Project Proposal

Institution / Programme of internship application: TLL

PI: Henning Seedorf

Mentor:
NA

Lab/Department: Genome and Ecological Biology

Name of intern (if applicable): TBD

Proposed internship period: TBD

Skills to have: Basic microbiology and some bioinformatics skills

Job Requirements:
Ability to work independently and collaboratively.
Strong organizational and communication skills.

Project title: Cultivation and Characterization of microorganisms from the intestinal tract of fish.

Objectives: The main objective of this project is to cultivate and characterize the microbial diversity of microorganisms of farmed (and non-captive) fish with the ultimate aim to use the obtained isolates for the development of aquaculture probiotics.

Methodology:
1. cultivation techniques for microorganisms;
2. Screening for antibiotic-resistant microorganisms;
3. Molecular biology techniques, such as DNA extraction, PCR, DNA sequencing, etc.;
4. Some basic bioinformatics, such as DNA sequence analysis;
5. Physiological and molecular characterization of microbial isolates from farmed fish.

Description:
Major efforts in microbiome research have focused in recent years on the characterization of microorganisms from the intestinal tract of humans. Several thousand strains have now been cultivated from human subjects and their genomes have been analysed. However, the cultivation and characterization of microorganisms from the intestinal tract of fish, such as Asian Seabass, is lagging behind and only a relatively small number of commensals from these hosts is currently available. Closing this knowledge gap may allow us to develop novel probiotics for use in aquaculture but will also increase our general understanding of fish gut-associated microbiota.

This project aims at isolating and characterizing novel bacterial strains from the fish

The student will learn 1. Some aerobic anaerobic cultivation techniques for intestinal microorganisms; 2. Molecular biology techniques, such as DNA extraction, PCR, DNA sequencing, etc.; 3. Some basic bioinformatics, such as DNA sequence analysis.

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Skills to have: Basic microbiology and some bioinformatics skills

Job Requirements:
Ability to work independently and collaboratively.
Strong organizational and communication skills.

Project title: Novel larvicides from Singapore soil

Objectives:
-Isolate novel microbial strains from the poorly characterized soil in Singapore, which is known to harbour a diverse range of species.
-Characterize the microbial strains for their ability to produce larvicidal compounds specifically targeting mosquito larvae, without disturbing the overall ecosystem.
-Develop an effective and eco-friendly larvicidal solution that can be used to control mosquito populations responsible for vector-borne diseases such as malaria, dengue, and Zika. This has been performed in other countries but not in Singapore.

Methodology:
-Cultivation techniques for aerobic and anaerobic microorganisms.
-Molecular biology techniques required for identification and characterization of microorganisms.
-Basic bioinformatics.
-Preparation of reports and presentations.

Description:

Vector-borne diseases, including malaria, dengue, and zika, continue to cause thousands of deaths globally, necessitating effective mosquito population control measures. Current methods often have a broad ecological impact, underscoring the need for targeted approaches that minimize disruption to surrounding ecosystems. Microbial larvicides, produced by naturally occurring microorganisms, offer a promising and ecologically sustainable solution for targeting mosquito larvae. This project aims to isolate and characterize novel larvicidal microbes from Singapore's underexplored soils, known to harbour unique microbial species. By leveraging

Singapore’s biodiversity, we seek to identify microbes that can specifically target mosquito larvae while preserving the ecological balance.

The student will learn 1. Some cultivation techniques for microorganisms; 2. Molecular biology techniques, such as DNA extraction, PCR, DNA sequencing, etc.; 3. Some basic bioinformatics, such as DNA sequence analysis.

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NA

Lab/Department: Genome and Ecological Biology

Name of intern (if applicable): TBD

Proposed internship period: TBD

Skills to have: Basic microbiology and some bioinformatics skills

Job Requirements:
Ability to work independently and collaboratively.
Strong organizational and communication skills.

Project title: Navigating microbial interactions of methanogens in the human gut microbiome

Objectives: The main objective is to characterize proteins that mediate the interaction between methanogens and other gut microorganisms. These will improve our basic understanding of microbe-microbe interactions in the gut and may guide the way for the development of novel strategies to mitigate methane emissions from animals.

Methodology:
-Cultivation techniques for aerobic and anaerobic microorganisms.
-Cloning of genes and protein purification.
-Molecular biology techniques required for identification and characterization of microorganisms.
-Basic bioinformatics.
-Preparation of reports and presentations.

Description:
Thousands of microbial strains have now been cultivated from human subjects and their genomes have been analyzed. However, the microbe-microbe and microbe-host interactions in gut remain poorly understood. The gut microbiome of animals and humans comprises a major reservoir of methane producing microorganisms, so-called methanogens. Adhesins are the large and abundant cell surface proteins of these microbes, that mediate interactions among microorganisms and their environment. We aim to characterize adhesins by expression of adhesin proteins and domains from human gut methanogens and to investigate the interactions with other gut symbionts.

The student will learn 1. Some cultivation techniques for microorganisms; 2. Molecular biology techniques, such as DNA extraction, PCR, DNA sequencing, etc.; 3. Some basic bioinformatics, such as DNA sequence analysis.

Project Proposal

- Please include the following information in your project proposal and submit it as a supporting document for the Internship Application Form.

- If this is a grant project, please attach confirmation from Grants and Intellectual Property Administration (GIPA) Department that the grant may be used to support this internship.

Institution / Programme of internship application:

PI: Shen Lisha

Mentor: Fan Sheng
(RO & above unless otherwise justified)

Lab/Department: Shen Lisha's group

Name of intern (if applicable):

Proposed internship period:

Skills to have: Basic knowledge in molecular biology

Job Requirements:

[For polytechnic internships only] Suitable for students with special educational needs? : YES / NO
(Polytechnics are moving towards building an inclusive and diverse society. Lecturer will work with PI to support students with special educational needs)

Project title: Unravelling the biological function of RNA-binding proteins in plant development

Objectives: To study the biological function of two RNA-binding proteins in Arabidopsis through observing the mutant phenotypes and identifying their downstream targets

Methodology: Molecular biology, biochemistry, and imaging

Description:

Appropriate timing of the transition from vegetative to reproductive development (floral transition) is crucial for crop breeding and utilizing plant biomass as a source of renewable energy. In *Arabidopsis thaliana*, this process is tightly regulated by a complex network of genetic pathways, including the photoperiod, vernalization, thermosensory, autonomous, gibberellin and age pathways. We have recently identified two RNA recognition motif (RRM)-containing proteins that control flowering time in Arabidopsis. In this project, we will focus on the characterization

of these two RNA-binding proteins to understand their function in flowering time regulation using a comprehensive set of physiological, molecular, genetic, biochemical, bioimaging and proteomics approaches. Achievement of the objectives in this proposal will allow us to gain significant insights into the molecular mechanisms of flowering in plants and the cognate processes in other eukaryotic systems. The derived knowledge will be practically important for creating novel and high-value varieties with desirable traits for economically important plants.

Additional information (if any):

Project Proposal

PI: Dr. Mookkan Prabakaran

Mentor: Dr Hongyi Xin
(RO & above unless otherwise justified)

Lab/Department: Molecular Viral Pathogenesis Group

Name of intern (if applicable):

Proposed internship period:

Project title: Molecular pathogenesis of Infectious Spleen and Kidney Necrosis Virus (ISKNV) & Scale Drop Disease Virus (SDDV) in Asian Seabass (Lates calcarifer)

Objectives:

1. Evaluate the progression of gross pathological changes during ISKNV & SDDV infections.
2. Utilize transcriptome analysis to elucidate dynamic changes in differentially expressed genes (DEGs) at various post-infection stages of SDDV and ISKNV in Asian Seabass (ASB) kidney cells.
3. Investigate DEGs associate with viral invasion, host metabolic pathways, and host immunological responses using real-time PCR.

Methodology:

1. Pathological: Gross pathological changes will be assessed using histological and immunohistochemical examinations across various tissues (spleen, kidney, liver, gill, heart, brain, muscle, and skin) of ASB. Viral titers will be determined using qPCR.
2. Transcriptome: RNA sequencing has proven valuable for understanding host-pathogen interactions. However, the pathogenic mechanisms and host responses following SDDV and ISKNV infections remain insufficiently characterized. This study will utilize transcriptome analysis to elucidate dynamic changes in DEGs at various post-infection stages in Asian Seabass kidney cells. DEGs identified from transcriptome analysis will be validated using real-time PCR to explore their roles in viral invasion, host metabolic pathways, and immunological responses.

Description: Infectious spleen and kidney necrosis virus (ISKNV) and Scale Drop Disease Virus (SDDV), both members of the *Megalocytivirus* genus, cause severe diseases in various fish species. These infections lead to severe diseases in various fish species, leading to substantial economic losses in aquaculture industries due to to high mortality rates. Understanding the molecular pathogenesis and host-virus interactions of SDDV and ISKNV will shed light on their virulence, host specificity, and resistance to antiviral measures, offering strategies for improved diseases management.

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PI: Pek Jun Wei

Mentor: Pek Jun Wei
(RO & above unless otherwise justified)

Lab/Department: PJW

Name of intern (if applicable):

Proposed internship period: 12 May to 1 Aug 2025

Project title: Investigating the role of circular RNA/peptide in reproduction

Objectives: To investigate the function of circular RNA/peptide during reproduction and aging

Methodology: The student will learn techniques in molecular biology (cloning, PCR, RNA work), fly genetics, cell biology, cell culture and imaging

Description: Circular (circ)RNAs belong to a class of transcripts that do not encode for any proteins. Although many circRNAs have been identified, their functional significance during ageing remains elusive. This project aims to study the roles of circRNAs during oocyte ageing in *Drosophila melanogaster* (fruit fly). With its powerful genetics, *Drosophila* offers an excellent system for functional analysis in vivo. The student will perform genetic analysis of circRNA mutant and overexpression flies to study their roles during ageing.

Additional information (if any):

Project Proposal

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- If this is a grant project, please attach confirmation from Grants and Intellectual Property Administration (GIPA) Department that the grant may be used to support this internship.

Institution / Programme of internship application:

PI: Zhang Dan

Mentor: Victor Ong
(RO & above unless otherwise justified)

Lab/Department: Zhang Dan's Group

Name of intern (if applicable):

Proposed internship period: 12 May – 1 August 2025

Skills to have: N/A

Job Requirements: N/A

[For polytechnic internships only] Suitable for students with special educational needs? : YES / NO
(Polytechnics are moving towards building an inclusive and diverse society. Lecturer will work with PI to support students with special educational needs)

Project title: A systematic *in vivo* screening of *C. auris* virulence factors

Objectives:

1. **To generate *C. auris* mutant library**
2. **To screen *C. auris* mutants with increased or decreased pathogenicity**
3. **To identify related virulence factors**

Methodology:
Microbiology techniques, Worm work, Molecular techniques, Bioinformatics analysis of sequencing data, Machine-learning-based image analysis

Description:
Candidiasis is a fungal infection caused by various *Candida* species, such as *C. albicans*, *C. glabrata* and *C. tropicalis*. These opportunistic pathogens are commonly carried by human and can become devastating to immunocompromised individuals under a variety of health conditions. As a result of climate change, new virulent *Candida* species or lineages have emerged and adapted, causing significant outbreaks. *C. auris* is one such emerging *Candida* pathogen. Clinical isolates of *C. auris* have evolved enhanced capabilities in multi-drug resistance and biofilm formation (in both human tissue and medical devices), imposing a rising

threat to disease treatment. However, little is known about virulence factors associated with *C. auris*. In this project, student will help to establish *C. auris* mutant libraries using piggyBac transposon-mediated, genome-wide mutagenesis and to conduct systematic screenings in the host *C. elegans* via our automated survival scoring platform for virulence factors. Students will be trained with microbiology and molecular techniques, worm work, bioinformatics analysis, and machine-learning-based image analysis.

Additional information (if any):