

SCELSE awarded Tier 3 funding for Air Microbiomes study

Have you ever thought of what's inside the air you breathe? We will soon know a lot more thanks to a new study by SCELSE researchers to characterise Singapore's air microbiomes. Until now, it has been difficult to identify the organisms that we breathe, but the SCELSE team is using state-of-the-art technology to reveal the sources, function and ecology of the microbial cosmos contained in Singapore's air. Led by Prof. Stephan Schuster, the team recently secured a Tier 3 grant from the Singapore Ministry of Education (MOE) for up to \$ 25 million, conditional to a 3rd year review and over the time span of 5 years, to perform the research investigation.

"Missing ecosystems, sources, function and ecology of urban air microbiomes", incorporates systems biology, aerosol physics, microbial physiology and ecology, environmental sequencing and bioinformatics to understand the ubiquitous, largely unexplored microbial

communities in Singapore's ambient air and indoor environments. The research will be divided in three major project themes headed by Prof. Schuster, Assoc. Prof. Federico Lauro, and Prof. Yehuda Cohen.

According to Prof. Schuster, the proposal was awarded the highest ranked grant in Singapore because it is innovative, it addresses a health concern and everyone can relate to the subject of research. "Consider this, all are concerned with food safety, with the microbial intake to their digestive system and bodies, but no one asks what are we breathing? There are about one million bacterial cells

inhaled per day," he said. The research grant proposal is aiming to understand how the climate in the tropics influences the not so-well understood microbial dynamics occurring in the air. The research investigation is divided in three main project themes: Environmental Genomics, Microbial Ecology, and Microbial Physiology.

the environmental physical/chemical parameters," Assoc. Prof. Federico Lauro said. He and his team will model the global ecology of the air microbiomes. They will assess the ecology of outdoor and indoor air microbiomes, which is best explained as dynamic, connected networks of sources and sinks. The team will be working with the data from airflow models and simulations to understand how microbes change across time and space. At a fundamental level, he said, some of the classic questions in microbial ecology like who is there, where are they coming from and, to a lesser extent, what are they doing, will be answered.



Stephan Schuster

Microbial Physiology

Microbial adaptive responses – knowing how microorganisms respond to stress and changing environments, will add another dimension to our understanding of air microbiomes. Such microbial adaptive responses will be investigated in controlled laboratory conditions simulating the air ecosystem. This component of the study, which is led by Prof. Cohen, addresses whether exposure



Yehuda Cohen

to specific environmental parameters induces unique molecular adaptive responses using well-defined laboratory scale aerosol experiments. "Bacteria residing in air particles from outdoor and indoor environments differ and that

it is the connection between the microbes and the surrounding conditions that prompts possible stress responses," Prof. Cohen said. SCELSE has the capacity, he continued, to handle the large sample numbers involved in sampling different air environments in Singapore. This puts SCELSE at the forefront of analysing tiny amounts of biomass, a constraint that has thwarted attempts at such studies in the past.

Assoc. Prof. Lauro believes the strength of this research lies in the high level of interdisciplinary collaboration and novelty of the project. "While there are other teams studying the air microbiome around the world, we are doing it on a scale of integration and interdisciplinary collaboration never attempted before. Moreover, we are bringing SCELSE's expertise in microbial genomics and bioinformatics to the table, and that's an incredible asset," he said.



Calendar

SCELSE Seminars
11am -12pm, SBS-08

- 03 Apr:** Isaac Kerlow (EOS, Sci. Comm.)
- 04 Apr:** Ruth K. Walker (Newcastle U.)
- 10 Apr:** Cao Bin (SCELSE & C Env. E)
- 17 Apr:** Alex Ludwig (Rhodes Telomere Gp)
- 24 Apr:** Chris Cummings (Sch. Comm., Sci. Comm.)

Meetings

Environmental Engineering meeting:
Fridays 9am, B3 Meeting Room

Workshops & Programs

April 14-17: Experimental design and data analysis., Dr Ezequiel Marzinelli. Venue TBA.
Aug '14 & Jan '15: Biophysical Platform Program, open for student intake. <http://www.scelse.sg/programs>

Conferences 2014

- 11-13 May:** Biofilms 6, Vienna, Austria.
- 24-29 August:** 15th International Symposium on Microbial Ecology. Seoul, S. Korea.
- 5-6 Sep:** Academic Medicine – Transforming Vision into Reality: SingHealth Duke-NUS Scientific Congress 2014, Singapore General Hospital.
- 10-12 Sep:** The Perfect Slime - Nature, Properties, Regulation and Dynamics of EPS, IWA Conference, Essen, Germany.

Environmental Genomics

Outdoor and indoor air harbour diverse microbiological communities with largely unknown composition and function. Prof. Schuster, the theme project PI, says that the contrast between the warm and humid air outdoors and the cool, dry air-conditioned air indoors may affect the components of the microbial communities found in the air. The implications of this study are far-reaching. "We will develop techniques that study single bacterial cells and their activity as we sequence not entire communities, but complete genomes within these communities," he pointed out. Such breakthroughs are enabled, he added, by techniques of single molecule sequencing. In other words, DNA sequences up to ten thousand base pairs can be read, and then matched by single cell techniques for sorting and imaging.



Federico Lauro

Microbial Ecology

"This project will advance our understanding of how microbes live and travel through air by studying the delicate interplay between genes/taxa and

Diane McDougald Visiting Assistant Professor

Relationships are intricate by definition, and bacterial ones are no exception. This is what the research focus of Visiting Assistant Professor Diane McDougald is all about. Her expertise includes the mechanisms of bacteria-protists and bacteria-macrophage interactions. At SCELSE, she is directing projects elucidating how bacterial pathogens cycle between hosts and the environment in Singapore's urban ecosystem. In collaboration with Prof. Mike Givskov and Asst. Prof. Yang Liang, she will be studying the adaptive evolution of *P. aeruginosa* in co-culture with macrophages and amoebae. "Predation is an important selection pressure that pathogens face in the environment and, as a result, pathogens may evolve phenotypes that not only increase their fitness in the environment, but may also increase their fitness in the human host. This will allow us to test key aspects of the Coincidental Selection Hypothesis," she says. The hypothesis states that the virulence of many opportunistic human pathogens may be the random by-product of selective pressure, not necessarily related to human disease. In other words, the "being at the right place at the right time" approach in the microbial world. She will also be investigating the role of heterotrophic

protists in engineered systems (sequencing batch reactors and membrane bioreactors) in collaboration with Associate Prof. Scott Rice and Prof. Stefan Wuertz, and in urban waterways and reservoirs with Associate Prof. Sanjay Swarup. Diane obtained her Master of Science degree in 1993 from the University of North Carolina-Charlotte (USA), where she worked on the "viable but non-culturable response of *Vibrio vulnificus*." In 2001, she obtained her PhD degree from the Centre for Marine Bio-Innovation (CMB) at the University of New South Wales (UNSW), where she worked under the supervision of Prof. Kjelleberg on the "Regulation of starvation and non-culturability in the pathogenic marine *Vibriosis*". She later became a Program Leader in the CMB, where she focused on cell-to-cell communication, biofilm formation, and bacterial stress responses from adaptations to mechanisms of molecular control. Her team investigated the role of quorum sensing in the pathogenesis of *Vibrio spp.*, and



Vg Asst Prof. Diane McDougald

on the development of novel inhibitors of quorum sensing as anti-virulence compounds. Recently, they have been investigating the interactions of bacteria with higher eukaryotes, particularly with heterotrophic protists. Diane has experience in Singapore's research landscape. In 2009, she started working at NTU's Advanced Environmental Biotechnology Centre (AEBTC) as the leader of the Marine Health and Biotechnology cluster, in which she managed projects including the investigation of the coral microbiome as an indicator of coral health and fouling inhibition in desalination membranes. In addition, her team investigated the temporal shifts in microbial community composition in a Singaporean reservoir and identified a bacterial species that is a potential indicator of cyanobacterial blooms in these reservoirs. She has been working with complex communities and predator/prey systems, which she finds much more challenging than working with single population experiments. The good news, she adds, is that such types of experiments give a more in depth view of what is happening in nature. "I find working in a team of bright young people to be the best aspect of my job," she said.

Predicting bioreactor performance with molecular data

Publication profile

Researchers all over the world work on linking microbial communities with the functions they perform in the environment. SCELSE researchers are taking it to the next level by predicting how microbial communities function in used water treatment, based on their diversity and dynamics. We used bioreactors in controlled experiments exposed to defined chemical stress to build a complex machine learning model called a Support Vector Regression that predicts how our reactors will perform at a given time point based on past performance data. We started out running

reactors with sludge fed on synthetic wastewater with and without 3-chloroaniline (3-CA), a xenobiotic stressor compound known to disrupt the wastewater treatment process. We found that the sludge could not adapt to the stress. We then started over, using the same regime, but this time, we "helped" the sludge by adding to all the reactors a strain known to contain part of the degradation pathway for 3-CA. Although the strain was maintained in the reactors throughout the two-month experiment and affected microbial community dynamics, the sludge did not

manage to respond to the stress input by degrading 3-CA. We then took all the molecular data from Terminal Restriction Fragment Length Polymorphism (T-RFLP) analysis of the 16S rRNA gene and amoA gene from both experiments and used diversity indices to see if we could predict the performance of the reactors. The predictions turned out to work well for the removal of general wastewater constituents like the removal of carbon and nitrogen. Current work in SCELSE uses metagenomic data to really zoom in on relating environmental and operational parameters of

a bioreactor (things we can measure or control easily) with community structure and function in a bioreactor (things that are not as easily measured or controlled). This would provide a more reliable model to predict process performance in wastewater treatment. In breaking news from the lab, Hari's reactors have recently evolved the metabolic capacity to remove 3-CA. The next step will be to test how microbial communities respond to bioaugmentation with a bacterial strain that carries the genes for the complete degradation of the toxicant.
-Hari Seshan, PhD student.

Latest SCELSE publications

Strain-specific parallel evolution drives short-term diversification during *Pseudomonas aeruginosa* biofilm formation

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Support vector regression model of wastewater bioreactor performance using microbial community diversity indices: Effect of stress and bioaugmentation

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