

BSPP News



The Newsletter of the
British Society for Plant
Pathology

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Front cover: An *Oxycarenous lavaterae* colony on the trunk of a lime tree. Colonies can be made up of several thousand individuals (photo courtesy of Emily Seward - see page 8).

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BSPP 2015 prize winners



The winner of the **PH Gregory Prize** for the best presentation made by a young scientist was Fay Newbery (middle right) of the University of Reading, for her talk "Maintaining oilseed rape yield in a changing climate: modelling for a warmer future".

The winner of the **J Colhoun poster prize** for best poster was Kathryn Hales (pictured left) of the University of Warwick for her poster "Understanding the ecology and epidemiology of *Pythium violae* to enable disease management in carrot crops".

Also pictured is Xiaolei Jin (far right) who won the competition to design the next **BSPP T-Shirt**, as seen on the BSPP website.

Matt Dickinson has chosen his winner of the **2015 Best Student Paper** competition in *Plant Pathology*. The winner is Stuart Fraser of the University of Aberdeen, UK, for his paper 'Intraspecific variation in susceptibility to dothistroma needle blight within native Scottish *Pinus sylvestris*'. S. Fraser, A. V. Brown and S. Woodward, in volume 64, pages 864–870. Doi 10.1111/ppa.12320.
<http://onlinelibrary.wiley.com/doi/10.1111/ppa.12320/abstract>

Marty Dickman has awarded the **2015 BSPP Best Student Prize** in *Molecular Plant Pathology* to Damián Cambiagno of the National University of Cordoba, Argentina for his paper 'The synthetic cationic lipid diC14 activates a sector of the Arabidopsis defence network requiring endogenous signalling components'. D. A. Cambiagno, C. Lonz, J-M Ruysschaert and M. E. Alvarez in volume 16, pages 963–972. Doi 10.1111/mpp.12252.
<http://onlinelibrary.wiley.com/doi/10.1111/mpp.12252/abstract>

A reminder of some future meetings and conferences

2016

Plant, Pathogens and People. Challenges in Plant Pathology to benefit humankind

New Delhi, India, 23 to 27 Feb 2016

Tackling emerging fungal threats to animal health, food security and ecosystem resilience

London, UK, 07 to 08 Mar 2016

5th International Symposium on Fusarium Head Blight and the 2nd International Workshop on wheat blast

Florianópolis, Brazil, 06 to 10 Apr 2016

9th International Symposium on Septoria Diseases of Cereals

Paris, France, 07 to 09 Apr 2016

5th International Symposium on Tomato Diseases

Malaga, Spain, 13 to 16 Jun 2016

11th International Symposium on Adjuvants for Agrochemicals

Monterey, USA, 20 to 24 Jun 2016

6th International Bacterial Wilt Symposium

Toulouse, France, 03 to 07 Jul 2016

XVII International Congress on MPMI

Portland, USA, 17 to 21 Jul 2016

3rd International Spongospora Workshop

Einsiedeln, Switzerland, 18 to 21 Jul 2016

2016 APS Annual Meeting

Florida, USA, 30 Jul to 03 Aug 2016

The 32nd International Symposium of Nematology

Braga, Portugal, 28 Aug to 01 Sep 2016

APPS meeting: 9th Australasian Soilborne Diseases Symposium

Canterbury, New Zealand, 14 to 18 Nov 2016

2018

11th International Congress of Plant Pathology (ICPP2018)

Boston, USA, 29 July to 03 August 2018

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Request for images

Do you have some great images in your collection that you would be willing to contribute to a BSPP image gallery, primarily for use in the future development of educational resources by the Outreach team?

We are after are clear pictures of:

- **Disease symptoms** of plant diseases caused by a range of bacteria, viruses or fungi
- **Plant defence reactions** - macroscopic or microscopic - in response to attack by a range of bacteria, viruses or fungi

The described feature needs to be very obvious to an untrained eye and preferably a high-res version. Please include a simple sentence describing what is shown. You and your institution will be credited for donating the image.

Picture and captions should be sent to outreach@bspp.org.uk



A Pathologist's Crossword 5 Solution by Cryptogam

from the Summer 2015 issue

ACROSS: 1 *John Vanderplank*. 6 *Bill Fry*. 8 *Chris Lamb*. 9 *Johanna Westerdijk*. 13 *George Agrios*. 14 *John Rishbeth*. 17 *Jakob Eriksson*. 21 *Eugene Nester*. 23 *Nick Talbot*. 25 *Miles Berkeley*. 28 *Corné Pieterse*. 31 *Deborah Fravel*. 33 *Brian Staskawicz*. 37 *Dieter Haas*. 38 *Joseph Kuc*. 39 *Ben Cornelissen*.

DOWN: 1 *Voltage*. 2 *Namer*. 3 *Raw*. 4 *Laser*. 5. *Nye*. 6 *Fei*. 7 *Yak*. 10 *Debts*. 11 *Jat*. 12 *Boss*. 15 *Sonar*. 16 *Her*. 18 *Ria*. 19 *Sitar*. 20 *Nab*. 22 *Eve*. 23 *Tup*. 24 *Bites*. 26 *Kirk*. 27 *Yeltsin*. 29 *Iat*. 30 *Evian*. 32 *Vials*. 33 *Suk*. 34 *Arc*. 35 *Agó*. 36 *Zil*.



Are you able to help any of these future plant pathologists looking for work experience?

If so then please contact the BSPP outreach officer Phil Smith at outreach@bspp.org.uk

Masters student ex. Hungarian University seeking ANY work experience. London based

I am a Hungarian but currently I am living in London and working as a volunteer. I am a Plant pathologist, I graduated from the Corvinus University of Budapest, Faculty of Horticultural Science in 2013. I would like to find a job in the UK. I would feel honoured if you could give me any advice where to find a job, an internship or how could I gain some work experience. CV available.

2nd year undergraduate seeking year-long placement (for sandwich year)

I recently came across the "Careers in Plant Pathology" section of your website, and thought it would be worth contacting you regarding arranging a possible work placement. I am currently going into the second year of my biological sciences degree at the University of Exeter and I have a sandwich year as part of course, so would a year-long work placement be possible to arrange?

I attended the Gatsby Plant Science Summer School in June and it made clear to me that a career in research is what I should aspire to. Pathology has interested me for a long time and the summer school opened my eyes even further and gave me a better understanding about the latest research in plant science and how the research sector works. I am available for placement in the 2016/2017 academic year, and have some ideas for projects

2nd year undergraduate seeking year-long placement (during 3rd year)

I am currently studying biology at Sheffield Hallam University, and I am about to go into my second year. I am interested at looking for a year long placement for my third year, and I noticed that you were offering work experience. I am very interested in working with plants, especially the genetic modification of plants to improve food yield, and I have found it difficult to find placements directed at my interests. Would it be possible to have a year long placement between summer 2016 and summer 2017, and if so, what would it entail?

Year 12 student seeking 1 week work experience. Cheltenham Ladies College / home Buckinghamshire

I am a pupil at The Cheltenham Ladies' College, about to commence my A Level studies, taking biology, chemistry, physics, maths and AS further maths. I am seeking an exciting work placement with a plant pathology department this year or in the coming year. I would be free at any time, but would prefer a time between during the school holidays.

JUNIOR FELLOWSHIP REPORT

Discovery and characterisation of *Phytomonas* in the Czech Republic

Phytomonas are single-celled eukaryotic parasites found globally in a broad range of plant hosts. They are transmitted between plants by insect vectors of the order Heteroptera and are known to infect more than 100 plant species from 24 different families. However little is known of their biology, host range or evolutionary history. Importantly, limited sampling has been conducted outside of South America, where several species cause economically important plant pathologies. Though two species are pathogenic the remainder of *Phytomonas* appear to cause no deleterious effect on their plant hosts and the mechanism by which they avoid triggering plant immune responses is unknown. Moreover, as this group of parasites do not generally cause pathologies, they have been overlooked by the scientific community and it is unknown whether there are species present in the UK.

The BSPP junior fellowship allowed me to learn the techniques required for sampling and characterisation of *Phytomonas* from the wild. This was made possible by collaboration with the world experts in isolation, identification and culturing of *Phytomonas*, Professor Julius Lukeš, Dr. Jan Votýpka and Dr. Petr Kment.

The trip began with the 45th Annual Protistology meeting in Dubovice, about 2 hours south of Prague. There I presented my work on comparative ge-

nomics of South American *Phytomonas* species. This allowed me to gain valuable presentation experience and gather feedback from a range of scientists with expertise on parasitic organisms. I was awarded a prize for my talk and established useful connections with scientists who have complementary research areas and are interested in future collaborations.

Once the conference was concluded I made my way to Prague. There both Jan Votýpka and Petr Kment, the two scientists who coordinated the *Phytomonas* isolation expedition, met me and outlined the basis of our plan. We were to sample over a dozen sites in the southern region of the Czech Republic, primarily looking for the insect *Oxycarenus lavaterae* but also other Heteropteran insects, the known vectors of *Phytomonas*. This strategy of sampling from insects was adopted as

Sweep netting and searching for insects in the undergrowth



Phytomonas can colonise a large diversity of plant tissues (including phloem, latex ducts, fruit, flowers and seeds) and thus sampling the right tissue from plants in the wild can be difficult (*Phytomonas* eluded discovery until 1909). Moreover, by looking in the insect host, where *Phytomonas* parasites can reach high infection loads in the gut and salivary glands, it enabled a more rapid and high throughput identification of parasites.

Over the following week we sampled insects from a variety of habitats and locations in the southern regions of the Czech Republic. The most easily collected species was *Oxycarenus lavaterae* as it overwinters in colonies on the trunk of lime trees (*Tilia*) (see front cover image) though we also used sweep nets and quick reflexes to collect other insect species.

Once back in the lab we dissected the insects and determined if they had a *Phytomonas* infection using microscopic analysis of insect tissue. I quickly learnt the tricks associated with accurate dissection of the insect digestive tract and salivary glands and was delighted to find multiple instances of *Phytomonas* infections in both *Oxycarenus lavaterae* and *Tritomegas sexmaculatus*.

Not only were we able to successfully find a wild species of *Phytomonas* in the Czech Republic, the *Phytomonas* we discovered in *O. lavaterae* is a new species with a striking and unusual morphology (see image right) that is much more elongated than other *Phytomonas* species described so far. Furthermore, a phylogenetic tree using analysis of the small ribosomal subunit sequence indicates that the newly discovered *Phytomonas* species is basal to other currently described species. This has excit-

ing implications for improving our understanding of *Phytomonas* biology, particularly with respect to adaptation to different plant hosts.

Overall this was a highly successful trip. It not only led to the discovery of a new species of *Phytomonas*, but also taught me the skills that are necessary to apply this type of sampling to insects in the UK. By improving our understanding of *Phytomonas* biology I hope to uncover how this fascinating group of plant parasites thrive in such a diverse range of hosts without provoking plant immune responses. This work was only possible thanks to the BSPP junior fellowship and the help and expertise of the Lukeš and Votýpka labs.

Emily Seward
University of Oxford



GRACE WATERHOUSE FELLOWSHIP REPORT

A comparative genomic study of *Xanthomonas vasicola* strains of different hosts including an isolate from *Eucalyptus grandis*

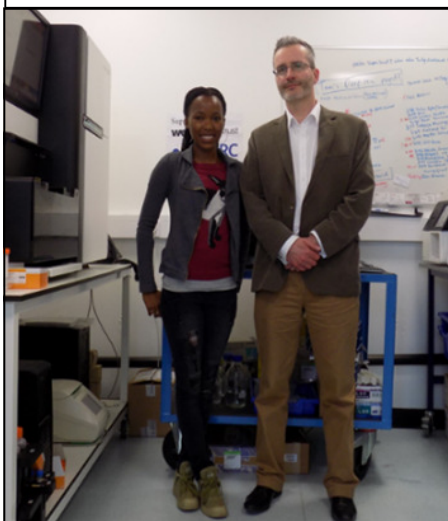
Xanthomonas is bacterial genus that belongs to the gamma division of the *Proteobacteria* family. All species in this genus are plant pathogens. One of them is *Xanthomonas vasicola* (Xv) which is a pathogen of various monocot plants, including Banana (Banana Xanthomonas wilt) which is currently threatening crops in East Africa. Recently a strain of Xv causing an outbreak of blight and dieback in *Eucalyptus grandis* was reported and this was the first time this pathogen was found to infect a dicot plant.

The genome of an Xv strain had been sequenced in Pretoria using the Illumina MiSeq platform. During my fellowship, I spent a month at the University of Exeter working with Dr David J Studholme, where I performed quality control, using TrimGalore and the FastX Toolkit and re-analysed the sequencing. Velvet and SPAdes genome assemblers were used. We thus managed to improve the genome assembly. A BWA alignment was undertaken in order to find genomic differences in the *E. grandis* isolate compared to other *X. vasicola* strains. The programme MUMmer was used to compare the assemblies and Harvest for the whole-genome phylogenetic analysis. From this data we observed that the isolate from *E. grandis* groups together with the sugarcane isolates. There was

a unique region that that was not found in any of the other *X. vasicola* strains, those from sugarcane, maize, banana and sorghum. Based on NCBI nt BLAST analysis 43% of this region matched with *X. campestris* pv. *vesicatoria* plasmid pXC183.

The skills I attained during my visit included learning to work within the Linux command line which can easily be extrapolated into various computational explorations. I feel that any further

Palesa and David in the lab at Exeter





Palesa and Jamie in the lab at Exeter

Exeter. As this was my first overseas trip, I valued the cultural experience in both Exeter and London. This was truly a once in a life time experience.

I would like thank everyone at the computational biology unit at the University of Exeter, with a special thanks to Jamie Harrison, and to Dr. David Studholme for giving his time to assist me and his patience teaching me new skills. Finally, I am truly grateful to the BSPP for giving me this opportunity to gain experience at the University of Exeter which has enhanced my genomic analysis skills.

analyses of next generation sequence data will be done more easily and with confidence. The skills I learnt will be shared with others in my Department at the University of Pretoria. I thoroughly enjoyed my visit to the University of

Palesa Madupe
University of Pretoria



BSPP Plant Pathology Promotion Fund

The BSPP wishes to promote an understanding and awareness of the importance of Plant Pathology to a wider audience than its membership. To that end it has established a fund for the Promotion of Plant Pathology. Applications for grants of up to a maximum of £2000 will be considered for projects that have as their aim the stimulation of interest in, and knowledge and awareness of, Plant Pathology to people who do not normally come into contact with the subject.

The projects can be parts of larger efforts for the promotion of the public understanding of science but should specifically address the role, function and activities of Plant Pathology. It is anticipated that central to any proposal will be the generation of resources/posters/displays and it is hoped that, where possible and appropriate, such resources should be made available to other members of the BSPP for similar promotional purposes. Application to the Fund is open to all members of the BSPP – see the website for more information.

MEETINGS REPORTS

Advances in Plant Virology Conference, Birmingham, UK 31st March - 2nd April 2015

Attending the Advances in Virology Conference with a travel grant from British Society for Plant Pathology (BSPP) was a great opportunity for me to have great insights into work that is being done in research on viruses and mechanisms that can be employed in the control of virus infections in plants and generate disease resistant plants. Talks mainly centred on understanding plant pathogen interactions between viruses and the hosts that they infect and how the relationships between the virus and the host subsequently determine if the plant is susceptible or resistant to the virus infection.

The gist of the conference is that it was organised in collaboration with the Society for General Microbiology 2015 annual general meeting and the sessions gave me the opportunity to attend a talk of the renowned scientist David Baulcombe who gave a talk on 'The small RNA link in antiviral defence'. David Baulcombe is the 2015 Society Prize medal winner. He discussed how RNA silencing was discovered and also discussed epigenetics and how epigenetic plants can be passed on to different generations of progeny plants.

More presentations centred on the best ways for breeding for plant resistance against viruses. Discussions were on identifying conserved proteins or regions in viruses as targets for plant resistance as this would allow the

development of plants that can be resistant to a broad spectrum of different strains of viruses.

In addition, there was an opportunity to have an audience with David Baulcombe who shared a personal experience on how to grow into a scientist in the current era and the challenges between being a scientist and developing a career in science. As a young upcoming scientist, I was inspired by this audience. Being a PhD student in my final year of study, I got a lot of insights on how I can plan my work and experiments in order to achieve results of the hypothesis that I set out to test.

Finally, on a very good note, I competed and won the student best poster award (Raymond/Roger Hull prize), the prize was the fifth edition of the Plant Virology text book written by Roger Hull. This book will help me so much as I prepare to write my final thesis.

I am really grateful for this opportunity to have received funding from the BSPP to attend and participate at the Advances in Plant Virology workshop.

Sarah Nanyiti
University of Bristol

The 25th International Conference on Arabidopsis Research, Vancouver, Canada 28th July - 2nd August 2014

I was fortunate enough to receive a generous grant from the BSPP to attend the International Congress of Arabidopsis Research (ICAR) last summer. The congress welcomed over 600 participants to the beautiful Chan Centre at the University of British Columbia (UBC) for five days of exciting science. ICAR is a broad meeting, covering many biological disciplines within the Arabidopsis community. I learned about new findings in fields not directly related to my own, as well as methods and technologies that have already informed and influenced my work.

Jeff Dangl (University of North Carolina) gave an excellent keynote lecture outlining research on plant-microbe interactions that has been the focus of his lab for the past 25 years. Peter McCourt (University of Toronto) delivered another great keynote on hormone signalling where he urged scientists to 'not give up on this little guy' - referring of course to the tiny Arabidopsis weed that was the focus of the meeting. I particularly enjoyed the plenary lecture by Sean Cutler (University of California) about agrichemical control of drought tolerance using engineered ABA receptors. Here he described engineering the flexible binding pocket of an ABA receptor to bind already available agrichemicals and improve plant yield. Plenaries by Joe Ecker (The Salk Institute) and Mark Estelle (University of California) stressed the importance of transcriptional waves in hormonal signalling pathways, and Keiko Torii (University of Washington)

gave a great talk about stomatal patterning.

At the concurrent session on *Modelling, Bioinformatics, and Systems Biology* I heard talks by Siobhan Brady (University of California), Ross Sozzani (North Carolina State University) and Sally Assmann (Penn State University) on different ways to use 'omics and high-throughput approaches to understand the complexity of plant growth and development. In the concurrent session on *Biotic Stress/Plant Defence* I learned about the most recent findings from Thorsten Nurnberger's (Univeristat Tubingen) group on a new class of microbial elicitors and their plant receptors. Yuelin Zhang (University of British Columbia) described a group of kinases that associate with the flagellin receptor FLS2 and are hyper-phosphorylated after microbial perception. In the section on *Signal Transduction and Integration*, Sorina Popescu (Boyce Thompson Institute for Plant Research) discussed using protein microarrays and network analysis to understand the plant immune response. During the poster sessions, many colleagues provided helpful feedback and ideas for future work, and I met with collaborators to discuss some of these future projects.

I also attended a few 'special interest' workshops. The first was on the new *Arabidopsis Information Portal* that was quite useful. Another was on *Small Molecules in Defence and Development*, where I heard from Clarice Souza (University of California) about

oligogalacturonide-induced immune signalling. Kate Warpeha (University of Illinois) discussed the role of phenylpropanoids in stress signalling. And finally, I also attended a workshop for *Early Career Researchers* focused on funding opportunities and academic job hunting, which I found very valuable.

The congress dinner was held at the stunning Museum of Anthropology, where we were offered a guided tour of

artefacts from all over the world. I found the Haida pieces the most interesting; in particular, Bill Reid's *The Raven and The First Men*.

In all, attending ICAR was a great experience. Thank-you so much for the travel grant!

Jacqueline Monaghan
The Sainsbury Laboratory

The 14th International Rapeseed Congress, Saskatoon, Canada 5th - 9th July 2015

The 14th International Rapeseed Congress brought together about 900 participants from more than 30 countries around the world. It is the most comprehensive forum for discussing advances, future opportunities and challenges in the rapeseed industry. The steering committee of the congress, co-chaired by Ag-West Bio and the Canola Council of Canada, put together a very comprehensive programme that included keynote sessions, plenary sessions and posters categorized under five main themes; Breeding, genetics and genomics; Crop protection, biotic stress, biology of canola pathogens; Seed chemistry, processing and utilisation; Crop production, abiotic stress, environmental impact; Economics, policies and trade. Also, there were workshops on specific topics such as phoma stem canker, the rhizosphere microbiome and seedling health, emerging technologies, etc.

Keynote sessions helped to give delegates a broader overview of the development of the brassica crop and the major areas of scientific improvement.

Keynote talks on the control of extracellular pathogens on oilseed rape (Prof Bruce Fitt, UK), blackleg resistance in oilseed rape (Dr. Regine Delourme, France) and sclerotinia stem rot management in oilseed brassicas (Prof. Martin Barbetti, Australia) helped to understand priority disease problems in different oilseed rape growing regions. I enjoyed the opening keynote talk by Dr. Keith Downey from Agriculture and Agri-Food Canada, who is known as one of the 'fathers of canola' after his involvement in the development of the first double low (low glucosinolate, low erucic acid) varieties of oilseed rape. His talk, titled 'Milestones on the road to the future', particularly focused on key stages in development of the crop and future prospects based on novel scientific knowledge. Dr. Isobel Parkin from Agriculture and Agri-Food Canada gave an interesting talk on 'The impact of genomics on brassica genetics and breeding - a sequence level view of the triangle of U'. Her presentation included the most recent advances in genome sequencing related to the triangle of U and discussed opportunities to incorpo-



Field visit to Bayer: A display of hybrid vigour in one of the hybrid production programmes

rate this information into further research on brassica genetics and genomics.

Dr. Boulos Chalhoub (INRA-URGV, France) presented their work on the sequencing of the *Brassica napus* genome. The allopolyploid *B. napus* genome has been identified as the most duplicated youngest genome sequenced, consisting of 101,040 gene models. It was stated that there is extensive cross-talk between the A and C genomes via homoeologous DNA exchanges, which is important for *B. napus* diversification. With an understanding of these processes, the *B. napus* genome sequence can be used as an important tool for crop improvement. Plenary sessions covered a broad range of topics under the five main themes of the conference. Incorporation of novel genetic and genomic approaches in to crop development has increased rapidly over the past few years and was featured in work presented by many researchers. As my research mainly focuses on oilseed rape genetics in relation to host resistance against *Pyrenopeziza brassicae*, I gained useful knowledge by attending the sessions on brassica genetic diversity, evolution/polyploid and emerging genetic technol-

ogies. Also, I enjoyed the parallel sessions on phoma stem canker host-pathogen interactions, identification and genetic mapping of disease QTL and genome wide association analysis (GWAS) of sclerotinia and clubroot genetics, which helped me to identify methods that were potentially applicable to my research work.

There was a considerable time allocation for networking activities on each day of the conference that allowed everyone to meet with research collaborators and also to build up new connections. It was very interesting that they held a networking reception at the Western Development Museum in Saskatoon, so we were able to experience the history of development in Western Canada while meeting with other researchers. During the poster reception, where I presented my research, I had useful discussions with various people, including researchers, post graduate students and plant breeders. It was fascinating that there was a substantial interest and involvement from the agricultural industries throughout the conference.

There was a pre-conference tour to Canadian light source (CLS) and the

POS Bio-Sciences. The CLS is one of the light source facilities around the world that use synchrotron light to analyse microstructures and chemical constituents of experimental samples. CLS has hosted a variety of research, including medical, environmental and agricultural research, archaeology and nuclear sciences. By visiting POS Bio-Sciences, I obtained a broader understanding about commercial production and purification of rapeseed oil.

The oilseed rape field visit, on the last day of the conference, provided me with the opportunity to experience oilseed rape cultivation in Canada and to see breeding programmes and cultivar testing done by various agricultural companies. The city of Saskatoon was renowned for its agricultural development and there is a history of over 6 decades of canola research, which made it an ideal venue for the conference. The city is built along the South Saskatchewan River, and owing to a number of bridges, the city is termed as the 'city of bridges'. I had the opportunity to visit the Agricultural Department of the University of Saskatchewan, which is over 100 years old, and to see their excellent research facilities.

Overall, the congress was a successful, well organised meeting and I would like to thank BSPP for their generous support that enabled me to attend this highly inspirational conference.

Chinthani K. Dewage
University of Hertfordshire

The conference was held at the TCU Place which had very good facilities. In the main conference hall, there was a very big screen with '14th International Rapeseed Congress' in a background of oilseed rape fields in flower. I have

been to many conferences and had never previously seen such a big screen which enabled the presentations to be seen from any corner of the conference hall. The opening ceremony was enhanced by local folk dancing. The performers were wearing traditional costumes and dancing according to the traditional 'first nation' drum music. This gave the participants a taste of the local 'first nation' culture.

It was a highly informative conference covering many aspects of oilseed rape research. The conference was split into five themes. I was interested in breeding and crop sessions which are related to my work and I attended the blackleg workshop, the disease I am working on, and obtained information on the latest blackleg research in other countries, especially Canada and Australia, where blackleg is a major disease problem on oilseed rape production.

I was delighted to see many Chinese colleagues and friends, and had discussions about collaboration on preventing the spread of the damaging pathogen *Leptosphaeria maculans* (phoma stem canker) into China. Importing into China a large amount of oilseed rape seeds from Canada and Australia, where *L. maculans* is present, increases the risk that *L. maculans* will spread into China.

I was impressed by the talks given by Gail Crockett and Mitchell Smith from US McDonald's Corporation. These talks demonstrated a good example of collaboration between McDonald and Cargill. Cargill's oilseed rape breeding programmes directly addresses the need of consumers through efficient delivery pipelines (e.g. breeding cultivars with special oil characteristics that directly supplied to contracted growers and oil processors, then oil directly supplied to

McDonald). Using the special oilseed rape oil, McDonald's can ensure that their restaurants provide consistent quality foods to customers. This is a good example of direct application of research results (e.g. special oil cultivar) to the end users (restaurant).

I attended the Crop Protection concurrent session. Having been working on phoma stem canker and monitoring virulent races of *L. maculans* populations in the UK, I enjoyed talks by Dr Regine Delourme (INRA-Rennes, France) on development of durable resistance for control of phoma stem canker, by Dr Marie-Hélène Balesdent (INRA-Bioger) on effector genes *AvrLm7* and *AvrLm3* evolution in French *L. maculans* populations, by Dr Kaveh Ghanbarnia (Canada) on comparative genomics to facilitate cloning of *L. maculans* effector gene *AvrLm2*. I have also attended talks on other oilseed rape diseases, such as stem rot (*Sclerotinia sclerotiorum*) and clubroot (*Plasmodiophora brassicae*), and some talks on phenotyping and disease resistance breeding.

The poster session was held in the evening section in a large hall where participants could move freely to view posters and talk to presenters. I was interested in the posters related to phoma stem canker. I was particularly attracted by two posters. One was presenting the recognition mechanism of *L. maculans* effector gene *AvrLm1* by the recently cloned resistance gene *LepR3* using the *Nicotiana benthamiana* model plant. The other one was presenting transcriptome profiles of Topas (susceptible) and near isogenic lines carrying different *R* genes (Topas-*LepR3* and Topas-*Rlm4*) in response to *L. maculans* infection. Having recently investigated effects of temperature on stability

of these two *R* genes, I had very useful discussion with the presenters on further investigation of mechanisms of temperature sensitivity of *R* gene-mediated resistance against *L. maculans*.

On the last day of the conference, there was an organised trip to visit field trials of oilseed rape companies, such as Bayer CropScience, Cargill, Monsanto and Dow AgroSciences. Big yellow patches were visible from airplane windows. It was very nice to see oilseed rape crops in flower in Canada. To prevent the spread of clubroot, everyone had to wear a pair of disposable boots before entering to the field. There were demonstration plots for different cultivars and information platforms, which were similar to those at Cereals' in the UK. After the conference, my colleagues and I visited Saskatoon Research Centre of Agriculture and Agri-Food Canada. Our visit was hosted by Dr Hossein Borhan whose group has cloned the first two *R* genes for resistance against *L. maculans*. We had discussions about collaboration and visited their facilities. I was impressed by their plant growth facilities and state-of-the-art lab equipment. With these good facilities, it is not surprising that they are the first to clone the *R* genes even through these *R* genes have been identified by other groups a long time ago.

I am very grateful to BSPP for the travel fund which enabled me to attend this conference. This not only gave me the opportunity to present our work, get up to date information about stem canker research in other countries and establish collaboration but also to experience Canadian culture.

Yongju Huang
University of Hertfordshire

The 9th International Conference on *Pseudomonas syringae* and related pathogens, Malaga, Spain 2nd - 5th June 2015

The International Conference on *Pseudomonas syringae* and related pathogens takes place every four years, with this year's conference hosted by Universidad de Málaga in Malaga, Spain. The conference took place over three days and the programme included 13 plenary talks by experts in different areas of research into species belonging to the *P. syringae* complex, as well as 30 shorter talks and a poster session where around 30 posters were displayed.

Of particular interest to me, was the session on Epidemiology and Disease Control. Dr Boris Vinatzer started off the session with a plenary talk introducing a possible novel system for classification and identification of pathogens using codes called Life Identification Numbers (LINs). LINs are unique numbers sequentially assigned to individual genome-sequenced organisms and are based on the level of sequence similarity between related organisms. The more related two strains, species or genera are the more similar their LIN numbers will be. Dr Vinatzer showed that the core genome phylogeny of species belonging to the *P. syringae* complex agrees with the LINs assigned to these strains. He indicated that the long term goal of this project is to assign a LIN number to every genome-sequenced organism, with the idea that this stable reference system could be applied to identification, epidemiology, taxonomy, biosecurity and plant/animal breeding certification.

Keeping with the theme of epidemiology, Dr Honour MaCann presented the evolution and population genomics of *P. syringae* pv. *actinidiae* (Psa). Kiwifruit has only been domesticated in the last 100 years and is native to China. Dr MaCann hypothesised that the Psa strain responsible for the most recent outbreak of bacterial canker of kiwi originated in China, and may have an ancestral association with wild kiwifruit. Sampling of symptomatic and non-symptomatic cultivated- and wild-kiwifruit was carried out in six provinces of China, and a selection of isolated Psa strains were genome sequenced. The phylogenetic analysis revealed that most strains were isolated from symptomatic cultivated kiwifruit and confirmed that the global outbreak of bacterial canker was caused by strains originating in China. The genomic population study also revealed that Psa strains have different effector complements, which are possibly new variants, and that there is an exchange of mobile genetic elements between pathogenic and non-pathogenic strains in the leaf niche. Future analysis of the data generated by Dr MaCann will surely reveal more about the evolutionary process of Psa.

Another talk I greatly enjoyed was given by Dr David Baltrus about phage-derived bacteriocins from *P. syringae* and their killing action against other *P. syringae* strains. A diverse range of *P. syringae* strains were assayed for killing action and the responsible bacteriocins were identified. Following deletion of

these bacteriocin genes in a model strain, the killing activity against other *P. syringae* strains continued. The genes responsible for the killing action were identified as a phage-derived bacteriocin locus. These produce phage tail proteins which target specific *P. syringae* pathovars. Dr Baltrus also found that it is possible to re-target the bacteriocin by inserting only two additional genes from the phage-derived locus of >20 genes. This exciting discovery provides a possible source of novel antimicrobials for use in agriculture.

Each day the sessions started at 9:00 am and ended at 7:00 pm, but even with a packed programme, there was ample time to enjoy the beautiful city of Malaga. A social event on the beach for the traditional football match was arranged one evening, with 'tinto con limon' and paella served afterwards. The final conference dinner was held at the Vinoteca El Patio de Beatas, a 'wine museum', where we were served typical Andalusian dishes and local wines. After three days of stimulating talks, the meeting was closed with the announcement that the next International Conference on *Pseudomonas syringae* and related pathogens will be held in Akureyri, Iceland in 2019. The organising committee at Universidad de Málaga are to be congratulated for an excellent, well-run and enjoyable conference.

Carrie Brady
University of the West of England

First of all, I want to thank the organisers and everyone involved for a fantastic meeting with a very interesting program, high calibre talks and a very engaging audience. I believe the intimacy of small conferences like this one makes these meetings even more valuable,

because it gives you ample opportunities to talk to fellow researchers, students or perhaps even the one person in this field that has inspired you to follow a particular path. I was really captivated by many of these talks and it is hard to pick out just a few. Here are some, in no particular order, that are relevant to my research:

Emilia López-Solanilla talked about how light perception influences the infection of a plant by phytopathogenic bacteria. She provided evidence that *Pto* swarming depends on light-intensity and quality, with white light exposure having an effect on flagellum synthesis. I particularly liked this talk because it showed me that as a researcher, one should remain open-minded and not forget about the big picture, e.g. in the case of pathogens, the influence of the environment on the plant-bacteria interaction.

David Guttman impressed with a comparative evolutionary genomics study of close to 400 whole genome sequences of different phylogroups of *P. syringae*, looking at compositional dynamics of the genome, host-associated genes and hot-spots of recombination and selection.

To me, Cindy Morris gave perhaps the most inspiring talk. I particularly like the way she drives her research in a direction that is important for agriculture. She is looking at ways of balancing the positive and negative effects of *P. syringae* in the environment by making use of the ice nucleation activity to influence rainfall, as droughts are becoming more and more of a problem for agriculture.

I was stoked to win the Best Poster Award for my poster entitled "The kiwifruit phyllosphere – a playground for



We also enjoyed a city tour of Malaga with a local guide and I was captured by the charm of the old town. One evening we were all carted to the beach, where most of us participated in the (quite rough) human Foosball event, (pictured above) which was great fun not only for the players, but also the audience.

P. syringae", with the gift being the book "Bacteria-Plant Interactions: Advanced Research and Future Trends".

Apart from the scientific side of things, let us not forget the social events, which make these meetings all the more fun! At the reception on the first evening we were treated to drinks and tapas on the terrace of the Universidad de Málaga with views of the Alcazaba.

Overall, it was a fantastic opportunity for me to mingle with specialists in *P. syringae* research and I came back with a lot more knowledge and a head full of new ideas. And finally – thank you, BSPP, for the travel grant, which heavily subsidised my travel costs and allowed me to attend this worthwhile conference.

Christina Straub
Massey University, New Zealand

The 6th Congress of European Microbiologist (FEMS 2015), Maastricht, The Netherlands 7th - 11th June 2015

International meetings such as the FEMS 2015 are unmissable dates on microbiologists' agendas. This year, the biannual Conference was celebrated in Maastricht - a lovely, history-rich and multicultural city in the south east of The Netherlands, but also the place where the Treaty, which finally led to the creation of the European Union, was signed in February 1992. This year's meeting attracted almost 2000 researchers from around the world and it was structured in 32 symposia, 21 workshops, 8 special events and 3 poster networking sessions. In total, there was an impressive collection of talks and posters which included more than 350 lectures and around 1600 posters.

Sessions of particular interest for BSPP members were those dedicated to plant-microbe interactions, cell polarity and virulence, horizontal gene transfer and evolution, fungal plant pathogens, cyclic di-nucleotides in bacteria, fungal-bacterial interactions, natural productions including secondary metabolites and the Type VI Secretion System.

The conference talks were opened with two plenary talks on Giant viruses and Human microbiome by Jean-Michel Claverie and Janet K. Jansson, respectively. The second day was kicked off by Pierre de Wit who gave an extraordinary plenary talk on the plant immune system and fungal effectors, but mainly

focussed on the co-evolution of the interaction between fungal pathogens and their plant host: an extraordinary battle for the survival.

Other remarkable highlights of the meeting are summarized below. Julia Vorholt described her current research on the isolation, characterisation and genome sequencing of phyllospheric bacteria. It was also great to have a general view on how phyllosphere bacteria change their gene expression profiles in this complex niche. Victor Carrion (in representation of Jos Raaijmakers) told us about the detection of metabolite production directly from live microbial colonies, as well as the production of sulphur-derivative volatile compounds by a plant-associated *Burkholderia* strain. The identified sulphur compounds resulted to show great potential to inhibit the growth of phytopathogenic fungi. Natalia Requena discussed the presence of effector proteins in mycorrhizal fungi, their similarities with those of plant pathogenic fungi and the importance of these effectors for establishing a successful symbiosis. Clay Fuqua gave a great talk on the regulation of the cell polarity in *Agrobacterium tumefaciens* and its implication in plant colonisation. Christoph Engl delved into the role of c-di-GMP in the virulence of *Pseudomonas syringae*, mainly through the characterisation of a novel dual function GGDEF/EAL protein. J. Allan Downie shed light to the implication of quorum sensing for nodule infection in *Rhizobium leguminosarum*. Rob Lavigne told us about how bacteriophage genes are expressed during bacterial infection and how this infection alters the metabolic profile of the host. It was also really exciting to attend Gabriel Waksman, Joseph Mougous, Eric Cascales and Marek Basler talks on structure and mechanisms of bacterial

secretion – one of the most covered topics during the FEMS 2015 conference.

In Masstricht, I also had the excellent opportunity of presenting my work on the isolation, characterisation and sequencing of generalised transducing bacteriophages infecting plant-associated bacteria – including biocontrol agents and phytopathogens belonging to *Serratia* and *Dickeya* genera. For this, I would sincerely like to thank BSPP for the very generous support provided to help my attendance at this fantastic conference; but also to allow me to come back to The Netherlands nine years after my stay in the Peter Bakkers' group in Utrecht (Plant-microbe Interactions, Faculty of Science).

Miguel A. Matilla
Spanish Research Council (EEZ-CSIC), Granada, Spain

I was offered the opportunity to present my poster entitled 'Characterising the virome of the entomopathogenic fungus *Beauveria bassiana*' in the 'Virome' poster session and to give a short overview of my work during the 'Virology' poster discussion session.

As a virologist, for me the highlight of FEMS 2015 was Professor Jean-Michel Claverie's plenary lecture on giant viruses isolated from marine protozoa. Unlike the tiny and minimalistic entities I am used to working with, these giant viruses consist of near micron-sized particles, contain double-stranded DNA genomes of more than 1 Mbp, comparable to that of a bacterium, and encode hundreds of proteins. However, only a small percentage *ca.* 10% of these putative open reading frames exhibit a



View from the Hoge Brug (Dutch for "high bridge") on the Meuse river, which divides Maastricht in two halves. Not a bad sight before arriving to the MECC Convention Center, the venue where the FEMS 2015 Conference was held

similarity to proteins of known functions. Interestingly, a large number of the viral gene products appear to be implicated in translation, a process necessary for the virus replication cycle but usually carried out using the host cell's machinery. Professor Claverie focused on the already renowned mimivirus together with two more recently discovered giant viruses designated as pandoravirus and pithovirus, the latter isolated from a layer of Siberian permafrost approximately 30,000 years old.

Additionally, I found particularly interesting Dr Philippe Marliere's presentation 'Accept no limit: why and how to restart chemical evolution in microorganisms' in the context of the 'High-throughput screening technologies' symposium. Dr Marliere described how a genetically engineered *Escherichia coli* strain unable to synthesise thymine was gradually adjusted to using 5-chlorouracil, a toxic chemical substance. Briefly, exposure of *E. coli* to sub-lethal concentrations of 5-chlorouracil under strictly controlled conditions provided an environment that favoured adaptive mutations which allowed the bacteria to

tolerate and use 5-chlorouracil instead of thymine. After 1000 *E. coli* generations and an ever-increasing ratio of 5-chlorouracil:thymine in the culture medium, bacteria capable to survive and proliferate solely using 5-chlorouracil were identified.

Since I have a partially medical background, Professor Janet Jansson's plenary lecture on the (human) microbiome also appealed to me. A number of high-throughput technologies are currently used in order to elucidate the composition and the function or the microbial communities in the gut and it was found that specific bacterial species, proteins and metabolites are associated with different types of inflammatory bowel disease (IBD). I was especially fascinated by a case study, a female patient suffering from severe IBD who did not respond to any of the conventional treatments. The patient exhibited an unusual profile of gut microbiome and was eventually cured when her husband's 'normal' gut microbiome was transferred to her by fecal transplantation.

In summary, attending FEMS 2015 gave me the opportunity to present my recent research findings to a wide audience, helped me expand my scientific horizons by exposing me to high-quality science quite different from my own and was a good opportunity for networking. I would like to express my gratitude to the BSPP for the financial support.

Ioly Kotta-Loizou
Imperial College London

My research focuses on identifying *Fg* effectors that are able to suppress wheat defence responses in fully susceptible cultivars infected by *Fg*. To test putative *Fg* effectors *in planta*, I use a *Barley Stripe mosaic virus*-mediated overexpression system. For this reason, the two sessions at FEMS entitled 'Fungal plant pathogens' and 'Fungal cell biology' were of great interest for me, covering recent topics on new effector discoveries, fungal sequencing, transport of peroxisomes and endosomes.

A workshop lecture given by Prof. Bart Thomma from Wageningen University entitled 'Pathogenomics of *Verticillium* wilt diseases' was very useful for my PhD. The main research subject of Prof. Thomma's lab is to understand fundamental processes in plant pathogenic fungi and oomycetes that occur in the rhizosphere, and the interactions with bacteria and their host plants. He showed that the avirulence gene *Ave1* in *V. dahliae* interacts with plant chitinases. This interaction was demonstrated *in vitro* and the mutant Δ *ave1* strain was unable to infect tomato. However, when a gene encoding chitinase in tomato plants was silenced, the mutant strain Δ *ave1* was able to infect the plant. In addition, he com-

pared two *V. dahliae* strains that were assembled (telomere-to-telomere) using long-read sequencing technology. Genomic rearrangements and structural variations were observed between these two strains. These variations could contribute to the evolution of virulence as these regions are enriched for *in planta*-expressed effector genes encoding secreted proteins. Based on his finding, it was hypothesised that evolution of *V. dahliae* is linked to segmental genome duplications mediated by improperly repaired DNA breaks.

Another talk which I found interesting was by Prof. Axel Brakhage from Leibniz Institute for Natural Product Research and Infection Biology entitled 'Pathogenicity and Immune Evasion of the Human-Pathogenic fungus *Aspergillus fumigatus*'. The study of virulence of *A. fumigatus* and Host-Pathogen Interactions is the one of the main topics in his lab. He demonstrated the main factors produced by the fungus to avoid recognition by resident macrophages. One is the hydrophobin protein RodA that masks essential molecular recognition patterns resulting in conidia being immunologically inert. Second, the conidia of *A. fumigatus* is covered by melanin DHN (dihydroxynaphthalene) and a strain with disruption of this gene showed attenuated virulence in a mouse infection model. It was also suggested that DHN inhibits the acidification step of phagolysosomes. *A. fumigatus* also produces a gliotoxin that has been shown to be important for virulence. Even though this talk was about human fungal pathogens, mechanisms of infection from plant and human fungal pathogens often overlap and similar approaches can be used to study both.

Prof. Gero Steinberg from University of Exeter talked about 'Molecular motors

in spatially organising the fungal cell wall'. His research aims to understand fungal pathogenicity and evolutionary conserved mechanisms of spatial organisation of eukaryotic cells. He had shown recently that in the pathogenic fungus *Ustilago maydis* early endosomes (EEs) have long-distance retrograde motility and this is necessary to trigger transcription of effector-encoding genes and secretion during host cell invasion. In his talk, he addressed the mechanism of peroxisome (PO) distribution in fungal cells. He shows that POs are evenly distributed in the cytoplasm. They show enhanced diffusion, which depends on the cyto-

skeleton. In addition, ~ 15% of POs move actively, which is driven by the motility of EEs.

I would like to thank BSPP by providing the opportunity to attend this event. Also, I would highly recommend the FEMS conference to anybody with an interest in advancing the understanding of current and future challenges in the study of microbiology and the next one will be held in Valencia, Spain in 2017!

Ana Karla Machado
Rothamsted Research



BSPP Fellowships

The BSPP runs three Fellowship schemes to support working visits by individual members to institutions other than their normal place of work for at least one month.

The **Senior Fellowship scheme** is open to anyone who has been a member of BSPP for at least two years and is intended to stimulate and facilitate studies or training to the benefit of plant pathology. Post-graduate student members may apply for **Junior Fellowships** where the aim is to encourage collaboration and interdisciplinary research, to enable students to acquire new techniques, and to make new contacts. Visits to laboratories in other countries are particularly encouraged. Any applicant must have been a member of BSPP for at least one year and be a post-graduate student at the time the Fellowship award is taken up. The **Grace Waterhouse Fellowship** has been set up to encourage links between the SASPP and the BSPP, with a particular focus on plant pathologists in the early stages of their careers. Members of the SASPP in the early stages of their career, studying in a southern African country, may apply for the Grace Waterhouse Fellowship to support a working visit of between one and three months to a laboratory in the UK.

Fellowships cover personal costs and a limited amount of research expenses. Members are strongly encouraged to apply and to take advantage of this generous scheme. Full details are on the web at <http://www.bspp.org.uk/funds/fellowships.php>.

UNDERGRADUATE VACATION BURSARY REPORTS

The effect of β -aminobutyric acid in the protection of tomato harvest against grey mould

During the summer of 2015 I carried out a project working under the supervision of Dr Estrella Luna-Diez. Her research focusses primarily on priming of the plant's immune system, whereby the defence response capacity of the plant is sensitised by specific signals, resulting in a faster and stronger upregulation of defence mechanisms upon subsequent attack. Non-biological agents can illicit priming. For example, β -aminobutyric acid (BABA) has been demonstrated to prime defence, making plants more resistant to a range of biotic stresses.

Grey mould (*Botrytis cinerea*) is a necrotrophic pathogen that infects green tissue of many plant species. However, it is also able to infect fruit, therefore representing a problem for growers of soft fruit, including tomatoes (*Solanum lycopersicum*). Due to its high spore production, mutations leading to fungicide resistance are common and subsequently many fungicides are incapable of controlling *B. cinerea*. Importantly, an experiment I carried out during my project showed that *B. cinerea* is able to grow at 4°C, thus indicating that the infection cannot be combatted by cold storage. As a result of these problems post-harvest losses in tomatoes can be up to 50%; therefore the possibility to control *B. cinerea* using BABA-induced resistance (IR) would be very useful. However thus far BABA has only been

shown to durably protect tomato green tissue. The aim of my project was to test whether BABA-IR persists until the fruiting stage and therefore protects tomato fruit post-harvest.

Micro-Tom tomatoes were grown in controlled environmental conditions. At the seedling stage (2 weeks old), plants were soil-drenched with either BABA or water. The plants were allowed to produce fruit and once they had matured and reddened, they were infected with *B. cinerea*. The subsequent results clearly demonstrated that the fruit from BABA-treated plants had smaller necrotic lesions and generally no disease progression. Therefore, BABA-IR is long-lasting and can persist to the fruiting stage, thus alleviating post-harvest losses.

In addition, I carried out a metabolomics analysis of the fruit. Firstly, metabolites were extracted from tomatoes of plants treated with either BABA or water. Then, samples were run through Ultra Performance Liquid Chromatography (UPLC)-qTOF mass spectrometer. The aims of this experiment were: to determine whether traces of BABA can be found in the tomatoes from BABA-treated plants, to analyse whether BABA alters beneficial agronomical characteristics in the fruit (such as carotenoid content) and to obtain a metabolomic fingerprint of the defence response.



Micro Tom tomatoes (*Solanum lycopersicum*) infected with Grey mould (*Botrytis cinerea*)

However due to the magnitude of the bioinformatics work required, the data analysis is currently being completed.

The studentship has allowed me to learn many techniques, which will be

invaluable for my future years of study. In addition the project has reinforced my interest in pursuing a career in research, specifically in the field of plant pathology. I am extremely grateful for the opportunity and also for the time and assistance my supervisor Dr Luna-Diez provided during the 8 weeks. Finally I would like to thank the BSPP as the money they kindly awarded allowed me to undertake this fantastic opportunity.

Samuel Wilkinson
The University of Sheffield

Molecular basis of potato immunity manipulation by *Phytophthora infestans*

The Late Blight causal oomycete *Phytophthora infestans* triggered the Irish Famine and continues to pose a threat to agriculture. It bypasses plant resistance genes due to its genome plasticity and possesses a plethora of effectors making it a powerful pathogen. PexRD54 is an RXLR effector which antagonises the activity of ATG8, a protein involved in host autophagy. This summer I was fortunate to work in Dr. Mark Banfield's Lab at the John Innes Centre. The Banfield Lab is interested in understanding the structure-function relationships of pathogen effectors and have been working on PexRD54 and ATG8 interactions for quite some time. The lab has solved the crystal structure of PexRD54, and a crystal structure of an ATG8 paralogue, ATG8c, bound to the ATG8 interacting motif (AIM) of PexRD54. These structures confirm that PexRD54 has an ATG8 interacting motif (AIM) located at its C-terminus. Previously, a student has characterised the

interaction of PexRD54 with ATG8c. There are different paralogues of ATG8 in potato and the aim of my project was to identify the key residues in the AIM which are essential for its binding to ATG8 paralogue ATG8x.

To determine the molecular basis of selectivity, the relevant proteins in the known interaction surface, and the selected mutants were expressed in *E.coli*, extracted and purified. The protein-protein interaction was studied *in vitro* using three techniques – Gel Filtration Chromatography (GFC), Peptide Array and Surface Plasmon Resonance (SPR).

Complexes of equal molar concentrations of wild type and mutant PexRD54 proteins with ATG8x were analysed by GFC. The fractions corresponding to protein peaks observed were collected and run on SDS-PAGE gels for verification. The GFC results showed weaker or no interaction only when the hydropho-

bic residues of the PexRD54-AIM motif were mutated to Alanine, indicating that these residues are important for binding to ATG8x. A peptide array of 200 AIM mutants (based on the sequence of the PexRD54 AIM) was then probed with ATG8x to elucidate the protein-protein interaction when each residue in the AIM was mutated to every other residue. The result of the peptide array confirmed that of GFC.

To quantitatively determine the interaction of the PexRD54 mutant proteins (specifically mutants in the hydrophobic residues) with ATG8x, SPR analysis was performed. ATG8x was captured on the chip and gradually increasing concentrations of its target proteins were flown over the chip. The sensorgrams obtained were used to determine the equilibrium dissociation constant (K_d) for the complexes. No binding was detected for the tryptophan mutant. The valine mutant had a K_d value significantly lower than that of the wild type RD54, confirming that a weaker interaction is observed.

I also assisted another project in the lab where we cloned DNA sequences encoding the several domains of two different rice blast resistance proteins in a vector, transformed them in *E. coli* cells and checked for protein expression levels in *E. coli*.

I would like to thank Dr. Mark Banfield for hosting me in his lab and Dr. Richard Hughes for his constant support, feedback and direction. Finally, I would like to thank the BSPP for awarding me the bursary. Working in the lab has been a challenging yet rewarding experience. Apart from learning molecular biology and advanced biochemical techniques, I gained a lot from discussions on the interpretation of results and ways to proceed further. This research experience has deepened my interest to work on plant molecular biology in the future.

Velin Marita Sequeira
VIT University, India

Genetic dissection of sulforaphane-mediated defence signalling in *Arabidopsis thaliana*

Sulforaphane, 1-Isothiocyano-4-methylsulfinylbutane, is a phytochemical that is found in cruciferous vegetables such as broccoli and kale. Well documented for its anti-carcinogenic properties in human studies, research is also focussing on its involvement in defence signalling in plants.

A recent study revealed that sulforaphane is released as part of the hypersensitive response (HR) in *A. thaliana* and it also induces cell death in naïve leaf tissue. When used as a pre-treatment on naïve *A. thaliana* leaf tis-

sue, it primes the plant for defence. When inoculated with the *Cala2* isolate of the oomycete *Hyaloperonospora arabidopsidis* (*Hpa*) post treatment, sporulation very much decreased compared to non-treatment. The *Hpa-Arabidopsis* pathogen model, which has been used for nearly 20 years, is incredibly important not only as a model to study host-pathogen interactions but also in translational research regarding important crops – *Arabidopsis* belongs to the Brassicaceae family, which also includes the aforementioned cruciferous vegetables.

Tissues treated with water, 400µl and 800µl sulforaphane had their total mRNA sequenced and differentially expressed genes were identified. The aim of this project is to determine the essential genes involved in the sulforaphane-mediated defence signalling pathway in *A. thaliana*.

Seeds of 14 different *A. thaliana* T-DNA mutants were sown in sets over a few weeks and grown under a 12/12 light cycle at 20°C with contamination controls in place. Once the seedlings were 10 days old, 25 of each accession were transplanted. Bioinformatics tools were used to find out the function and structure of each gene and oligonucleotides were designed for each gene. At 2 weeks old, the putative mutant line for each gene was tested for homozygosity. Tissue PCR was performed using Extract-N-Amp kit. Columbia wild-type and a no DNA control were routinely included in the experiment. Homozygous lines were transplanted to larger pots to be grown up for seeds. In order to examine the T-DNA insertion point, the gene needed to be amplified and sequenced. The Cetyltrimethylammonium Bromide (CTAB) protocol was used to extract DNA from homozygous lines. T-DNA inserts were amplified using a T-DNA and a gene specific primer. The PCR product was used for sequencing.

So far I have identified 13 homozygous lines of which the selected plants are being grown to obtain seeds for the next stage of the project. Bioinformatics analysis determined that these genes code for various heat shock proteins.

The next stages will involve the homozygous plants undergoing self-pollination for seed collection. The seeds will be sown as described before, along with pots of wild-type Columbia

and the susceptible *Arabidopsis* mutant *Ws eds1-1* randomly assorted in a tray, two of this setup for each accession. Seven day-old seedlings will be inoculated with the Col-0 compatible isolate *Hpa-Noks1* by spraying. These will be kept covered to maintain humidity and to avoid contamination. Fifteen seedlings from each of the trays will be examined for the number of sporophores on each cotyledon. The infection will be classified according to the number of sporophores; 1-10 being a light infection to 20 plus being a very high infection.

My project supervisor, Professor Mahmut Tör, has been a source of support and guidance throughout this project, along with Elena Fantozzi and Osman Telli and they all receive my warmest thanks. I would also like to say a big thank you to the BSPP for not only funding this project, but for allowing me to develop my skills as a plant pathologist and it has encouraged me to pursue postgraduate study. I have become much more confident in the laboratory environment as a result and I have very much enjoyed the project so far!

Lisa King
University of Worcester

The impact of different fungicide regimes on the development of fungicide resistance in *Botrytis cinerea*

Botrytis cinerea is a particularly virulent species of the genus with a broader range of potential hosts than many other members of its group. The overall area of work involves studying *B. cinerea* fungicide resistance in order to develop guideline strategies for fungicide use that could reduce resistance risk. A detached leaf assay had already been developed to study the frequency of fungicide resistance. The aim of the project was to further develop the detached leaf assay to facilitate the collection of useful data. The assay involved subjecting infected leaves, from 3 different plant species, to different Succinate Dehydrogenase Inhibitor fungicides (SDHI) and Quinone outside Inhibitor (QoI) fungicides. The data collected would be used to determine the effect of the different fungicides on around 100 *Botrytis* isolates, the frequency of resistance and to support the findings of a plate assay which was being carried out at the same time.

The work involved carrying out a detached leaf assay to determine the efficacy of six fungicide treatments. Tomato, bean and cucumber plants were grown until mature enough to bare appropriately sized leaves for the assay. Meanwhile agarose plates were prepared as a medium to inoculate the leaves. *B. cinerea* isolates were sub cultured onto multiple PDA plates containing streptomycin as an antibiotic. Plugs carrying the fungal hyphae were cut from the PDA plates and placed onto the cuticle of leaves of each plant species, six for each treatment: water (control), Boscalid, Cyprodinil, Fenhexamid, Fludioxonil, Iprodione and Pyraclo-

lostrobin. The tomatoes were kept in a growth cabinet at 20°C with 16 hours of light per day for 4 days and the beans were kept in the same conditions for 7 days.

To determine the level of control provided by each treatment, the average diameter of the lesions was recorded by taking two measurements perpendicular to one another, this produced twelve data points for each isolate, treatment and leaf type. Data was then analysed using a *t*-test to detect significant results between the control and each treatment, and ANOVA to determine if a particular treatment had an effect on the level of infection.

The initial tests did not show any of the treatments to be effective. Clearly this was not likely to be a true reflection of the resistance profile of the fungi. In order to overcome this, the fungicide concentration was increased from 1 part per million (ppm) to 5ppm to improve the odds of observing differences between fungicide treatments. Assays experimenting with alternative concentrations, 2ppm and 5 ppm, showed that 5ppm was the most effective for collecting meaningful results.

Overall the level of control offered by the fungicides was highly variable. The results from the twelve assays successfully completed, using bean leaves with 5ppm fungicide concentrations, suggested that Boscalid, Fludioxonil and Pyraclostrobin offered significant control most frequently. Boscalid was successful in four assays; Fludioxonil and Pyraclostrobin were successful in five. The

fungicide that frequently provided the least control was Iprodione with only one of the twelve showing significant prevention of infection. There were noticeable differences observed between the isolates, with some growing extremely aggressively and others showing no significant signs of infection on the leaf.

Whilst taking part in this period of research I have gained a valuable insight into the research world and had the opportunity to improve skills that apply both, specifically to a laboratory environment, and the workplace generally. Specific laboratory processes I have become familiar with include: the production of PDA plates, sub culturing *Botrytis* fungi, setting up and optimising assays as well as collecting and managing data. In addition I have been in-

involved with a number of meetings regarding the overall work that is being carried out on *Botrytis*. My involvement with the project has made me consider how I collaborate, communicate, manage projects and work with others. I have very much enjoyed this experience and will be able to use it inform my career decisions going forward.

I would like to thank my supervisor, Dr Ashleigh McKenzie, for her support during this project and giving me the opportunity to be involved in her research work. I'd also like to thank Jeanette Taylor for her technical support during this project and BSPP for financial support.

Marcus C Murray
SRUC Edinburgh

Conventional chemistries under threat: Can alternative chemistries complement a reduced fungicide programme?

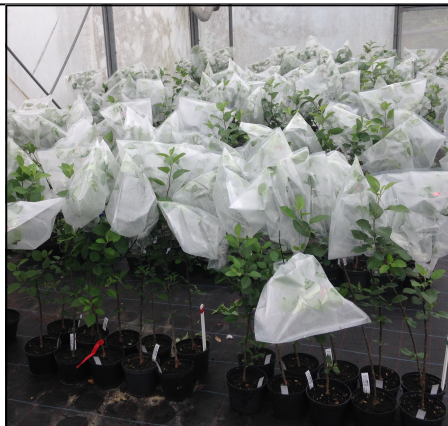
The foliar diseases apple scab, caused by *Venturia inaequalis*, and powdery mildew, caused by *Podosphaera leucotricha*, are 2 of the 3 most important pathogens of apples in the UK. In addition to the foliar symptoms reducing yield, both diseases can reduce fruit quality, making fruit unmarketable. Currently, control of these diseases is largely reliant on conventional fungicides, however new regulations will reduce the amount of fungicides available to growers, making it extremely difficult to achieve the level of disease control necessary to be a viable fruit grower. Alternative treatments are available on the market that have the potential to be integrated into reduced conventional fungicide

programmes e.g. compounds which elicit the plant's own defence, increase plant health or have a direct (physical or biological) mode of action on the pathogen. During my placement I conducted studies to evaluate the efficacy, persistence and systemic nature of a selection of these treatments. A field trial was conducted at East Malling Research (EMR) to evaluate the efficacy of alternative treatments for powdery mildew control as part of a reduced fungicide programme and compared to a current industry standard programme. A poly tunnel experiment using the apple-scab pathosystem was conducted alongside the field trial to investigate the persistence and systemic nature of

selected treatments (coded throughout this report for commercial sensitivity) which confer an elicitor effect and to understand how these treatments can be incorporated into a season-long programme.

The field trial was conducted in a mature orchard of cv. Gala with treatment plots arranged in a randomised block design with 4 replicates of 3-tree plots per treatment. Each treatment plot was separated by guard trees/rows. The trial relied upon natural infection. Treatments (which included the 2 elicitor treatments used in the poly tunnel trial) were applied at 7-10 day intervals throughout the season and compared to a reduced fungicide programme. Assessments of mildew incidence were recorded throughout the season to track the disease epidemic. Fruit set and chlorophyll content were also assessed to measure pleiotropic effects of treatments and fruit quality will be measured at harvest.

The poly tunnel trial was conducted on MM106 (scab susceptible) rootstocks. This trial was inoculated. The trees were sprayed to run-off with the treatments; 2 elicitor treatments, Systhane (positive control) and water (negative control). The rootstocks were treated 10, 7 and 3 days (second experiment only) 7 days or 3 days prior to inoculation. Field inoculum (collected from naturally infected leaves) of *V. inaequalis* was prepared (1×10^5 spores/ml) and 2ml was applied to the youngest leaves of actively extending shoots. The inoculated shoots were covered for 24 hours with bags to maintain humid conditions for the fungus to germinate and infect the leaves. An assessment was conducted once sporulating scab lesions became evident (experiment 1



Treated and inoculated rootstocks with extending shoots covered with bags

= 27 days post inoculation (dpi), experiment 2 = 18 dpi). The number of sporulating lesions on the upper and lower surfaces of the 3 youngest leaves at the time of inoculation was scored for each tree.

In the field trial the disease pressure was extremely high as conditions were conducive for the disease, inoculum built up on untreated guard trees and the host (cv. Gala) is a very susceptible variety. The 2 elicitor treatments performed poorly on their own in the field, probably due to the high disease pressure and moderately well when combined with a reduced fungicide programme but not as well as a full fungicide programme. Other alternatives did show promising results despite the high disease pressure. In both polytunnel trials infection was high, with an average of 2.52 and 7.21 lesions per leaf in experiment 1 and 2 respectively. Overall the fewest lesions were visible on Systhane-treated plants (with an average of 4.45 lesions per leaf), followed by the 2 elicitor treatments (4.65 and 6.21). Untreated

rootstocks had an average of 5.01 lesions per leaf. Systhane had the greatest systemic activity and persistence as the treatment had similar efficacy whether applied 7 or 3 days prior to inoculation and the number of lesions was reduced, relative to negative control, on leaves that were yet to emerge at the time of treatment. Both elicitor treatments had similar efficacy as water after 7 days. Elicitor A reduced the number of lesions significantly compared to untreated rootstocks at 3 days, suggesting localised/short term effects are achieved with this treatment. Elicitor B reduced lesions further after multiple applications, suggesting the effects of this treatment accrue over time. These findings will be important to consider

when advising growers on spray programmes.

I would like to thank BSPP for allowing me to undertake this fascinating project, which has greatly expanded my understanding of plant pathogens, which will be invaluable for me to pursue a career in plant pathology. I would also like to thank Dr Robert Saville for supervising and helping me through the placement and to Jennifer Kingsnorth and all the staff at EMR for all their teaching, support and outstanding warmth over the 10 week placement.

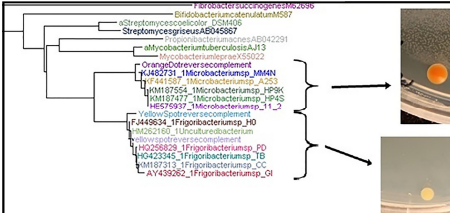
Michael Long
University of Reading

Naturally-occurring endosymbiotic bacteria in plant tissues - where and what are they, and what are the implications for plant pathogen genome sequencing?

This summer I spent ten weeks working at The James Hutton Institute. During my placement with Professor Lesley Torrance and Dr Alison Roberts, I worked to identify the bacteria that have been causing contamination of sterile *Spongospora subterranea* cultures. The lab has been working to sequence the genome of the *Spongospora* pathogen, but pure cultures have not yet been obtained due to microbial contamination. Despite experiments showing that the pathogen source is free from microbial contaminants, whenever *Spongospora* sporeballs are added to sterile plant tissue cultures for studies of the life cycle, the plants become infested with a range of microbial 'contaminants' which prevent isolation

of pure *Spongospora* zoospores and ultimately kill the plants. It is assumed that sterile plant tissue cultures are free of all microbes, but under simple light microscopy, what appear to be bacteria could be seen in the root hairs of potato plants that were grown under sterile conditions.

My studentship involved finding out more about the contaminant microorganisms and identifying them. A series of experiments were carried out to determine if the seed coat was the source of contamination, whether soaking the seed to reduce the depth of ridges in the seed coat would reduce contamination, and whether the method of surface sterilisation was effective. In summary,



Part of a phylogenetic tree containing the Actinobacteria where two of my samples were found to be microbacterium and frigoribacterium

because they were not cultured on the agar media so these results are only a snapshot of the endophyte communities present in 'sterile' tissue culture.

To enable more of these endophytes to be cultured on agar media some research has suggested the addition of plant tissue to the media. This was investigated in two different ways. Firstly, roots from several sterile tissue potato and barley plants were crushed and plated out on various media, half of these plates contained only the crushed root liquid and the others also included additional plant root tissue. In another experiment plant tissue extract was added to the agar medium used to culture the organisms. Neither experiment increased the microbial culture efficiency or diversity of organisms that were cultured.

surface sterilisation was complete and the coat is not the source of contamination. Even seeds which had their coats removed and dissected embryos gave rise to plants which contained microbial contaminants. At the point we discovered all tissues, at all stages contained microbes, we decided to refer to them as endosymbionts instead of contaminants!

The next aim was to try to isolate, culture and identify the endosymbionts, which was done by crushing roots from each plant and plating them out on several different media (V8, YEB, TSA and Pea Broth). Once microbial colonies could be seen, a loop of each bacteria was removed and added to a one step DNA extraction kit, in order for the DNA to be amplified using PCR. PCR was completed using 16s primers and then sent to the sequencing lab. The sequencing results were then run through a BLAST search and aligned to create a phylogenetic tree. This experiment found that the endosymbionts cultured were from four main phyla including Actinobacteria, Bacilli, Betaproteobacteria and Alphaproteobacteria and a number of these have known benefits to the host plant such as nitrogen fixation and are confirmed plant endosymbionts. However there is likely to be a large number of bacteria that were not sequenced

This summer studentship has allowed me to improve my skills in PCR, sterile tissue culture, microscopy, general microbiology and sequencing, which will be a great benefit during my honours project in my final year at university and in the future. I would like to thank the BSPP for their generosity in funding this project, Lesley Torrance and Alison Roberts for all their advice and supervision and everyone in the lab who encouraged and helped me complete this project.

Beatrix Clark
University of Edinburgh

Investigating a potential link between take-all disease progression and root system phenotypes in two important elite winter wheat cultivars

Take-all root disease in wheat can be responsible for > 50% yield loss, posing challenges for future food security. Take-all is caused by the ascomycete fungus *Gaeumannomyces graminis* var. *tritici* (*Ggt*) which infects roots penetrating the inner cortex and preventing flow of water and nutrients. The fungus has little impact on first wheat yields because during this period take-all inoculum builds in the rhizosphere but is not highly infective. Without rotation subsequent wheat crops suffer from the accumulated soil inoculum resulting in higher levels of root infection. By a fifth wheat rotation, changes in soil microbiota mean *Ggt* is outcompeted causing a decline in disease. When grown as first wheats, cultivars differ in the amount of take-all inoculum which accumulates in the rhizosphere. A cultivar with low accumulation of inoculum is referred to as a LowTAB (low take-all build-up) cultivar. My project focussed on comparing a LowTAB cultivar to a HighTAB (high take-all build-up) cultivar in order to understand their root architecture phenotypes and its potential contribution to the LowTAB trait.

Field trials on the Rothamsted Research Farm in Hertfordshire, UK were used to assess take-all build-up using a soil core bioassay method. Monthly soil cores were taken from a first wheat site and baited with seeds of wheat cultivar Hereward (highly susceptible to take-all). After 5 weeks in a controlled environment seedlings were visually assessed for take-all lesions. Infection levels in pot bioassay seedlings have

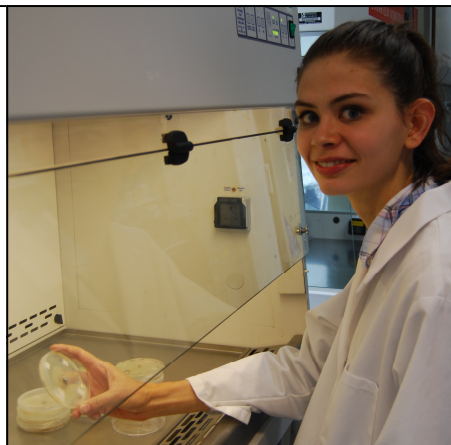
been proven to correlate well with levels of take-all that occur if second wheat is sown. In 2015, in the field site selected the LowTAB trait behaved differently to expected, with similar levels of take-all build up between the LowTAB and HighTAB cultivars ($p = 0.364$). This is likely to result from overall low levels of inoculum accumulating in the soil (in LowTAB 6.8% roots infected in bioassay compared to 6.1% in HighTAB).

To investigate root architecture I assessed roots from whole plant samples. To achieve this I utilised both a first wheat and a third wheat field trial, with a higher take-all infection level expected in the third wheat. Comparing current commercial cultivars in these trials revealed no significant difference in the susceptibility to take-all or total number of crown and seminal roots. However, we found a significant difference (two-way ANOVA, $p < 0.05$) in root dry mass with mass lower in the LowTAB cultivar for samples taken for April, May and June. In light of these findings one key question arose: What is the cause of the lower dry mass? To answer this we examined root architecture in more detail, focusing on the June sample, as a previous BSPP Summer Student, Joseph Earley in 2014, also found a significant difference in dry root mass at this time. To deepen our study we used a WinRHIZO scanner. The analysis showed no difference in root length or diameter between cultivars. However, there was a significant interaction effect between rotation position and cultivar in one of the other parameters measured.

Due to the low level of take-all build-up the correlation of differences in root architecture found with the LowTAB trait would be unreliable.

At Rothamsted Research, under guidance from Joseph Moughan, I designed my own experiment to understand the role of root exudates in take-all infection. The experiment consisted of an agar filled petri-dish centrally inoculated with one of four *Ggt* isolates, then measurements of the average growth of hyphae from the central inoculum towards the four equidistant squares of filter paper. One piece of filter paper on each plate was infiltrated with: water, take-all active fungicide, LowTAB cultivar root exudates and HighTAB root exudates. The results of the experiment showed significantly reduced hyphal growth towards the fungicide and significantly increased towards the water relative to the other four treatments. There was no significant difference between growth of hyphae towards the two cultivars.

My summer studentship has challenged me to question further the causes of food insecurity. Whilst also providing me with an understanding of new tools, techniques and approaches, namely experimental design, disease assess-



Erin checking take-all isolate growth in a root exudate chemotaxis assay

ment, statistical analysis, culturing and linking laboratory and field methodologies. Such skills will help in my endeavour to answer questions on improving food security in my pursuit of a PhD. I would like to thank Rothamsted Research, specifically Dr Vanessa McMillan, Prof. Kim Hammond-Kosack and Joseph Moughan for his day-to-day supervision.

Erin Baggs
University of Bath

Modelling the distributions of pests and pathogens in China

An estimated 30-40% of attainable crop yield is lost annually to pests and pathogens. Under current scenarios of future climate change, crop losses due to pests will become even more severe. In order to secure future food security we need tools that will allow accurate modelling of the geographic distributions of pests over space and time.

Studies have shown that pest occurrence is correlated with economic factors such as international trade, and physical factors such as host availability. At Exeter University, Dan Bebbler and colleagues have developed a predictive model of pest occurrence that incorporates many of these factors. The model uses data from the Plantwise

Knowledge Bank of CAB International (www.cabi.org), currently the most complete database of crop pest occurrence data worldwide.

China is the world's second largest economy and Chinese crops and their pests will play a key role in future food security. Currently, however, when the model is run for China, it is unable to accurately predict pest distributions. Several pests thought to be absent based on the CABI database nevertheless have high predicted probabilities from the model. Likewise, there are many pests that are known to be present, but for which the model predicts low probability of occurrence. My question as a BSPP summer student at Exeter University was: why is the model unable to produce better predictions for China, and how can we make the model better?

A major problem is that the model is calibrated using an incomplete database. Chinese efforts to monitor crop pests are extensive, but most Chinese publications are inaccessible to the international community, being published only in Chinese. Thus, there is likely to be a large amount of distribution data for China that is absent from the CABI database. We believe that it is this knowledge gap that prevents us from modelling pest distributions in China more accurately.

To explore the extent of this knowledge gap, I took 100 randomised predictions from the model, all for pests currently thought to be absent, and used these to search the Chinese literature for pest presence data. This work was carried out with three Chinese PhD students from the Kunming Institute of Botany (KIB). The aim was to see how many of these pests would turn out to be actual-

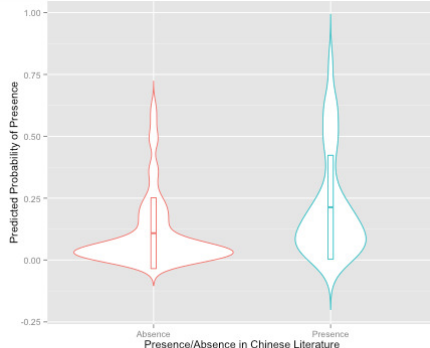


Figure 1: Summary of our findings when 100 predictions from a model of pest occurrence were tested against the Chinese literature to estimate actual presence/absence. Violin plots show the probability distribution of data points, with box plots in the centre showing lower quartile, median, and upper quartile. The reason why most pests had very low predicted probabilities was because we used a randomised sample of those pests already thought to be absent based on the CABI Plantwise Knowledge Bank.

ly present based on the literature, and to compare this with their probability of occurrence from the model.

The model had some successes in predicting pest occurrence: pests that were present in the literature had a slightly higher median probability than those found to be absent from the literature (see violin plot in figure 1). A logistic regression revealed that probability of pest occurrence was a significant factor in predicting pest presence/absence. The relationship is not hugely significant, however. This could be for several reasons: 1) as suspected, the model is currently limited by lack of distribution data, 2) sample size remained small ($n=100$); 3) we lacked the ability to quantify true pest absence – a pest was simply assumed to be absent if we didn't find it in our searches; 4) the literature itself is incomplete; 5) there are other factors missing from the model. Lack of true absence data is a recognised hindrance in the development of accurate species distribution models and this prevented us from testing the model as rigorously as possible.

My study confirms that China is a “black hole” for the international scientific community working on pest and pathogen distributions. Although in some cases the model was able to accurately predict pest occurrences, there is still a long way to go. Our work reiterates the importance of true absence data in accurate species distribution modelling. This study has initiated a future collaboration between Exeter and KIB, who will attempt more literature searches to test the model.

Many thanks to Professor Sarah Gurr and Dr Dan Bebber at the University of

Exeter, and to Dr Peter Mortimer at KIB, for their guidance and supervision. A special thanks to Gui Heng, PhD student at KIB, and his team Ye Lei and Hui Li, who all worked extremely hard on the data mining. And a huge thanks to Dr Kate LeCocq, for travelling with me to China! Thank you to BSPP for giving me this opportunity to develop my skills as a scientist, and to gain an insight into one of the most interesting and rapidly developing areas in plant pathology.

Elsa Field
University of Oxford

Identifying direct protein-protein interactions between barley powdery mildew effectors and components of cereal Receptor-Like Kinases required for non-host resistance in wheat and barley

Blumeria graminis is an obligate biotrophic fungus causing powdery mildew in a number of economically significant cereals. Sequencing of the *B. graminis* f.sp. *hordei* genome revealed a comparatively large percentage of protein coding genes are members of the candidate secreted effector protein (CSEP) family. Host-Induced Gene Silencing studies revealed that some members of this family have significant roles in haustoria formation in infected epidermis. My placement was part of a larger study in the laboratory of Professor Pietro Spanu, which aims to outline if these effectors physically interact with with Pathogen Recognition Receptors, specifically Receptor-Like Kinases (RLKs), using yeast two-hybrid screening.

Under the supervisor of Dr Joe Yu my overall aim was to generate Mav203

transformants, containing a pDEST32 bait vector with one of seven RLKs and a plasmid library of ~500 CSEP prey. These could then be screened on Sc-Leu-Trp-His+3AT+X-gal plates to investigate protein-protein interactions (PPIs). One limitation of this system is poor MaV203 transformation efficiency. In order to optimise this, the standard protocol was amended to investigate a number of variables. Firstly, modified YAPD medium and cell plating density were investigated for single transformation. Competent MaV203 cells were incubated with modified YAPD medium prior to heat shock, and then plated to varying densities on single drop out plates. After 3-4 days incubation, colony number was counted to estimate transformation efficiency. Significantly improved transformation efficiencies were obtained from these optimised

conditions, with highest values at 1.08×10^7 CFU/(mg plasmid DNA $\times 10^8$ cells).

Similar experimental conditions were then repeated, with the additional variables of cycloheximide (added to the transformation mix prior to heat shock) and heat shock temperature. Addition of cycloheximide and higher heat shock temperatures did not significantly improve transformation efficiency. Using these optimised conditions, heat shock time and concentration of bait/prey plasmids were investigated for co-transformation with two plasmids. Again, significantly improved transformation efficiencies were obtained, with highest values as 1.11×10^6 CFU/(mg plasmid DNA $\times 10^8$ cells).

In order to establish if bait plasmids had been successfully transformed into MaV203 a standard miniprep protocol was followed for plasmid extraction, which could then be sent for identification by sequencing. Results were initially poor, with low quality and quantity of DNA, and were not sufficient for sequencing. To overcome this, we transformed the extracted plasmids into *E. coli* for amplification. This allowed for successful sequencing of the 7 RLK baits. Transformations of the prey li-

brary were also completed and interactions screened for on Sc-Leu-Trp-His+3AT+X-gal plates. Unfortunately, there was not sufficient time to evaluate these results, however once potential interactions have been indicated by the blue-white screen this can be further investigated with other techniques such as split YFP.

This was my first experience working in a professional research environment, and I feel it has given me invaluable insight into a research career. This placement has given me the opportunity to learn new techniques and protocols, such as isolation of plasmid DNA from yeast, and to further understand the key factors involved in experimental design. I thoroughly enjoyed working in the lab at the forefront of research on plant pathology, and I hope the results I obtained will contribute to further research in this project. I would like to pay many thanks to Professor Pietro Spanu and Dr Joe Yu for providing me with this opportunity, I am immensely grateful to BSPP for providing the support to make this placement possible.

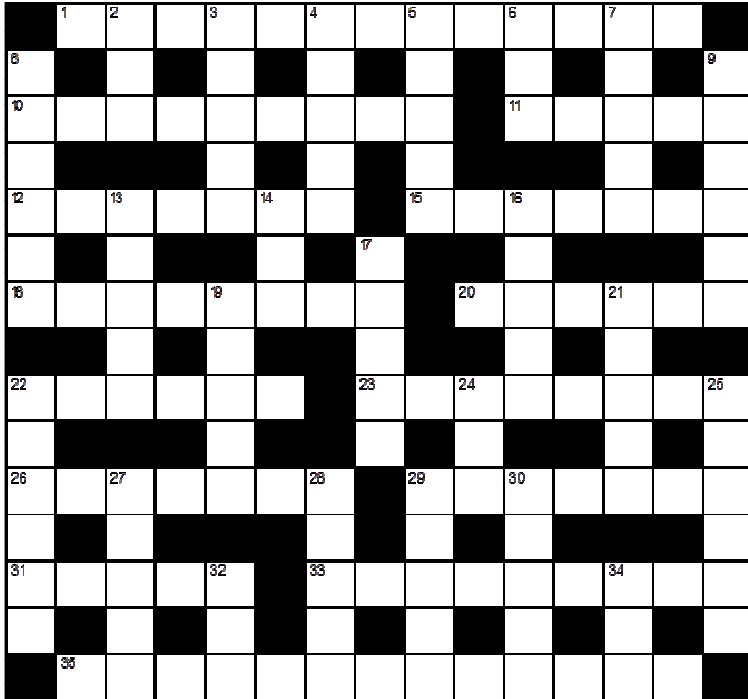
Emily Read
Imperial College London



- | | |
|--|---|
| from Typhoon Ursula (7) | (8) |
| 15 Sip tea and give it a stir (7) | 26 Topless sycamore near building (7) |
| 18 Bohemian composer takes first place (8) | 29 Romeo cut from Shakespearean scene (7) |
| 20 Covered up in whitewash by auditor (6) | 31 Revealed by Caliph Omar (5) |
| 22 Cryptogam is in disrepute (6) | 33 Wickedness received by applause (9) |
| 23 Pointless speculation ends in Iowa | 35 Gloomy novices in distress (13) |

A Pathogen's Crossword 6 by Cryptogam

Across solutions are genera of plant pathogenic fungi. The clues have a word-play part only and no further definition. Down clues are normal cryptic clues and aren't obviously relevant to plant pathology.



Across

- 1 Call and call again for finding in forensic trial (13)
- 10 A cosy chat will sort it out (9)
- 11 Heard you rode but took a tumble (5)
- 12 Our son, though injured, escaped from Typhoon Ursula (7)
- 15 Sip tea and give it a stir (7)
- 18 Bohemian composer takes first place (8)
- 20 Covered up in whitewash by auditor (6)
- 22 Cryptogam is in disrepute (6)
- 23 Pointless speculation ends in Iowa

(8)

- 26 Topless sycamore near building (7)
- 29 Romeo cut from Shakespearean scene (7)
- 31 Revealed by Caliph Omar (5)
- 33 Wickedness received by applause (9)
- 35 Gloomy novices in distress (13)

Down

- 1 Call and call again for finding in forensic trial (13)
- 10 A cosy chat will sort it out (9)
- 11 Heard you rode but took a tumble (5)
- 12 Our son, though injured, escaped

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