computational biology [[www.skblab.org](http://www.skblab.org)]. Thus, the supervisory team has complementary skills that enhance the project and make it ideal for this proposed collaborative research work under Monash-IITB academy.

## What is expected of the student when at IITB and when at Monash?

### At IITB:

- 1) The student will set up the infection assays, using different plant hosts (rice, barley, millet and wheat) and the fungal pathogen *M. oryzae*. Note: *M. oryzae* belongs to the BSL-1 category, and hence will not require any containment facility. The assays will be conducted in a portable plant growth chamber or the greenhouse on the campus.
- 2) Biological samples from the above-mentioned assays will be collected, processed for total RNA extraction towards RNA sequencing.
- 3) A relevant genetic modification (based on the findings from the global transcriptome analysis – to be done at Monash) in a plant host and biological assays thereafter to assess enhanced disease resistance, if any.

### At Monash:

- 1) The student will be trained in computational analysis of genomes and transcriptomes.
- 2) The student will analyse the RNA-seq data for a) transcriptional differences, b) splicing differences, c) any patterns among differentially transcribed or differentially spliced genes.
- 3) Carry out molecular experiments (cloning, generating constructs etc) based on the results of the computational analysis.

## Expected outcomes

The proposed research study will help us understand the molecular mechanism(s) by which the blast fungal pathogen manipulates the host gene expression machinery, and thus hijacks plant immune response to cause the disease. Further, the findings from this research study might shed light on a possible evolutionary aspect of the pathogen-induced altered splicing, during adaptation to a different host or host jump by the blast fungus.

## How will the project address the Goals of the above Themes?

The research findings from the proposed project would help us design novel/innovative strategies to confer disease resistance towards the devastating blast disease. This, in turn, will help us in reducing the crop yield losses due to the fungal disease and therefore in global food security for the future.

## Potential RPCs from IITB and Monash

### IITB members:

- 1) Prof. Swati Patankar – works on host-pathogen interaction using the model parasite pathosystem.
- 2) Prof. Anirban Banerjee – works on host-pathogen interaction using the bacterial pathosystem.
- 3) Prof. Kiran Kondabagil – works in the area of virology and Next gen Sequencing analysis.

### Monash members:

- 1) Prof John Bowman – Expert on evolutionary analysis and would be helpful in the host-specificity evolution part of the project.
- 2) A/Prof David Powell – Director, Monash Bioinformatics Platform, An expert on genomics and bioinformatics.

## Capabilities and Degrees Required

- 1) Four year Bachelor's Degree (e.g., B.Tech) or Master's degree in life sciences or allied subjects, including a research component.
- 2) Hands-on experience in handling microbial cultures and/or model plants.
- 3) Hands-on experience in molecular biology would be preferred.
- 4) Willingness and an interest in learning and applying bioinformatic skills. Some experience in python and/or R programming would be desirable.

## Necessary Courses

- 1) Research Philosophy (BB602)
- 2) Biostatistics (BB621)
- 3) Modelling Biological Systems & Processes (BB626)

## Potential Collaborators

There is potential to develop national international collaborations through this project. Some potential external collaborators include Prof Ashis Nandi (JNU, India), Prof Wangsheng Zhu (Chinese Agricultural University, China).

Select up to **(4)** keywords from the Academy's approved keyword list (**available at <http://www.iitbmonash.org/becoming-a-research-supervisor/>**) relating to this project to make it easier for the students to apply.

**BioScience, Biochemistry,**