



## **TRAVEL, CONFERENCE or SCIENTIFIC EXCHANGE REPORT 2015**

### ***Part 1 - Summary Details***

---

*Please use your TAB key to complete Parts 1 & 2.*

**CRDC Project Number:** UNE1505  
**Project Title:** The 6<sup>th</sup> Congress of European Microbiologists – Maastricht, the Netherlands  
**Project Commencement Date:** 04.06.15      **Project Completion Date:** 14.06.15  
**CRDC Research Program:** Conference Travel

### ***Part 2 – Contact Details***

---

**Administrator:** Dr. Kathryn Dougall  
**Organisation:** The University of New England  
**Postal Address:** University of New England  
Science and Technology W34  
Armidale NSW 2351  
**Ph:** 02 67733262      **Fax:** 02 67733523      **E-mail:** kjacques@une.edu.au

---

**Principal Researcher:** Sarah Cooper  
**Organisation:** UNE  
**Postal Address:** University of New England  
Science and Technology W34  
Armidale NSW 2351  
**Ph:** 02 67732077      **Fax:** 02 67733267      **E-mail:** scooper4@myune.edu.au

---

**Supervisor:** Associate Professor Lily Pereg  
**Organisation:** UNE  
**Postal Address:** University of New England  
Science and Technology W34  
Armidale NSW 2351  
**Ph:** 02 67732708      **Fax:** 02 67733267      **E-mail:** lperegge@une.edu.au

---

**Signature of Research Provider Representative:** \_\_\_\_\_

**Date Submitted:** \_\_\_\_\_

## **Part 3 – Travel, Conference or Scientific Exchange Report**

---

(Maximum two pages)

### **1. A brief description of the purpose of the travel.**

The purpose of the travel was to attend and present my research at the 6<sup>th</sup> congress of European Microbiologists (FEMS Federation of European Microbiological Societies), Maastricht, the Netherlands. This conference is one of the leading meetings of its kind and brings together approximately 3000 microbiologists from around the world. As part of my communication strategy this congress provided the perfect opportunity to disseminate my research to the wider scientific community and it was a privilege to present my PhD findings at such a renowned congress. It is a biennial conference and I am thankful for the opportunity to attend this conference within my candidature. It is important that my results be presented as soon as possible and attending this congress enabled me to do so.

The conference abstract can be found on page four of this report and a copy of the presentation can be found attached.

### **2.**

#### **a) Major findings and outcomes**

#### **b) Other highlights**

The congress had a number of sessions, which covered current topics and issues relating to microorganisms. It provided new concepts and ideas that have contributed to the research being conducted in my project. Topics ranged from microbial genetics, hyphal structure and growth, to interactions in soil microbiomes and biofilms and ecosystem resilience. Of particular interest were a number of presentations, one on chitinase production by fungi, a discussion of the genomic flexibility of *Verticillium dahliae*, one on siderophores and trace element availability, a presentation on fungal highways and bacterial movement.

The plant-fungal pathogens plenary lecture included discussions on the production of chitinases by fungal root pathogens and discussed the control and induction of chitinase production. This presentation provided valuable information that assisted in the development of a medium that induces the production of chitinases by the *Trichoderma* isolates in my project.

Another valuable aspect of the conference was some of the research being done on the same microorganisms that I am working with, *Verticillium dahliae*, *Aspergillus fumigatus* or in the same genera as with *Fusarium solani*. In these projects they often applied different techniques and used different fields of science to investigate these microorganisms. Alternatively, they applied different approaches to similar questions, this provided a different, wider perspective and a way of thinking about and analysing these microbes. An example of this was the work being done in the project entitled '*Plant-microbiome interactions in the heavy metal polluted environments*'. The mobilization of trace elements, in particular, the work on the mechanisms of siderophore production and other secondary metabolites is genetic based (mine involves plate assays). What they are doing could easily be used for my project and maybe a better way to do it in the future. Another study '*Pathogenomics of Verticillium wilt diseases*' introduced genomic flexibility a characteristic of *Verticillium dahliae* that enables it to escape host immunity whilst maintaining its aggressiveness. It was a really interesting study and something that should definitely be addressed when looking at disease control for this pathogen.

The concept of 'fungal highways' was discussed by a number of presenters; this is where bacteria use fungal hyphae as a way to move around the soil and plant roots. This may be something to consider when bacterial bio-inoculations are being applied to soil. It provides a mechanism for a non-motile bacterial inoculant to disperse in the soil. It could be that when some of the bacterial agents identified in my study are used they need a mechanism to disperse through the soil in order to work more effectively. Fungal highways may be the biologically sustainable way to achieve this.

The symposium and workshops I attended during the conference are listed following. Abstracts for these can be found at the following link: <http://fems-microbiology.kenes.com/Documents/FEMS%20abstracts.pdf>

### **Introduction**

**Plenary Session: Giant viruses** J.M. Claverie<sup>1</sup>, C. Abergel<sup>1</sup> <sup>1</sup>Structural and Genomic Information Laboratory, Mediterranean Institute of Microbiology, Marseille, France

### **Day One:**

**Plenary Session: (human) microbiome** J.K. Jansson<sup>1</sup> <sup>1</sup>Biological Sciences, Pacific Northwest National Laboratory, Richland WA, USA

### **Symposium: Plant Microbe Interactions**

- i. *The Phyllosphere microbiota: Responses to and Impacts on Plants*, J.A. Vorholt
- ii. *Plant-microbiome Interactions in the Heavy Metal Polluted Environments*, A. Sessitsch, E. Corretto, M. Puschenreiter, K. Fallmann, M. Kuffner, S. Hann, Y. Schindlegger, G. Brader
- iii. *Back to the roots: Microbiology and chemistry at the root-soil interface*. J. Raaijmakers
- iv. *Plant-fungal communication During Arbuscular Mycorrhizal Symbiosis*, N. Requena

### **Workshop: Publication Workshop**

#### **Workshop: Fungal Plant Pathogens**

- i. *Transcriptional networks controlling Pathogenicity and Polarised growth in U. maydis*, B.Faist, J. Ulrich, K. Heimel, J. Kamper
- ii. *Pathogenomics of Verticillium wilt diseases*, B. Thomma, M. Seidl, X. Shi, J. Boshoven, M. Van Damme, J.Li, E. Rojas Padilla, Y. Song, G. Van den Berg, L. Faino
- iii. *My Presentation*
- iv. *Evaluation of genetic diversity among phytopathogenic isolates of Fusarium solani complex causing Shisham dieback disease in Pakistan*, I. Mukhtar, R. Bajwa, G. Nasim, F.Y. Hafeez
- v. *Application of Trichoderma strains against GTD Pathogens*, C. Kovacs, E. Sandor, P. Balling, Z. Bihari, F. Peles

### **Day Two**

**Plenary Session:** Plant-Fungal pathogens, P.J.G.M. De Wit

#### **Symposium: Establishment of the fungal Mycelium**

- i. *Heterogeneity of the Fungal Mycelium*, H.A.B. Wstösten, R. Fischer
- ii. *The Microtubules cytoskeleton in Aspergillus nidulans*, R. Fischer
- iii. *Signalling cascades associated with fungal cell-cell communication and trophic growth*, S. Seiler
- iv. *Insight into the early regulation of Conidiospore development in Aspergillus nidulans*, U. Ugalde, M. Iradi

### **Poster Discussion: Environmental Microbiology**

#### **Workshop: Fungal Bacterial interactions**

- i. *Microbial Logistics- Mycelia as a Networks for Functional Transport of Bacteria and chemicals*, L. Wick
- ii. *Fungi-bacteria interactions: from soil functioning to complex behaviour*, P. Junier, A. Lohberger, V.Herve, A. Simon, T. Junier, S. Bindschedler, G. Cailleau, R. Bshary, E. Verrecchia
- iii. *Effect of dispersal networks on bacterial dispersal and biodegradation at varying water potentials*, A. Worrich, M Kästner, A. Miltner, L.Y. Wick
- iv. *Strategies of Streptomycetes for fungal targeting and inhibition*, H. Schrempf, P. Merling
- v. *Role of Volatiles in Antifungal activity of a lactobacillus paracasei against Penicillium strains*, S. Aunbjerg, A. Honoré, P. Ebrahimi, F. Vogensen, V.T. Skov, S. Knøchel

- vi. *The fungal highway toll: Metabolisms and genes involved in fungal- driven bacterial dispersal in natural ecosystems*, A. Simon, A. Al-Dourobi, S. Bindschedler, L.Y. Wick, J. Zopfi, D. Job, E.P. Verrecchia, P. Junier

### **Day Three:**

**Plenary Session:** How to eat without a mouth or gut: symbioses between chemosynthetic bacteria and gutless Marine Worms, B. Schink

### **Symposium: fungal cell Biology**

- i. *Molecular motors in spatially organizing the fungal cell*, G. Steinberg
- ii. *Peroxisome biogenesis and proliferation in yeast*, I.J. van.der. Klei
- iii. *Genetic Networks in Budding Yeast*, B. Andrews
- iv. *The importance of fungi and their movement in crops*, S. Gurr

### **Poster Discussion: Social Interactions Between microbes**

#### **Workshop: Fungal human Pathogens**

- i. *Components of the fungal cell wall that turn on and turn off the immune inflammatory response*, N.A.R. Gow
- ii. *Pathogenicity and immune evasion of the human-pathogenic fungus *Aspergillus Fumigatus**, A. Brakhage
- iii. *First metabolic network of the seborrheic dermatitis associated yeast *malassezia furfur**, S.Triana, A. Gozalez, S. Restrepo, A. Celis
- iv. *Prospective study on oral candidial infection after intensity-modulated radiation therapy for non-metastatic nasopharyngeal carcinoma: correlation with the radiation dose to the parotids*, V.H.F. Lee, C.J. Seneviratne, H.L. Fong, S.S.W. Wong, D.L.W. Kwong, K.O. Lam, T.W. Leung, L.P. Samaranayake.
- v. *Rapid detection of *cyp51A*-promoter based voriconazole resistance in *Aspergillus fumigatus* isolates in a high incidence population*, J. Fahren, TT. Severs, W.S. Voskuil. C.H.E. Boel, P.J.A. Haas, J.F. Meis, J.G. Kusters

### **Day Four:**

#### **Plenary Lecture: Mechanisms of bacterial secretion, G. Cornelis**

#### **Symposium: Bacterial Spores**

- i. *Collaborating with the innate immune system to combat multidrug-resistant bacterial pathogens*, V. Nizet.
- ii. *Meningococemia A disease of the Endothelial cells*, X. Nassif.
- iii. *Buruli ulcer: from disease to pain control*, P. Brodin, O. Song, E. Marion, Y. Comoglio, G. Sandoz, L. Marsollier.
- iv. *The use of Antibiotics drive the evolution of resistance by activating competence for DNA uptake: molecular mechanisms involved in *streptococcus pneumoniae**, J.W. Veening

Closing Session:

Awards: Lwoff awards, Poster awards, Closing ceremony

- i. *Transmission: A basic Process in Microbiology*, F. Baquero
- ii. *The Microbial Methane Cycle*, R.K. Thauer

**3. Detail the persons and institutions visited, giving full title, position details, location, duration of visit and purpose of visit to these people/places. (NB:- Please provide full names of institutions, not just acronyms.)**

NA

- 4. a) Are there any potential areas worth following up as a result of the travel?**
- b) Any relevance or possible impact on the Australian Cotton Industry?**

Two potential areas of that would be worth following up include:

1. The possibility of using 'fungal highways' to aid in the dispersion of bacterial biocontrol agents. This is a possible future direction for my project and something to consider when making microbial mixes for bio-inoculations.
2. The genomic flexibility of *Verticillium dahliae* and what implications this has on its spread and virulence to Australian cotton. Can the studies of comparative genomics in this project be applied to the control of this pathogen in Australia?

**5. How do you intend to share the knowledge you have gained with other people in the cotton industry?**

The knowledge I have gained from attending this conference will be shared with people from the cotton industry when I attend the 2015 Australian cotton conference in Toowoomba later this year.

**6. Please list expenditure incurred. (Double click inside the table to enter the data)**

---

Please email your report 30 days after travel/conference to: [research@crdc.com.au](mailto:research@crdc.com.au)

**A novel method for rapidly isolating fungal suppressive microbes directly from soil**

Sarah Cooper<sup>a</sup>, Lily Pereg<sup>a</sup>

<sup>a</sup>School of Science and Technology, University of New England, Armidale, NSW 2351, Australia

Soilborne fungal root phytopathogens are some of the most damaging and difficult to control pathogens faced by agricultural production in the field, nurseries and greenhouses worldwide. There are many detrimental issues with current chemical control methods and this has increased interest in biological control using soil microorganisms that suppress the growth of phytopathogens. Antibiosis is one of the most important mechanisms responsible for fungal antagonism, with some significant antifungal compounds including, antibiotics, volatile organic compounds, hydrogen cyanide and lytic enzymes (Bhattacharyya & Jha, 2012; Compant *et al.*, 2005). Up to date methods for the isolation of fungal-suppressive microorganisms from the soil are time consuming and tedious. We have established a simple method for isolating fungal pathogen-suppressive microbes (bacteria and fungi) directly from the soil as well as procedures for confirmation of disease suppression. We will report on these methods, which were so far tested with three cotton fungal pathogens *Thielaviopsis basicola*, *Verticillium dahliae* and *Fusarium oxysporum* and a pathogen of button mushrooms *Verticillium fungicola*. We have isolated a diversity of *T. basicola*- suppressive fungi and bacteria from two vastly different soil types. Identification of the antagonistic isolates revealed that they are a diverse lot, some belonging to groups known to be suppressive of a wide range of fungal pathogens, endorsing the power of this technique to rapidly and directly isolate soil-borne microbes antagonistic to a wide variety of fungal pathogens.

**References:**

- Bhattacharyya, P. N., & Jha, D. K. (2012). Plant growth-promoting rhizobacteria (PGPR): emergence in agriculture. *World Journal of Microbiology and Biotechnology*, 28, 1327-1350.
- Compant, S., Duffy, B., Nowak, J., Clément, C., & Barka, E. A. (2005). Use of plant growth-promoting bacteria for biocontrol of plant diseases: principles, mechanisms of action, and future prospects. *Applied and Environmental Microbiology*, 71(9), 4951-4959.