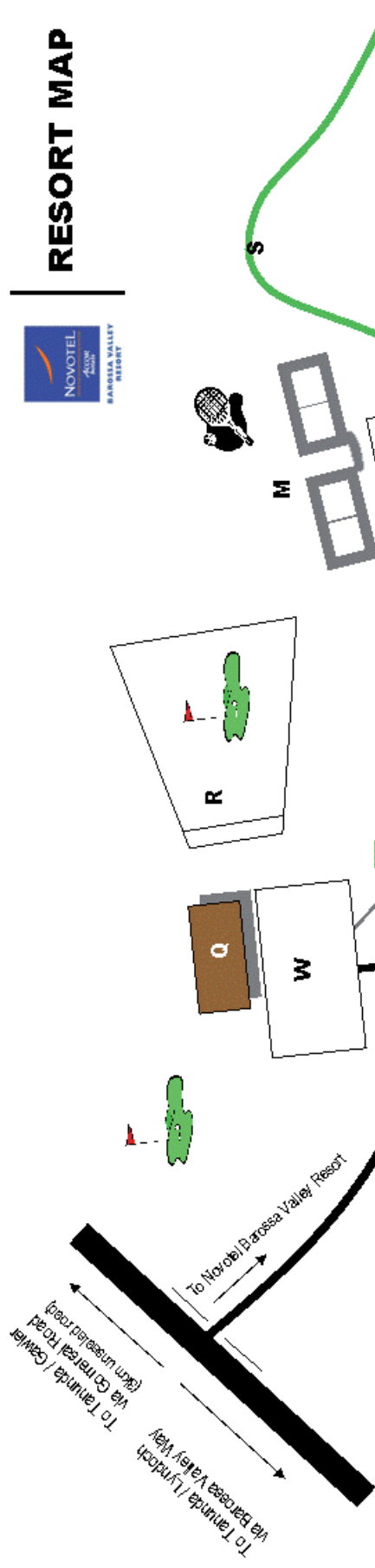


science exchange

2011





first floor rooms – 101 to 170
second floor rooms – 201 to 270

A. Reception	B. Conference Centre	C. Gramps bar	D. Harrys Restaurant
E. Gym	F. BBQ Area	G. endota day spa	H. Pool Bar
I. Pool	J. Volley Ball, Bocce, Badminton	K. Giant Chess Set	L. Car Park
M. Tennis Courts	N. The Baumè Room	O. Half Basket Ball Court	P. Archery
Q. Golf Clubhouse	R. Golf Driving Range	S. Running/walking track	T. North Para River
U.To Jacobs Creek	V.The Tasting Room	W.Golf Club Car Park	



Welcome

On behalf of the Cooperative Research Centre for National Plant Biosecurity, we would like to welcome you to the 2011 Science Exchange.

After six successful years in operation, we continue to grow and the Science Exchange provides us with a wonderful opportunity to get together to meet a range of representatives working in the same field.

The 2011 Science Exchange – which will run over two-and-a-half days – will provide you with the opportunity to take in a series of presentations, attend meetings, take in interactive displays and view a range of posters, while also giving us a chance to mingle and discuss projects with other colleagues at a range of functions.

The topics on the conference program include communication and capacity, biology and ecology, pest identification, tools for detection and diagnostics, sampling design and analysis, eradication and control, predicting incursions and spread, and decision making, which we hope will provide you with a diverse look at a range of plant biosecurity issues.

Like the 2009 Science Exchange, we will be holding poster sessions on the Wednesday afternoon and Thursday morning, where we encourage you to view your peers work and vote for the 'People's Choice Award', which will be announced at the Science Exchange Awards Dinner on the Thursday evening.

While on the subject of the Science Exchange Awards Dinner, we are looking forward to enjoying some of the local produce at a beautiful local winery, catching up with colleagues and finding out who will win the Science Committee awards.

The awards will honour achievements covering collaboration, innovation, impact on industry and excellence. These awards play an important role in recognising the time and effort project teams devote to ensuring the sustainability of Australia's plant industries.

Finally, we would like to reiterate our welcome. We hope you find the 2011 Science Exchange an interesting and informative event while also experiencing the sights and flavours of the Barossa Valley.

A handwritten signature in dark ink, appearing to read "John Lovett".

Professor John Lovett
Chairman

A handwritten signature in dark ink, appearing to read "Simon McKirdy".

Dr Simon McKirdy
Chief Executive Officer



Wednesday 9 February 2011 (Shiraz Rooms)

Session 1: Communication and Capacity - Chair Martin Barlass			Page
8.30am – 9.00am	Welcome	John Lovett and Simon McKirdy	
9.00am – 9.15am	Improving knowledge exchange in the grains industry	Sharyn Taylor	7
9.15am – 9.30am	Detecting and reporting high priority pests in the Western Australian grains industry	Nichole Hammond (PhD Student)	8
9.30am – 9.45am	Biosecurity through community engagement	Paul Royce (PhD Student)	9
9.45am – 10.00am	Biosecurity governance: negotiating citrus biosecurity with local governments and communities in West Timor, Indonesia	Wayan Mudita (PhD Student)	10
10.00am – 10.15am	Building sustainable Indigenous biosecurity management workforces in northern Australia	Ruth Wallace	11
10.15am – 10.30am	The National Postgraduate Curriculum in Plant Biosecurity	Glynn Maynard	12
10.30am – 11.00am	Morning Tea		
Session 2: Genetics, Biology and Ecology - Chair Shane Hetherington			
11.00am – 11.15am	Identification of effectors in <i>Venturia inaequalis</i>	Daniel Jones (PhD Student)	14
11.15am – 11.30am	Wheat stripe rust infecting barley grass, is there cause for concern?	Jordan Bailey (PhD Student)	15
11.30am – 11.45am	Mechanisms of phosphine toxicity and resistance	David Schlipalius	16
11.45am – 12.00pm	The role of native plants during an insect incursion: survival and development of glassy-winged sharpshooter (<i>Homalodisca vitripennis</i>) on Australian native plant species	Anna Rathe (PhD Student)	17
12.00pm – 12.15pm	Insights into the spatiotemporal dynamics of <i>Tribolium castaneu</i> across an ecological landscape gained through trap data and population genetics	Greg Daglish	18
12.15pm – 12.30pm	Individual-based modelling of phosphine resistance in lesser grain borer (<i>Rhyzopertha dominica</i>)	Mingren Shi (PhD Student)	19
12.30pm – 1.15pm	Lunch		
Session 3: Pest Identification - Chair Mike Cole			
1.15pm – 1.30pm	The pan-genome of <i>E. amylovora</i> provides insights into host specificity and better diagnostic design	Rachel Powney (PhD Student)	21
1.30pm – 1.45pm	The impact of taxonomy: How a successful invasive species could achieve world heritage list protection by changing its name	Bobbie Hitchcock (PhD Student)	22
1.45pm – 2.00pm	Recombinant antibodies for immunodetection of banana viruses	Jenny Vo (PhD Student)	23
2.00pm – 2.15pm	Getting to know the locals: A systematic revision of the Australian macropsine leafhoppers	Linda Semeraro (PhD Student)	24
2.15pm – 2.30pm	Resolving the <i>Bactrocera dorsalis</i> complex	Tony Clarke	25
2.30pm – 2.45pm	A diagnostic framework to identify nematode pests for plant biosecurity using novel molecular techniques	Matthew Tan (PhD Student)	26
2.45pm – 3.00pm	National trapping program for <i>Trogoderma</i> and related Dermestids	Oonagh Byrne	27

3.00pm – 4.30pm	Afternoon Tea and Poster Session 1 (Cabernet Rooms)		Page
Communication and Capacity			
Poster 1	Effective international, national, and local policy frameworks for biosecurity	Theo Litaay (PhD Student)	29
Genetics, Biology and Ecology			
Poster 2	Ecological research for pre-harvest control of Queensland fruit fly as part of systems approach – an overview	Solomon Balagawi	30
Poster 3	The South African Citrus Thrips (<i>Scirtothrips aurantii</i>) in Queensland is highly polyphagous, and does not show strong preferences for its only recorded host in the field	Brian Garms (PhD Student)	31
Poster 4	Retention time of infectious potato spindle tuber viroid (PSTVd) on common surfaces	Alison Mackie (PhD Student)	32
Poster 5	Presence of pathogenicity genes in <i>Fusarium oxysporum f.sp. cubense</i>	Rachel Meldrum (PhD Student)	33
Poster 6	<i>Bactrocera tryoni</i> adult preference and larval performance on five citrus varieties	Sakuntala Muthuthantri (PhD Student)	34
Poster 7	Life outside the silo: stored grain pest ecology in the Riverina	Mark Stevens	35
Pest Identification and Tools for Detection and Diagnostics			
Poster 8	Investigating the receptors involved in chemical communication for the pest beetle <i>Tribolium castaneum</i>	Kelly Bailey	36
Poster 9	New recombinant antibodies for virus detection	Paul Campbell	37
Poster 10	Dermestidae species differentiated using a novel approach to quantitative PCR	Mark Castalanelli (PhD Student)	38
Poster 11	Systematics of the <i>Ustilago</i> , <i>Sporisorium</i> and <i>Macalpinomyces</i> complex of smut fungi	Andrew Geering on behalf of Alistair McTaggart (PhD Student)	39
Poster 12	Performance analysis of flying spores detection system for plant biosecurity management	Felipe Gonzalez	40
Poster 13	The description of three novel species of <i>Phytophthora</i> from native vegetation in Western Australia	Giles Hardy on behalf of Alex Rea (PhD Student)	41
Poster 14	A learning method for emergency plant pest detection on hyperspectral image	Pattaraporn Khuwuthyakorn (PhD Student)	42
5.30pm – 7.15pm	Pre-dinner drinks and special function (Volleyball lawn)		
7.15pm – 10.15pm	Dinner: MC John Sandow (Shiraz Rooms)		

Thursday 10 February 2011 (Shiraz Rooms)

Session 4: Tools for Detection and Diagnostics - Chair Rohan Rainbow			Page
8.30am – 8.45am	Evaluation of novel platforms for their ability to identify new biomarkers for bacterial pathogens	Deb Hailstones	44
8.45am – 9.00am	New technologies for the detection and monitoring of begomoviruses and their whitefly vectors	Sharon Van Brunschot (PhD Student)	45
9.00am – 9.15am	Project review: the development of new diagnostic platforms to assist post entry quarantine plant pathology laboratories	Linda Zheng	46
9.15am – 9.30am	Sniffing out grain infestations with the Red Flour Beetle, <i>Tribolium castaneum</i>	Bradley Stevenson	47
9.30am – 9.45am	Development of a smart spore trap	Les Zeller	48
9.45am – 10.00am	Using CSI methods to detect fungal spores on clothing	Dominie Wright	49
10.00am – 10.15am	Digital tools for diagnostics	Gary Kong	50
10.15am – 11.45am	Morning Tea and Poster Session (Cabernet Rooms)		
Predicting Incursions and Spread			
Poster 15	A review of the climate change implications for the pest status and vectoring potential of the bird cherry-oat aphid, <i>Rhopalosiphum padi</i>	Kyla Finlay	52
Poster 16	A simulation technology approach to <i>Bactocera spp</i> : lessons from a past incursion for improving future responses	Juan Jose Garcia Adeva	53
Poster 17	Modelling the 1996 lupin anthracnose incursion in Western Australia	Michael Renton	54
Poster 18	Can mechanistically parameterised, anisotropic dispersal kernels provide a reliable estimate of wind-assisted dispersal?	David Savage (PhD Student)	55
Poster 19	The impact of elevated CO ₂ on Barley yellow dwarf virus and its aphid vector <i>Rhopalosiphum padi</i>	Jo Luck on behalf of Piotr Trebicki	56
Poster 20	Invasion genetics of Russian wheat aphid, <i>Diuraphis noxia</i> , in Western China and worldwide	Bo Zhang (PhD Student)	57
Sampling Design and Analysis			
Poster 21	Trapping to prove area freedom	Shirani Poogoda on behalf of Francis de Lima	58
Poster 22	Bayesian statistics for biosecurity	Samantha Low Choy	59
Poster 23	Estimating time-varying components of Qfly dispersal in the benefit-cost analysis of a monitoring system	Rohan Sadler	60
Poster 24	Evaluating surveillance and control in benefit-cost analysis of area-wide management	Ben White	61
Poster 25	Sampling irrigation water for plant pathogens - coherently working together or organised chaos?	Rebecca Zappia (PhD student)	62
Eradication and Control			
Poster 26	Strong phosphine resistance eradication in Western Australia	Michelle Chami	63
Poster 27	Numerical study of wind induced pressure fluctuations on grain storage bunkers	Wei He	64
Poster 28	Ensuring grain storage structural integrity for grain biosecurity	YongLin Ren	65
Poster 29	Fate of phosphine in grains	YongLin Ren	66
Poster 30	Contingency plans for exotic pests of grain	Jo Slattery	67
Poster 31	Widening the toolkit: developing biosecurity solutions from chemical ecology	Max Suckling	68

Session 5: Sampling Design and Analysis - Chair Phil Clamp			Page
11.45am – 12.00pm	Sampling within heterogeneous systems: choosing the right model	David Elmoultie	70
12.00pm – 12.15pm	'Alluring appeal' - evaluation and development of female fruit fly lures for improved market access	Katina Lindhout	71
12.15pm – 12.30pm	Evidence for area freedom: prospects for Bayesian modelling in plant biosecurity	Mark Stanaway (PhD Student)	72
12.30pm – 12.45pm	The statistical analysis of rare events	Susan Barrett	73
12.45pm – 1.30pm	Lunch		
Session 6: Eradication and Control - Chair Kathy Ophel-Keller			
1.30pm – 1.45pm	Eradication of black rot from vineyards using a drastic pruning protocol	Mark Sosnowski	75
1.45pm – 2.00pm	Achieving successful impact management of invasive plant pests using sterile insect release and mating disruption	Bill Woods	76
2.00pm – 2.15pm	Alternative to phosphine – nitrogen storage	YongLin Ren	77
2.15pm – 2.30pm	Three-dimensional computational fluid dynamics model for forced convective flow in grain storages	Ming Zhao	78
2.30pm – 2.45pm	Development of a fumigant monitoring system for stored grain	Paul Kamel	79
2.45pm – 3.00pm	Afternoon Tea		
3.00pm – 5.00pm	Project meetings Participants Committee meeting (Cabernet Rooms)		
5.30pm	Buses depart for dinner		
6.00pm – 7.00pm	Pre-dinner drinks and wine tasting (Offsite)		
7.00pm – 11.00pm	Science Exchange Awards Dinner (Offsite)		

Friday 11 February 2011 (Shiraz Rooms)

Session 7: Predicting Incursions and Spread - Chair Rod Turner			
8.30am – 8.45am	Targeting detection and risk assessment capability for exotic plant parasitic nematodes	Sunil Singh (PhD Student)	81
8.45am – 9.00am	Meta modelling of biological invasion for rapid response	Michael Renton	82
9.00am – 9.15am	Using TOPS to identify host hot spots for rust incursion management: Lessons learnt	John Weiss (PhD Student)	83
9.15am – 9.30am	Factors affecting the dispersal of fungal pathogens: Chickpea ascochyta blight as a model	Steven Coventry (PhD Student)	84
9.30am – 9.45am	Sudden Eucalypt death? Australian native plant susceptibility to <i>Phytophthora ramorum</i> , and its potential global distribution	Kylie Ireland (PhD Student)	85
9.45am – 10.00am	Climate change, biosecurity and migratory insect pests: Integrating population dynamics with 'over the horizon' invasion ecology	Hazel Parry	86
10.00am – 10.15am	The CUBAn Crisis: The story of how prophet can triumph over evil	David Cook	87
10.15am – 10.45am	Morning Tea		
Session 8: Decision Making - Chair Shashi Sharma			
10.45am – 11.00am	AQIS Operational Science Program and R&D challenges for CRC	Mark Whattam	89
11.00am – 11.15am	Biosecurity risk assessment systems: an international comparison	Kerrie Mengersen	90
11.15am – 11.30am	Economic analysis of surveillance and quality assurance as strategies to maintain grain market access	Hoda Abougamos (PhD Student)	91
11.30am – 11.45am	Towards a new framework for the appraisal of R&D investments to safeguard biosecurity within pest management systems	Veronique Florec	92
11.45am – 12.00pm	Science Exchange Close	John Lovett	
12.00pm – 12.15pm	Prepare for departure. Packed lunch will be provided to delegates		
12.15pm	First buses depart for Adelaide airport (Delegates will be advised which flights need to take this bus)		
12.45pm	Final buses depart for Adelaide airport		

Communication and Capacity

Chair: Martin Barlass



Improving knowledge exchange in the grains industry

Sharyn Taylor^{1,2}, Jo Slattery^{1,2} and Terry Rose¹

¹Plant Health Australia, ²Cooperative Research Centre for National Plant Biosecurity

In many regions of Australia, the fumigant phosphine is central to the management of pests of stored grain as it has the combined attributes of being cheap, effective for most commodities, compatible with grain handling logistics and accepted by most international and domestic markets as being residue free. In the past 15 years, insect resistance to phosphine has increased in both frequency and strength such that it now threatens its continued use and, as a result, its role as a tool for maintaining market access. This increase in insect resistance is thought to occur as a result of use of phosphine in poorly sealed storage facilities, and/or at incorrect rates or application methods, resulting in doses of the fumigant which do not kill all stages of insects.

This project assessed the stakeholders within the supply chain that will be impacted by or contribute to the development of phosphine resistance and ways that information exchange occurs within the grains industry. It found that while the issue of phosphine resistance is significant for many different stakeholders, parts of the grains supply chain continue to use phosphine incorrectly for a number of reasons. These reasons included confusion over the information being delivered, lack of incentives to use phosphine correctly or disincentives to deter its use incorrectly, and a need for information to come from a trusted source.

The project investigated potential methods for information delivery and exchange to improve the use of phosphine and ensure uptake of messages through identification of trusted sources to 'seed' information exchange and identification of drivers that encourage best practice in use of phosphine. To achieve this, the project contributed to funding for Grains Biosecurity Officers appointed across Australia, whose role in developing and delivering awareness material will encourage best practice of phosphine use for controlling insects of stored grain.

About the author:

Dr Sharyn Taylor joined Plant Health Australia as a Program Manager in February 2007. In this role Sharyn is responsible for managing biosecurity planning and implementation projects including Industry Biosecurity Plan development and review, development of Farm Biosecurity Manuals and the National Plant Surveillance Reporting Tool. Dr Taylor is also responsible for identifying and leading specific biosecurity risk mitigation projects for government and industry including the Grains Farm Biosecurity Program, development of Contingency Plans for exotic pests and methods for capturing surveillance data.

*Dr Taylor was previously employed at SARDI as a Senior Research Scientist and has 16 years experience as a Nematologist working in dryland cropping systems in southern Australia. In 2000, she completed a PhD on root lesion nematodes (*Pratylenchus* spp.) in broad acre agriculture in South Australia and has published several journal articles in this field.*

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Detecting and reporting high priority pests in the Western Australian grains industry

Nichole Hammond^{1,2,3}

¹ Cooperative Research Centre for National Plant Biosecurity, ² School of Veterinary and Biomedical Sciences, Murdoch University, ³ Department of Agriculture and Food, Western Australia

Passive surveillance activities are an important part of early detection and demonstrating area freedom for high priority pests (HPPs). Passive surveillance uses data that has been generated for other purposes and often includes reports of suspect cases to the authorities. This information can be collected from many sources such as, from National and Regional Plant Protection Organisations, government agencies, universities and research institutions, scientific societies, diagnostic laboratories, producers, consultants, museums, published literature, unpublished data and reports from the public.

Much of the data available from passive surveillance in the WA grains industry is collected through reports of endemic and unusual plant pests and diseases. Many of these reports are obtained from samples sent to diagnostic services and reports made to the Department of Agriculture and Food, WA (DAFWA) by growers, agricultural consultants and researchers. Reporting systems and diagnostic laboratories routinely produce absence data that are not quantified. These systems have the potential to provide a lot of information that could form part of a surveillance system and aid in demonstrating freedom from HPPs.

A cross-sectional survey of members of the grains industry in WA was performed using both random and opportunistic sampling. One hundred and forty-five growers, agricultural consultants, researchers and other people working within the grains industry responded to the survey. The questionnaire considered knowledge of advisory services, factors that influence reporting of suspect HPPs reporting of past plant pest and disease problems, the likelihood of detecting specific HPPs in grain or crops and actions that would be taken if a specific HPP was detected.

This is the first study of this kind in the WA grains industry. Information from the survey was analysed and provides insight into areas that could be improved to increase the likelihood that a suspect HPP is detected and reported. The information gathered from the survey was also used to inform a quantitative evaluation of this component of the passive surveillance system operating within WA for detection of HPPs in the grains industry.

About the author:

When Nichole Hammond started her PhD in January 2007 she was the CRC's first female PhD student. Her PhD thesis is titled 'Evaluation of emergency plant pathogen surveillance systems and surveillance methods'.

*The PhD continued her studies at Murdoch University where she successfully completed a Bachelor of Science in Biotechnology and an Honours project (Biological Sciences) on the characterisation of *Rhizoctonia solani* isolates collected from potato crops in Western Australia using anastomosis groupings, pectic isozyme groupings and polymorphism of the ITS region of the rDNA.*

Prior to starting her PhD Nichole worked for the Western Australian Department of Agriculture and Food in a number of biosecurity related fields within the plant pathology section, including diagnostics, surveillance, pest risk analysis and plant health policy.

Since completing her PhD Nichole has returned to the Western Australian Department of Agriculture and Food as a Research Officer within the Plant Biosecurity group.

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Biosecurity through community engagement

Paul Royce^{1,2,3}

¹OrdGuard, ²Charles Darwin University, ³Cooperative Research Centre for National Plant Biosecurity

At present, biosecurity information is informed by quantitative, scientific experimentation and provided to communities by centralised agencies in structured, partisan and one way mediums. While the availability and provision of factual, accurate and current material is important to reducing the risks of biological incursions, such a process does not allow for a two-way dialogue in which local people have the opportunity to ask questions, put forward their own opinions, challenge other viewpoints, share their experiences and learn from the experiences of others. As a result, the opportunity to build an understanding of biosecurity is limited to the written material provided by external agencies, which offers people a very narrow field to determine whether biosecurity information is correct, relevant and meaningful to an individual and the community in which they live. Similarly, such a process does not allow for the mutual development of trusting, respectful and reciprocal relations, which are central to the effective exchange of information, because the only interface between local people and biosecurity agencies is the brochures, websites or road signs they provide.

While there is no question that considerable and quality work is being undertaken by government agencies, local growers and industry bodies to address issues of biosecurity in Australia, the methods used to engage with communities and exchange relevant information does not encourage an increase in biosecurity interest or participation outside the agricultural sector. Unfortunately, biosecurity proponents still maintain the assumption that information provision equals social change; the greater the volume of information, the greater the probability that people will adopt biosecurity knowledge, which will in turn bring about a change in biosecurity attitudes, practice and behaviour. However, this study found that people will not take up biosecurity information and translate it into new knowledge and social change unless the perceived net result of this information is likely to impact on them personally or more specifically, the lifestyle and livelihood they currently or will potentially lead. This presentation will therefore examine the likely methods used by individuals to access information that is of personal interest or importance, how individuals gather this information, where this information is gathered from, the volume of information an individual is likely to gather and the credibility attached to the information they are provided with. Effective community engagement processes and initiatives will also be introduced in order to offer up new ways of increasing broad community awareness and participation in biosecurity practice.

About the author:

Born into a farming family in the mid-west region of WA, Paul travelled to many destinations around Australia and the world before returning to Perth to complete a Bachelor of Social Science (Youth Work) at Edith Cowan University. With 18 years experience in the community services sector, Paul has held a number of grass roots and senior management positions in the areas of social and community planning, programme development and service delivery, primarily to support Indigenous and non-Indigenous young people and their families.

In early 2005, a move to the Northern Territory enabled Paul to take up a lecturing position in youth and community services at Charles Darwin University while also completing a Masters in International and Community Development at Deakin University. In late 2005, Paul was offered a CRCNPB scholarship to study the implications of applying community engagement principals to biosecurity strategies in the Ord River irrigation region around Kununurra, WA. It is expected that the research findings from this PhD will assist to bring about a change in biosecurity attitudes, practice and behaviour in the immediate and broader community, which will reduce the risk of biological incursions occurring in the region.

Since July 2010, Paul has worked for the Department of Child Protection and with his partner, live on a four acre property on the Ord River growing mangoes, grapefruit and limes.

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Biosecurity governance: negotiating citrus biosecurity with local governments and communities in West Timor, Indonesia

I Wayan Mudita^{1,2}

¹Charles Darwin University, ²Cooperative Research Centre for National Plant Biosecurity

Citrus was once a widely cultivated crop in West Timor, Indonesia, but has been severely declining during the last decade. Despite growing evidence that *huanglongbing* (HLB), previously known as citrus greening, is the primary cause of the decline, local governments remain afraid that officially acknowledging the disease will harm all efforts that have been made to promote the local mandarin cultivar. On the other hand, because of the lack of access to information sources beyond their village boundaries, the majority of community members have not heard about the disease.

This paper describes the outcomes of mixed qualitative and quantitative research methods to negotiate official acknowledgment of HLB existence by local governments in order to promote public communication about the disease with local communities. For the purpose of providing a sound basis for negotiation, interviews were carried out with community members and government officials to understand how members of local communities interact between themselves and with local governments.

To provide rigorous evidence that HLB is the primary cause of citrus decline, citrus specimens were sent to a highly reputable university for PCR (Polymerase Chain Reaction) tests, and collaboration was sought with the local office of the national quarantine agency for the necessary institutional and legal supports. Results suggest that, while local communities consider citrus cultivation as a mean of strengthening ties with their relatives and fellow villagers, local governments view it as an opportunity for implementing an intensification programme by replacing the means of citrus propagation from previously using seeds into using grafted seedlings without properly communicating the risk of disseminating graft-transmissible diseases. The negotiation that was carried out to explain the possibility of this risk by presenting evidence from the PCR tests has received mixed responses. The provincial and the TTU (Timor Tengah Utara or North Central Timor) district governments did not oppose the moves, but the TTS (Timor Tengah Selatan or South Central Timor) government refused all evidence of the disease unless the evidence is provided by an institution under its official authorization.

Regardless of these mixed responses, however, the publication of this negotiation process by local newspapers has raised awareness among growers that to better manage biosecurity risk requires not only measures that could effectively control the disease but also policy that seeks better cooperation among all concerned stakeholders. This raised awareness has helped citrus growers to be more active in seeking information regarding the disease and its management beyond their village boundaries, thereby improving bridging ties with fellow growers from outside their villages and linking ties with universities and other research institutions. It is these ties, and the reciprocity bound up with them, that are expected to put more pressure on local governments to engage in better biosecurity governance in assessing, managing, and communicating risks posed by HLB to the citrus industry in the region and beyond.

About the author:

Mr Mudita is currently a PhD student at Charles Darwin University, Darwin, NT, Australia, with support from Cooperative Research Centre for National Plant Biosecurity. His research is focused on encouraging better cooperation between local governments and communities in managing citrus biosecurity against *huanglongbing* (HLB), of which presence in West Timor, Indonesia, is currently not yet officially recognized by local governments in the region. He joined Nusa Cendana University, Kupang, East Nusa Tenggara Province, in 1986 as assistant lecturer after obtaining his undergraduate degree from Mataram University, Mataram, West Nusa Tenggara Province. He promoted to be a full lecturer after obtaining his master degree in plant disease management from Macdonald Campus of McGill University, Montreal, Canada, in 1991. Since then he has been a full lecturer in the same university with teaching and research responsibilities in the area of crop protection and environmental management. His interest in community management of biosecurity has developed since he joined a research project led by Prof. Ian Falk who is now his principal supervisor.

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Building sustainable Indigenous biosecurity management workforces in Northern Australia

Ruth Wallace^{1,2}

¹Charles Darwin University, ²Cooperative Research Centre for National Plant Biosecurity

The expanse of Northern Australia provides a challenge for plant biosecurity authorities in the region and relevant industries. The potential of Indigenous based enterprise development to support sustainable biosecurity management strategies and activities across Northern Australia. These enterprises participate in surveillance, management and education activities related to biosecurity, the decisions Indigenous people make about their land and economic development also have significant implications for biosecurity management. Indigenous biosecurity related enterprises may be directly employed in biosecurity management or have their cultural and economic business impacted by biosecurity incursions. The core issues have been explored through a CRCNPB study.

This presentation discusses some examples of enterprise structures and processes that have been identified through research in workforce and enterprise development and the issues that need to be addressed to recognise their potential. In addition, the key features of developing and supporting biosecurity management related Indigenous enterprises are outlined. The challenges identified for this approach are also discussed, which include; developing business models of plant biosecurity management that integrate business and social enterprise models and Indigenous and non-Indigenous policy, governance and leadership models, building the capacity of stakeholders to engage those enterprise and the capacity of Indigenous people to meet enterprise contracts and access specific enterprise, robust data management and the development of biosecurity skills in Aboriginal workforces.

About the author:

Ruth Wallace is the Director of the Social Partnerships in Learning Research Consortium, Charles Darwin University. Ruth has extensive experience in innovative delivery of compulsory, post school and VET programs in regional and remote areas across Northern Australia. Her research is concerned with understanding learner identities, training frameworks in Indigenous contexts and partnerships across industry, communities and training institutions.

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The National Postgraduate Curriculum in Plant Biosecurity

Glynn Maynard^{4,7}, Kirsty Bayliss^{1,7}, Anthony Clarke^{2,7}, Michael Keller^{3,7}, Kim Plummer^{5,7} and Penny Wurm^{6,7}

¹Biological Sciences, Faculty of Science, Engineering and Sustainability, Murdoch University, ²Biogeosciences, Faculty of Science and Technology, Queensland University of Technology, ³School of Agriculture, Food and Wine, Waite Campus, The University of Adelaide, ⁴Office of the Chief Plant Protection Officer, Commonwealth Department of Agriculture, Fisheries and Forestry, ⁵School of Life Sciences, La Trobe University, ⁶School of Science & Primary Industries, Charles Darwin University, ⁷Cooperative Research Centre for National Plant Biosecurity

The traditional research disciplines underpinning plant biosecurity are the plant protection fields of entomology and plant pathology. However, biosecurity is more than just pathology and entomology and encompasses, in addition to these fields, areas such as risk analysis, community engagement, emergency response planning, invasion biology and quarantine. Beginning as a research project in 2007, the *National Curriculum in Plant Biosecurity* is now a fully recognised postgraduate degree program covering a Postgraduate Certificate, Postgraduate Diploma and Masters of Plant Biosecurity. The degrees are offered externally through Murdoch University and the Queensland University of Technology and are delivered by a national consortium which, additional to Murdoch and QUT, includes the University of Adelaide, La Trobe University and Charles Darwin University. The CRCNPB is also an official consortium member, while DAFF provides the services of the Executive Officer.

The units within the degrees are flexibly delivered and all are written explicitly for the biosecurity curriculum: they are thus bespoke units for these degrees. Educationally, the degrees are targeted to those already in the plant biosecurity field and wishing to advance their formal education, or those looking to enter plant biosecurity for the first time. The availability of the plant biosecurity degrees has two major implications for stake-holders. Firstly, the education provided will increase breadth and quality of knowledge in those working in plant biosecurity. While this will hopefully increase the generally quality of plant biosecurity within Australia, it also has more specific benefits. Firstly, the degrees will aid employers by allowing them to up-skill staff through externally recognised avenues. Secondly, for those wishing to enter the biosecurity field, it will offer an avenue of formal training not currently available. Both of these benefits are in-line with recommendations of Beale. Information on the courses can be found at www.plantbiosecurity.edu.au

About the author:

Glynn Maynard completed her degrees in entomology at the University of Queensland in 1983 and then worked for Queensland Lands Department and CSIRO entomology on biological control programs. She returned to the University of Queensland in 1997 to undertake a PhD in entomology which she completed in 1992. She then moved to Canberra to work for the Australian Government with the Australian Biological Resources Study then part of the Australian National Parks and Wildlife Service, The University of Queensland and Griffith University. In 1995 she moved to the Department of Primary Industry and Energy to a position in Australian Quarantine and Inspection Service and has worked at various positions within this various formats of this organisation since then in Canberra, Cairns and Melbourne. During 1995 and 1996 she worked with the United Nations Food and Agricultural Organization (FAO) in Rome and outposted to various locations, whilst at FAO she worked with the International Plant Protection Convention and FAO Forestry department. Currently she works in the Office of the Chief Plant Protection Officer.

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Genetics, Biology and Ecology

Chair: Shane Hetherington



Identification of effectors in *Venturia inaequalis*

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Venturia inaequalis and *V. pirina* are the causative agents of apple and pear scab respectively. This project aims to identify and characterise effectors in these species.

Effectors are pathogen proteins involved in infection. Effectors can also be recognised as foreign by plant receptors, which then initiate a signal transduction cascade that results in plant resistance. Breaking of resistance can occur if either the plant receptor gene or the effector gene is lost, or if the receptor is unable to recognise the effector due to a mutation. Due to this evolutionary pressure, effectors often vary across species and races.

Effectors are therefore of interest for three reasons: for their direct role in infection; for their role in triggering plant resistance; and for use in developing molecular tests that can differentiate strains of *V. inaequalis* (including resistance-breaking strains) and other species of *Venturia*.

Western Australia is currently free of *Venturia inaequalis*, but maintaining area freedom status is costly because of the lack of cost-effective surveillance methods, and the difficulty of rapidly developing new surveillance methods. However, next-generation whole genome sequencing is now cheap, effective, and fast. With the whole genome of a pathogen, it is possible to identify genes that are unique to that pathogen. These genes are targets for DNA or protein-based surveillance tests that can rapidly and cost-effectively identify the presence/absence of the scab pathogen and also differentiate this pathogen from related non-pathogenic species. Additionally, genes unique to a pathogen may be determinants of host specificity, and genes that display characteristics specific to effectors, or are unique to pathogens with a characteristic mode of infection (e.g. *V. inaequalis* and *V. pirina*), may be involved in the infection process. Therefore, the whole genome of a pathogen is an output that will inform all future studies on this pathogen and related pathogens.

We have successfully sequenced and *de novo* assembled the genome of *V. pirina*; this represents the first genome sequence of this important pear pathogen. We have validated this genome assembly by identifying candidate effector genes in the genome. A further genome assembly may use the existing *V. inaequalis* genome as a scaffold. Comparison and annotation of the genomes of these closely related *Venturia* species will follow. This will facilitate differentiation of the apple and pear scab pathogens (pear scab being well established disease in W.A.).

We intend to compare proteins from both *Venturia sp.* grown on cellophane/PDA culture against proteins on PDA culture, since previous work shows that both *Venturia sp.* grow pseudostroma *in vitro* on cellophane + PDA (but not on PDA alone) which are similar to structures produced during infection. Initial comparisons indicate that the proteomes of the different species and different culture conditions are broadly similar but not identical, suggesting that a protein differential-display approach is appropriate. Proteins present in cellophane culture may be involved in the formation of infection structures and thus are candidate effectors, while proteins that differ between species may be involved in host specificity. Differentially expressed proteins will be isolated using 1-D or 2-D gels. Proteins isolated by this method can be rapidly identified by comparing the mass of peptide fragments to theoretical masses generated from predicted genes in the whole genome sequence.

About the author:

Mr Daniel Jones is a Cooperative Research Centre for National Plant Biosecurity PhD candidate enrolled at the Department of Botany, La Trobe University. Most recently he was a Biosecurity Risk Analyst at the Ministry of Agriculture and Forestry, New Zealand, assessing the biosecurity risk from import of *Phaseolus spp.* beans and table grapes.

Daniel has worked in many different areas at the University of Auckland including developing virus tests in ornamental plants, microbiology of wastewater, stream ecology, and apple flowering genetics. He gained a Masters in Science at the University of Auckland and Scion (Rotorua) working on genetic mapping in two species of *Pinus*.

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Wheat stripe rust infecting barley grass, is there cause for concern?

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Wheat stripe rust is caused by the fungal pathogen *Puccinia striiformis* f. sp. *tritici* (*Pst*), an obligate biotroph. *Pst* has host specificity for wheat but is also capable of infecting barley, rye, triticale and certain grasses.

Pst comprises a range of pathotypes which are defined according to their unique combination of avirulence/virulence characteristics, this is determined via disease response on wheats of known resistance genotypes. There are two major pathotype groups within Australia: those pathotypes derived from the first incursion of *Pst* in 1979 in eastern Australia, and those derived from the more recent 2002 incursion in Western Australia.

The 1979 *Pst* population developed virulence for weedy barley grass populations, in the years after its introduction to Australia. The evolution of *Pst* towards virulence for weedy *Hordeum* spp. has had little impact on wheat resistance genes deployed in commercial production and the role of *Hordeum* spp., as hosts for *Pst* within and between winter cropping seasons, remains unclear.

The genus *Hordeum* belongs to the grass tribe Triticeae and contains 33 species. *Hordeum* species occur in mainly open habitats, often in steppe or meadow vegetation, along streams and ditches, and their distribution within Australia is restricted mainly to the south. The species *H. leporinum* and *H. glaucum* are the two most common species in Australia and comprise the barley grass differential used in this study. They can be easily differentiated by anther colour and ploidy level.

The now dominant *Pst* pathotypes, from post 2002, are of different origin and genotype, compared to the 1979 population, and appear to have the same infection type on *Hordeum* spp. as the 1979 population had when it was first introduced. However, recent isolates have been recovered from *Hordeum* spp. and research is being undertaken to examine the hypothesis that the post 2002 *Pst* pathotype population may also develop affinity for Australian barley grass. To test this hypothesis, a barley grass differential set has been assembled, comprising several *Hordeum* spp. This set is able to define virulence for *Hordeum* spp. among isolates of pathotype 104 E137 A- (1979 *Pst* population) and shall be used to further assess the 104E137A- population, and its single-step-mutation descendants, as well as the post 2002 *Pst* population.

About the author:

Jordan Bailey graduated from the University of Sydney in 2009 with a degree in Agricultural Science. Jordan has a keen interest in the plant sciences and began her PhD in August of 2009. Jordan is working on the wheat stripe rust pathogen *Puccinia striiformis* f. sp. *tritici*, at the University's Plant Breeding Institute. This project will investigate the pathogen's history within Australia, focusing on foreign incursion events and the occurrence of new pathotypes as well as stripe rusts virulence for wild barley grass populations within Australia.

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Mechanisms of phosphine toxicity and resistance

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Phosphine resistance is a serious developing problem for food security worldwide, especially for stored grains. The Australian grains industry especially is heavily reliant on this fumigant to maintain insect-free grain. In order to enhance resistance management strategies, we have aimed to identify the genes responsible for resistance in order develop genetic markers, so that rapid testing of field collected insects can be performed.

We have used genetic linkage and next-generation genomic sequencing approaches to identify the genes responsible for phosphine resistance in the pest insects *Tribolium castaneum* (Rust Red Flour Beetle) and *Rhyzopertha dominica* (Lesser Grain Borer). To date, we have found through genetic studies that high-level resistance is conferred by two loci, *rph1* and *rph2* that have synergistic interactions. We have also found through genetic complementation studies that these resistance loci are highly conserved within species. We have identified one gene at the *rph2* locus, responsible for high-level resistance in both *T. castaneum* and *R. dominica*, demonstrating that resistance is also well conserved between species. Sequencing of the mutations that confer resistance in this gene from multiple high-level resistant strains has highlighted the probable mechanism for phosphine mode of action as well as mechanisms for resistance. The biological effect of the phosphine mode of action has strong implications for redox biology and also fumigant chemistry.

About the author:

Dr David Schlipalius began his PhD at the University of Queensland in 1999 on a GRDC scholarship studying the molecular genetics of phosphine resistance in the Lesser Grain Borer, *Rhyzopertha dominica*, and produced the first genetic linkage map of that beetle.

He has also spent a couple of years working on honeybee genomics as a postdoctoral researcher at Purdue University in Indiana, USA. He is listed as part of the Honeybee Genome Sequencing Consortium that published the Honeybee Genome Project and worked on the construction of a detailed genetic linkage map to help define genes involved in behaviour, including the stinging behaviour of Africanised ('killer') bees in the Americas.

Since then he has returned to Australia and the stored grains research field to complete the detailed genetic analysis of phosphine resistance.

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The role of native plants during an insect incursion: survival and development of Glassy-winged sharpshooter (*Homalodisca vitripennis*) on Australian native plant species

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The glassy-winged sharpshooter, *Homalodisca vitripennis* Germar (Hemiptera: Cicadellidae), is an important insect vector of the xylem-limited plant pathogen *Xylella fastidiosa* Wells which causes diseases in numerous plant species including food and feed stock crops, ornamentals and weeds. Both the pathogen and the vector are native to the Americas and are considered to be highly invasive but, to date, neither have been detected in Australia. The wine and table grape industry is particularly concerned about the arrival of *H. vitripennis* because of the potential economic impact on this important Australian commodity.

Past *H. vitripennis* invasions, such as that which occurred in French Polynesia, have demonstrated the need for rapid detection and containment of an incursion. This requires identification of regions that have climatic and environmental conditions conducive to establishment as well as a detailed knowledge of host plants utilised by *H. vitripennis* for feeding and/or oviposition. These regions and host plant species can then be targeted for monitoring in order to increase the possibility of early detection of an incursion. The research to be presented includes the host status of a range of Australian native plant species in terms of feeding, oviposition and nymph development of *H. vitripennis* based on field and greenhouse trials completed in California.

About the author:

Anna is originally from New Zealand where she graduated from the University of Otago, Dunedin with an honours degree before moving to Australia. She has been based at Industry & Investment NSW, Gosford for the past two years where she is completing a PhD through Charles Sturt University. Her PhD project is based on a plant pathogen and its insect vector with a particular focus on the risk that these species pose to Australia. She is supported by the Cooperative Research Centre for National Plant Biosecurity and the E H Graham Centre.

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Insights into the spatiotemporal dynamics of *Tribolium castaneum* across an ecological landscape gained through trap data and population genetics

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¹Agri-Science Queensland, Department of Employment, Economic Development and Innovation, ²Cooperative Research Centre for National Plant Biosecurity, ³University of Queensland, School of Biology, ⁴Queensland University of Technology, ⁵CSIRO Ecosystem Sciences, EcoSciences Precinct

The rust-red flour beetle, *Tribolium castaneum* (Herbst), is a major pest of grain in Australia and many other countries. This species is assumed to be a good coloniser of grain storages through the human movement of grain with active dispersal by flight being considered unlikely. We combine an ecological study of dispersal with an analysis of gene flow using microsatellites to investigate the spatiotemporal dynamics of *T. castaneum* in an ecological landscape in eastern Australia.

Flying beetles were caught in pheromone traps for most of the year at grain storages and in fields at least one kilometre from the nearest stored grain. Traps at storages caught significantly more beetles than traps in fields and almost no beetles were caught in native vegetation reserves many kilometres from the nearest stored grain. Genetic differentiation between beetles caught at storages and in fields was low, indicating that although *T. castaneum* is predominantly aggregated around grain storages; active dispersal takes place between to the extent that significant gene flow takes place between them. Combining ecological and molecular techniques reveals much greater active dispersal in *T. castaneum* than previously thought, with this active dispersal being realised as gene flow. We conclude that the degree of movement is enough to mitigate founder effects and genetic drift.

About the author:

Greg Daglish is a Principal Research Scientist from Agri-Science Queensland, in the Department of Employment, Economic Development and Innovation. He has a strong interest in postharvest protection of grain from insects, including the practical application of knowledge of resistance and insect ecology. Greg was leader of CRC50089 'Grain Insect Ecology' and currently leads CRC5D149 'Grain Insect Ecology Phase 2'. He is based at the EcoSciences Precinct in Brisbane.

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Individual-based modelling of phosphine resistance in lesser grain borer (*Rhyzopertha dominica*)

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We describe the construction of individual-based models to investigate some genetic and operational factors which influence the development of phosphine resistance in lesser grain borer (*R. dominica*). The models are based on assumptions of resistance being conferred through one-locus or through two-loci. We show that the simulation of population dynamic of *R. dominica* in the absence of phosphine fumigation describes the statistically discrete analogue of the Hardy-Weinberg equilibrium.

We compare the one-locus model with aggregated two-locus model and verify the declaration in the literature that the trait of phosphine resistance is not conferred by a single gene; using a one-locus model to develop pest control strategies will therefore be unreliable. We use the two-locus model to investigate the impact of different duration of life stages and the impact of different initial frequencies of genotypes on the effect of fumigation. We conclude that extending the exposure duration of fumigation is a much more efficient control strategy than increasing the phosphine concentration. Furthermore, for more resistant pest population with n times the resistance allele frequency of a more susceptible population, we need to increase exposure duration only by only n days at most compared to the susceptible population, not n times.

About the author:

Mingren received his first PhD degree in Applied Mathematics from Murdoch University in 1997. He has worked as a Postdoc at UWA, as a Research Fellow at UNSW, and a lecturer in Statistics/Operations Research at USQ. He has also worked as a Coordinating Lecturer and Teaching Assistant at UWA where he was lecturing and tutoring in Industrial Statistics and Total Quality Management, Engineering Mathematics in 2008.

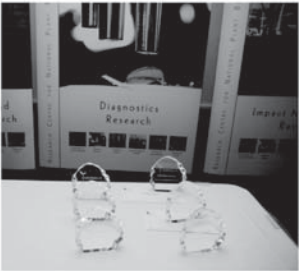
He enrolled in April, 2009, as a PhD student at the School of Plant Biology, UWA, working for a CRCNPB's project under the supervision of Dr Michael Renton. His project is "Simulation Modelling of Population Dynamics and evolution of resistance to Phosphine in Lesser Grain Borer."

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Pest Identification

Chair: Mike Cole



The pan-genome of *E. amylovora* provides insights into host specificity and better diagnostic design

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Erwinia amylovora, the causal agent of fire blight, is a destructive phytopathogenic bacterium of plants in the family Rosaceae. *E. amylovora* is known not to occur in Australia and is therefore, a major biosecurity threat to the Australian pome fruit industry. Better understanding of the biology of this organism and its interaction with host plants, aids in our preparedness for, and ability to prevent future incursions.

The pan-genome of a bacterial species is composed of a core set of genes present in all strains (core genome), and a dispensable set of genes present in two or more strains and genes unique to single strains (flexible genome). It has been shown in many clinically important bacterial populations that the pan-genome of a species can provide important information on the diversity of a species. In particular, the pan-genome can have wide implications for development of control strategies, diagnostics and greater biological understanding of an organism.

We have identified the pan-genome of *E. amylovora* using multiple complete genomes of diverse strains of *E. amylovora*. We will present highlights of this research including an analysis of the flexible genome of *E. amylovora* which identified new candidates for host specificity including genes involved in secondary metabolite production and toxin biosynthesis, putative effector proteins and plasmids. We will also discuss how the core genome of *E. amylovora* has been used in a genomics based pipeline for molecular diagnostic target identification.

About the author:

Rachel Powney has a Bachelor of Science from the University of Melbourne and an Honours degree in Applied Science (Agriculture) from the University of Tasmania.

Rachel has worked at the Department of Primary industries Victoria in the Plant Health/Bioprotection platform since 2005 and is currently a CRC Plant Biosecurity student doing her PhD with Latrobe University and DPI Victoria.

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The impact of taxonomy: How a successful invasive species could achieve world heritage list protection by changing its name

Bobbie Hitchcock^{1,2}

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Epiphyas is an indigenous Australian genus of more than 60 moth species. A notorious member of the genus is the horticultural pest species *E. postvittana*, also known as the light-brown apple moth. Presumably through trade, *E. postvittana* became established in New Zealand and Hawaii during the 1880s, in England after 1936 and more recently in the American State of California. The light-brown apple moth is considered to be a significant economic threat to horticultural industries in many countries.

Epiphyas postvittana has also been found on islands near Australia such as Lord Howe, a small volcanic island in the Pacific Ocean about 700km northeast of Sydney. Without human inhabitants before 1788, the island was described in 1956 by scientist S.J. Paramonov as 'a riddle of the Pacific' due to the inexplicable origins of the island's unusual flora and fauna. International recognition of the island's unique ecosystems was achieved in 1982 when the Lord Howe Island Group was added to UNESCO's World Heritage list.

The Australian National Insect Collection contains *E. postvittana* collected on Lord Howe Island between 1966 and 2005, but after inspecting the collection at the British Museum, I now know that two *Epiphyas* species have been found on the island. A single adult male moth was collected on Mount Lidgbird in 1953 by J.D. Bradley, who identified the specimen as *Epiphyas aulacana*, a species visually distinct from *E. postvittana*, but belonging to a group of four similar looking *Epiphyas* species known only from the Australian mainland and Tasmania.

The Lord Howe Island Board of Management stated in 2009 that pest plants and animals are a main threat to the island's ecology, but without knowing when the two *Epiphyas* species arrived on Lord Howe, the threat posed to the island's indigenous biota by these putative exotic species is difficult to estimate. Might either of these species have arrived *before* 1788, when human settlement of the island began? What then would be the implications for the management of these species within the island's ecosystems?

To confirm the species identifications, particularly that of *E. aulacana*, and to estimate a time window for the arrival of each species to the island, I went to Lord Howe to look for fresh specimens from which to extract DNA-based information. I came back with larvae and adults, a host plant record and the seeds of a story which exemplifies the taxonomic challenges addressed and achievements made during this 2007-2010 revision of the genus *Epiphyas*.

About the author:

Bobbie has a First Class Honours degree in Chemistry from the Australian National University and a Bachelors degree in Zoology and Chemistry from La Trobe University in Melbourne. She is now a PhD Candidate in the School of Biology at the Australian National University and the Cooperative Research Centre for National Plant Biosecurity at CSIRO Ecosystem Sciences in Canberra.

Since July 2007, she has been working on a revision of the moth genus *Epiphyas* in the Australian National Insect Collection with her supervisor Dr Marianne Horak. Her other advisors are Dr Andrew Mitchell, formerly with the DPI-NSW in Wagga Wagga and now at the Australian Museum in Sydney; Dr John Trueman and Professor Mike Crisp, who are both in the School of Biology at the ANU in Canberra.

The revision of this genus would not have been possible without access to the resource collection at the ANIC, other collections within Australia and the British Museum in London. The DNA-based component of this project was developed with contributions from moth enthusiasts and research collaborators in Australia and overseas and by members of the CRC40136 project team led by Bill Woods at DAFWA in Perth.

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Recombinant antibodies for immunodetection of banana viruses

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This major aim of this study is to develop recombinant antibodies to economically important banana viruses including the various badnaviruses that cause banana streak disease. These viruses are particularly difficult to detect as badnaviral DNA is integrated in the nuclear genome of the banana and DNA-based detection methods are incapable of distinguishing replication-defective integrated sequences from those that are actively replicating. In order to generate recombinant antibodies to *Banana streak MY virus* (BSMYV), chickens were immunised with purified virus and the spleen harvested for RNA extraction. An antibody response was observed, suggesting that the immunizations were successful. Antibody gene repertoires amplified from chicken splenocytes will be cloned into the pCANTAB-link phagemid vector for affinity selection by biopanning. Bound scFv will be eluted and sequenced. After functional tests, scFv fragments will be expressed as soluble antibodies and purified for immunoassay development.

We have investigated a new purification strategy for BSMYV using solution-phase isoelectric focusing. Intact viral particles were found within the pH range 4.5-9.1 and fractions with a pH of ~ 6.8-8.4 contained the most viral particles. This purification method is much faster and simpler than conventional methods and results in highly pure virus preparations. Research has also been done to characterize the coat protein of BSMYV to allow *in vitro* expression of the protein for use in antibody production and epitope mapping. The coat protein forms part of a large polyprotein that also contains movement protein, aspartic protease, reverse transcriptase and RNase H1 domains. This polyprotein is processed through the action of the aspartic protease to form the mature proteins, but the cleavage sites are unknown and can only be determined empirically. Putative coat proteins of BSMYV were identified by SDS-PAGE analysis of the purified virus and two coat proteins identified by electrospray ionization mass spectrometry (ESI-MS) and N-terminal sequencing. This is the first time that the coat protein of any badnavirus has been characterised.

About the author:

I completed a Bachelor of Biotechnology with Honours (H1) in 2007 at the University of Queensland. I am currently completing my PhD with the Cooperative Research Centre for National Plant Biosecurity. I am enrolled through the University of Queensland at the School of Australian Institute of Bioengineering and Nanotechnology. My research is based at Ecosciences Precinct (Queensland Department of Employment, Economic Development and Innovation). My interest is to develop new diagnostic methods to detect plant and animal viruses.

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Getting to know the locals: A systematic revision of the Australian macropsine leafhoppers

Linda Semeraro^{1,2,3}, Murray J. Fletcher⁴ and Andrew Mitchell⁵

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Leafhoppers are phytophagous insects which can cause serious damage to plants through direct feeding and their ability to transmit plant diseases.

Four leafhopper species, belonging to the genera *Macropsis* and *Oncopsis* (Cicadellidae: Macropsinae), are known to transmit phytoplasma diseases overseas. These include rubus stunt phytoplasma (RUS), peach yellows and alder yellows.

These diseases and their vectors are not currently known to occur in Australia. However, at least half of the 46 species (in 9 genera) of macropsines described from Australia are placed currently in the holdall genus *Macropsis* Lewis.

In this project, the taxonomy and phylogeny of the Australian genera of Macropsinae leafhoppers, are revised. The objectives are to (1) clarify whether *Macropsis* and/or *Oncopsis*, occur in Australia (2) determine which macropsine genera are represented in Australia and (3) infer the relationships between Australian and worldwide genera/ pest species of macropsines.

This revision of the macropsine leafhoppers combines both morphological and molecular characters to help better define genera/ species and determine relationships within the subfamily. This study will improve understanding of the endemic Australian macropsine fauna and help more readily identify exotic macropsine pests should they be introduced to Australia. It will also provide a better understanding of how closely related the Australian macropsine species are to pest species known to transfer phytoplasma diseases of concern.

Initially, we evaluated morphological characters including generic characters as derived from literature. A morphological character matrix, coding for more than 100 characters of around 600 specimens, has been created.

DNA sequences of the mitochondrial Cytochrome Oxidase I (COI) gene and a nuclear gene (28S) in the ITS region of ribosomal DNA are acquired and analysed. Non-destructive DNA extraction techniques are employed and newly designed primers are used to amplify smaller fragments within the gene region of interest, to overcome issues of DNA degradation when using older collection material.

Morphological examination resulted in only two Australian specimens matching with the genus *Macropsis*. One specimen is a female paratype, misidentified as *Macropsis victoriensis*. But, females are difficult to identify with certainty based on morphological characters alone. The other specimen is a male of an undescribed species, identified in this study as belonging to a subgenus, *Parapediopsis*, which doubtfully represents *Macropsis* (*sensu stricto*).

In this study, it was found that there are at least 100 macropsine species in Australia, twice as many species as currently described. At least one new generic record and one new Australian genus have been found.

Partial COI (550 - 650 basepairs) and 28S (~700 basepairs) gene sequences were acquired for over 70 specimens, representing 40 macropsine species and 10 genera / subgenera from Australia and overseas. Preliminary analysis of these data shows that most of the Australian species form a distinct clade separate from the overseas species. However, a small number of Australian species are more similar to *Macropsis* from overseas than to the Australian clade.

Further analysis, using Neighbour Joining, Maximum Parsimony and Bayesian methods, will further elucidate the relationship between Australian species and overseas pest macropsines.

Results of these analyses will be presented and discussed.

About the author:

I am CRCNPB PhD student, studying at La Trobe University and based at the Department of Primary Industries, Victoria (Knoxfield). I am currently in the final stages of completing my PhD thesis on the systematics of Australian macropsine leafhoppers. I will be returning to full-time employment with Department of Primary Industries, (DPI) Victoria, where I have been working for the last 10 years. In my position at DPI, I am involved with helping to provide a service for diagnosing insect / mite plant pests for state government bodies, quarantine and other clients.

Working in this area, I have developed an appreciation of the importance of rapid and accurate diagnoses, which is essential for detecting, containing and eradicating introduced pests. This work relies on having a solid taxonomic framework and sound understanding of the group of pests in questions and their closest relatives. Through this basic taxonomic and systematic study, I would like to improve tools available to diagnosticians and contribute to an increased understanding of the Australian leafhopper fauna.

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Resolving the *Bactrocera dorsalis* complex

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Pest fruit flies of the *Bactrocera dorsalis* complex dominate NAQS, AQIS and industry target lists. Three species within the complex (*B. dorsalis* s.s., *B. papayae* and *B. philippinensis*) are category two pests in the Deed. Unfortunately, despite their importance, these three species cannot be adequately resolved from each other, nor from endemic, non-regulated fruit fly species. Also, a fourth non-Australian pest species, *B. carambolae*, is closely related to these three species and is morphologically and genetically similar. Project CRC20115 is simultaneously bringing together, for the first time, a series of parallel data sets focussing on molecular, morphological, and behavioural information relating to each of these four pest species. The chief objective of this study is to retest their original classification to determine the validity of their taxonomic identities, and whether the current classification is biologically meaningful. Once species boundaries have been resolved, definitive molecular markers will be developed.

Molecular characterisation is being achieved by amplifying and sequencing six genetic markers from both the nuclear (ITS1, ITS2, CAD) and mitochondrial genomes (COI, ND4-2), together with transcriptome analysis on, so far, three of the four pest species. Geometric morphometric shape analysis on wings is being applied to determine the capacity of the technique to achieve fine-scale resolution between populations or species. Behavioural aspects specific to the mating systems of the four species are being examined, mainly via mating compatibility studies being undertaken at FAO/IAEA research laboratories situated in Seibersdorf, Austria.

Results so far demonstrate that, similar to previous studies on these species, *B. carambolae* is genetically the most distinct species from the remaining three. Geometric morphometric data based on DEEDI collection material can resolve differences in wing shape variation among different populations of the species and is a promising tool for further development. Ongoing mating compatibility studies have so far revealed that *B. carambolae* and *B. dorsalis* exhibit relatively high levels of mating isolation under field-cage conditions (remaining species yet to be tested).

Remaining work for this project is to:

- a) complete the collection of sequence data for all selected specimens;
- b) extend the use of shape analysis to *de novo* collected material; and
- c) complete mating compatibility studies to include recently acquire live material of *B. philippinensis* and *B. papayae*.

Once collected, this data will be analysed together to provide a recommendation as to the relationships between these pest species and their subsequent classification to be applied to trade and quarantine purposes. This project is now intimately tied and working in collaboration with the FAO/IAEA Coordinated Research Project, 'Resolution of cryptic species complexes of tephritid pests to overcome constraints to SIT applications and international trade'.

About the author:

Tony Clarke completed his PhD in entomology from The University of Queensland in 1992. After graduating, he spent 10 years as a research fellow working on insect ecology at the University of Tasmania, The University of Queensland and Griffith University. In 2002 he took up a tenured position as an ecologist with the Queensland University of Technology, where he is now an Associate Professor. Most of his research has focused on sustainable insect pest management with an emphasis on forestry and horticultural crops. He has participated in several international projects which have seen him work with colleagues in Asia and the Pacific. His current research is focused plant biosecurity, particularly with respect to tropical fruit flies. Tony is the author or co-author of over 80 refereed publications and he has graduated 14 masters and PhD students.

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A diagnostic framework to identify nematode pests for plant biosecurity using novel molecular techniques

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Plant parasitic nematodes are one of the four most important agricultural and horticultural plant pests. The worldwide annual losses to agricultural production attributable to nematode infection are about USD\$120 billion. Although nematodes cannot move more than few metres annually by themselves, human activities have resulted in the effective spread of these major pests around the world. The transportation of infected plant materials from one continent to another can put Australian agricultural production and trade at risk. There is a continuing need to develop and improve robust, rapid and accurate diagnostic methods for nematodes, to expedite the inspection time of plant materials being traded, and to reduce the potential for nematode spread. The aim of this project is to develop new protocols for the diagnosis of exotic nematodes.

Classical taxonomic identification of nematodes requires a trained specialist and identification is time consuming, especially when exotic nematodes must be identified. The development and application of molecular techniques to identify phyto-nematodes can improve the time taken for nematode identification. Molecular techniques of diagnostics have proved to be increasingly reliable and rapid compared to classical approaches. In this project both DNA and protein-based diagnostic methods have been developed to identify a range of root lesion (*Pratylenchus* spp.) and cyst (*Heterodera* and *Globodera* spp.) nematodes. Characteristic sequences of ITS regions have been generated and phylogenetic relations of these nematodes studied. Similarly, protein biomarkers have been established that can be used to identify both genera and species of these nematodes. Application of these diagnostic tests will help reduce potential entry of exotic nematodes into Australia, and so help to reduce potential production and trade losses.

About the author:

Mr Matthew Tan completed his undergraduate training at the University of Queensland and completed his Honours Degree in Nematology in 2008. During his Honours research, he studied the intraspecific variation within Australian *Radopholus similis* isolates (Burrowing nematode) on banana plants. Based on these results, it was concluded that the burrowing nematode has been introduced into Australia, although the genus *Radopholus* is indigenous to Australia. After completing his degree, he worked in the National Parks Board (NParks) in Singapore for 15 months. Currently, he is completing his PhD at Murdoch University (Western Australia) with Dr Vivien Vanstone (DAFWA) and Professor Mike Jones. Matthew is aiming to develop novel technique for plant parasitic nematode identification. Currently, promising results have been obtained from protein profiling of nematodes which has potential for use as a molecular diagnostic approach for species identification.

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National trapping program for *Trogoderma* and related Dermestids

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The Khapra beetle, *Trogoderma granarium* Everts (Coleoptera: Dermestidae) is recognised as one of the world's most destructive pests of grain products and is the subject of strict quarantine measures in many countries. Khapra beetle is listed in the 100 'World's Worst Invasive Alien Species' by the Global Invasive Species Programme. Plant Health Australia has identified Khapra beetle as one of the top five biosecurity threats to the Australian Grains Industry. Australia is free of Khapra beetle, with records of intercepts only and one incursion that was swiftly eradicated in WA in 2007. If Khapra beetle became established in Australia there would be large trade and production impacts.

There are over 120 described *Trogoderma* species worldwide and many have yet to be discovered. Apart from the Khapra beetle, there is the less significant pest the Warehouse beetle, *Trogoderma variabile* Ballion, which is already established in Australia. There are another four minor pest species, 52 described native Australian species and many native Australian species remain undescribed, any of which could accidentally get into grain stores - as they have done so on a number of occasions, and be misidentified.

The Khapra beetle can only be reliably identified by a limited number of highly skilled taxonomists. Expert morphological determination requires keying-out specimens, dissection and slide mounting of diagnostic features. Suspected *Trogoderma* specimens found in grain products are usually the larvae or larval skins which are very difficult, sometimes impossible to diagnose morphologically. Adult specimens are usually scarce and damaged. Due to their similarity, warehouse beetle, or native *Trogoderma* spp. could be mistakenly identified as *T. granarium*, or could mask the early detection of Khapra beetle. Their misidentification has the potential to seriously compromise the Australian grain exports.

The national trapping program for *Trogoderma* has been designed as a 'targeted' baseline survey of the distribution of *Trogoderma variabile* and related native *Trogoderma* spp. in Australia. Trapping sites were selected from locations in which *T. variabile* and related Dermestids were previously collected in CSIRO trapping surveys conducted in 1991-92 and 2001-2003, as well as in previous surveillance catches in WA. The trapping in the 2009-10 season included 64 sites across WA, SA, VIC, NSW and QLD using participating CRC-affiliated grain companies (CBH, GrainCorp and Viterro).

More than 600 trap sample catches are providing material for diagnostic capacity building. Trap catch data was collected using the Urban Surveillance Database application developed in CRC30014 (PDA-Assisted Surveillance). The trapping program plays an important role in supplying the National *Trogoderma* Reference Laboratory with specimens for taxonomic studies, diagnostic imaging, biogeographical diversity studies and validation of diagnostic DNA markers for exotic and native *Trogoderma* species.

This research supports the National Reference Laboratory for *Trogoderma* in its capacity to becoming an accredited facility for rapid diagnosis of suspect specimens of *Trogoderma* species detected in Quarantine and Biosecurity surveillance, and demonstrates to international markets Australia's pest-free status. This work addresses the 'International importance of accredited diagnostic laboratories using accepted diagnostic procedures' as written in the International Standards for Phytosanitary Measures (ISPM 27).

About the author:

Dr Oonagh Byrne (BSc in Zoology and MSc in Biotechnology), emigrated from Ireland to Australia in the mid 1990's and soon after, took up a GRDC-funded research position at the Centre for Legumes in Mediterranean Agriculture at the University of WA. Dr Byrne's research has included breeding field pea for resistance to pea weevil, developing protocols for field pea resistance screening, and has published on the genetics of pea weevil resistance. In 2009 Oonagh took up her current position as Research Officer in Entomology at DAFWA on CRC project 'Khapra Beetle Diagnostics'. Oonagh's research focus is in the establishment of a National Reference Laboratory for *Trogoderma* and related Dermestids (CRC20137).

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Poster session 1:

- Communication and Capacity
- Genetics, Biology and Ecology
- Pest Identification and Tools for Detection and Diagnostics



Effective international, national, and local policy frameworks for biosecurity

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An integrated biosecurity management strategy incorporates effective policy and related regulatory frameworks (including instruments and activities) to analyze and manage risk, including environmental risks. These policy frameworks operate internationally, nationally, and locally. The United Nations Food and Agriculture Organization (FAO, 2008, p. 6) sees biosecurity as a strategic and whole-of-jurisdiction domain. For them, biosecurity is: *'a strategic and integrated approach that encompasses a policy and regulatory framework for analyzing and managing relevant risks to human, animal and plant life and health, and associated risks to the environment.'*

For any country's policy framework to be effective, it must be developed and implemented at the regional and local level, and guarantees policies at different levels of governance work in harmony towards effective implementation. Clearly, in such a complex overarching policy environment, the question arises as to how such policies actually engage with the various levels of governance in a real live country example? That is, how does engagement occur in practice so that all these policies can be adopted?

Using biosecurity management in provinces in Eastern Indonesia as a case study of how international, national, and local legal policy frameworks engage with local knowledge to create a new development paradigm, this research assesses the underlying factors that hamper opportunities to implement a new biosecurity policy paradigm. A paradigm that utilises local knowledge to benefit from technological advances in development (old paradigm). The research also answering the need – using policy frameworks – to develop a new paradigm of biosecurity framework in countries such as Indonesia.

About the author:

Theofransus Litaay since 2007 is a researcher in the Australian-Indonesian Biosecurity Community Management Project (Ausindo-Biocom). This is the project of CRCNational Plant Biosecurity conducted at Northern Australia and Eastern Indonesia regions by Charles Darwin University. In Indonesia, this project is supported by several partners such as Satya Wacana Christian University (Salatiga, Central Java), Mahasaraswati University (Denpasar, Bali), Nusa Cendana University (Kupang, West Timor), BaKTI (Eastern Indonesia Knowledge Exchange, Makassar, South Sulawesi), JiKTI (Eastern Indonesian Researcher Network in 12 Eastern Indonesia provinces), Pattimura University (Ambon, Maluku), etc.

In 2010, he organized a workshop in cooperation with the government of Maluku Province (Indonesia) and a group of local researchers that produced three districts' plant biosecurity strategy. Two of the districts are in direct border with Australia and East Timor. His background is Law. He finished his undergraduate degree at Satya Wacana Christian University (SWCU) in Salatiga (Central Java, Indonesia) and finished his master of laws degree (LL.M) at Vrije Universiteit, Amsterdam. In September 2008, he started his Ph.D study as external student of Charles Darwin University, conducting research in greater Papua, Maluku, and East Nusa Tenggara provinces. He is a researcher at the Center of Eastern Indonesia Studies of Satya Wacana Christian University (SWCU) and lecturer at the faculty of law of SWCU.

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Ecological research for preharvest control of Queensland fruit fly as part of systems approach – an overview

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Background: Fruit flies directly impact on fruit quality and are the single most significant phytosanitary barrier in Australia for domestic and international market access. In the near future, some of the common chemicals currently registered for fruit fly management are likely to have their usage significantly reduced for crops with edible peel. Alternative treatments for pest fruit flies such as the Queensland fruit fly, *Bactrocera tryoni* (Froggatt), require development in order to maintain crop protection and market access. Systems approaches, which link two or more independent management techniques, offer a promising alternative for fruit fly control. Unfortunately much of the underpinning science needed to develop systems approaches for *B. tryoni* management is not available. This project is helping address this issue.

Methods: The first task of this project was to undertake a formal scientific literature review to identify the knowledge gaps in *B. tryoni* biology and ecology pertinent to the development and/or refinement of management tools. The review identified key areas of scientific weakness including knowledge of how and why the fly moves within and between crops. Having identified the gap, research is pursuing this area by quantifying where flies are distributed within orchards and plants with special emphasis on how, why and where flies forage for protein and cue lure resources.

Results: The first study investigated the distribution pattern of *B. tryoni* in different orchard types using strawberry and apple as models. Results from this study show that in a strawberry farm, a higher proportion of *B. tryoni* were caught on the field edges early in the production season. In contrast, flies were found to be evenly distributed within apple orchards throughout the production season. We presume differences in foraging and sheltering behavior influence these patterns and research to test these hypotheses are continuing. Studies on *B. tryoni* foraging patterns for protein within a host plant showed that more *B. tryoni* search for protein on a fruiting host plant than on a non-fruiting plant. A higher proportion of flies were also found feeding on protein placed on mid to upper canopy than lower (<1.3m) in the canopy.

Conclusions: We conclude that *B. tryoni* effectively forages for protein at heights higher than 1.3m from ground, indicating greater efficacy of protein baits when applied at foliage higher in the canopy. While preliminary, results from the strawberry farm study suggest farm edges as sites for intensive management, while management effort for *B. tryoni* in an apple orchard should be evenly distributed throughout the orchard.

About the author:

Solomon Balagawi is a Research Fellow in the discipline of Biogeosciences at QUT. He has been conducting ecological research on fruit flies whilst as a young researcher employed on an ACIAR fruit fly project in PNG, and later as a subject of his PhD studies at Griffith University. Solomon's current research is focused on understanding the ecology of Queensland fruit fly relating to its distribution pattern in the field. It is anticipated that information generated in this research should provide the ecological basis for improving the current preharvest management strategies. The information should further assist in the effective implementation of systems approach technology to gain market access for fresh horticultural commodity produced in Australia.

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The South African Citrus Thrips (*Scirtothrips aurantii*) in Queensland is highly polyphagous, and does not show strong preferences for its only recorded host in the field

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The South African Citrus Thrips *Scirtothrips aurantii* (SACT) was first discovered in Australia on Mother of Millions *Bryophyllum delagoense* (MoM) at Sherwood, Queensland in 2002. The presence of SACT in Australia was a cause for biosecurity concern as in its native range it is highly polyphagous and is a controlled pest of both citrus and mango.

Surveys in SACT infested areas failed to detect the insect on these or any other plants save MoM, and preliminary lab studies found collected thrips only able to survive and breed on MoM. While this has led to suggestions that the Queensland population of SACT might be a cryptic species or specialized host race, morphological and molecular taxonomy has found no difference between the thrips population on MoM in Australia and those collected from citrus in South Africa.

My research shows that the Queensland SACT population can indeed successfully reproduce on a number of hosts, and colonies can be maintained on alternate hosts for several generations.

Host preference tests indicate that this insect does not have an inherent strong preference for MoM, and thrips reared on alternate hosts do not seem to exhibit strong learning or imprinting effects towards new hosts.

About the author:

I am a PhD student studying entomology at the Australian National University. For my thesis I am studying several invasive plant-insect systems. Given the complex and dynamic nature of a biological invasion, my work emphasises controlled experiments to better understand both current field observations and how the impact of an invasive species might change in the future. This improved understanding of current events and future risk can be applied to both monitoring and management regimes to more effectively manage invasive species.

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Retention time of infectious potato spindle tuber viroid (PSTVd) on common surfaces

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Potato growing areas of Australia are currently considered free of Potato spindle tuber viroid (PSTVd) and this pathogen is classified as an emergency plant pest (Category 3) under the Emergency Plant Pest Response Deed (EPPRD).

Three strains of PSTVd have been detected so far in the PSTVd outbreaks in Australia. The “Naaldwijk strain” was detected in glasshouse grown tomatoes in southern Western Australia (WA) in 2001 and a survey of field tomatoes in New South Wales detected a common European strain (PTVCGA). The last three detections in WA since 2004 have been of the “Chittering strain” of PSTVd and each instance the initial detection was in glasshouse or field grown tomatoes. It is unclear at this point what the source of PSTVd inoculum for these outbreaks was, by what pathway the pathogen reached the tomato crops and what the impact of these PSTVd strains was on tomato fruit yield and quality under Australian conditions.

Following an incursion of PSTVd in Australia an important aspect of the eradication program that follows is the cleaning and sanitizing of machinery and equipment used on the affected farm. However, some aspects of PSTVd epidemiology are poorly understood, including the stability of infectivity of PSTVd inoculum on different common surfaces such as those associated with machinery, mulches, staking and handling plants, eg. cotton, metal, plastic, unpainted wood, glass, rubber, string and leather.

In a preliminary experiment, fresh undiluted sap from PSTVd infected tomato plants was extracted and pipetted onto various surfaces (cotton, metal, plastic, unpainted wood, glass, rubber, string and leather) and left to dry out for 4 different time intervals (5 minutes, 1 hour, 6 hours and 24 hours). For each surface, after each time interval, the sap was rehydrated using distilled water and each extract was inoculated to five cv. Grosse Lisse tomato plants.

The outcome was that PSTVd contaminated glass, wood, plastic, leather and string surfaces were still infective after 24 hours; contaminated cotton was still infective after 6 but not 24 hours, and contaminated metal was still infective after 1 but not after 6 hours. The results for rubber were inconclusive will need to be repeated. The results to date indicate that further time periods (for example, 2 weeks, 1 month and 6 months) need to be incorporated into this work.

About the author:

Alison Mackie is currently a Cooperative Research Centre for National Plant Biosecurity student doing her PhD with University of Western Australia and Department of Agriculture and Food, WA. Alison's PhD project will investigate the phylogeny, pathogenicity and epidemiology of potato spindle tuber viroid (PSTVd) and related pospiviroids in Australia.

Alison has been employed by the Department of Agriculture and Food, Western Australia (DAFWA) since 1999 and has worked on a number of projects in the plant pathology section, including culture collection, diagnostics, surveillance and horticulture pathology.

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Presence of pathogenicity genes in *Fusarium oxysporum f.sp. cubense*

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Fusarium wilt is caused by a range of *Fusarium oxysporum* formae speciales, classified based on the host they infect. Banana Fusarium wilt occurs when the pathogen *Fo f.sp. cubense* enters banana plants, eventually leading to the death of the host. *Foc* is classed into races, each race affecting a different host range. Race 4 is the most important, affecting Cavendish cultivars, the most commercially significant banana variety. Pathogenicity genes in *Fo f.sp. lycopersici* have been identified based on proteins 'secreted in xylem' upon infection of tomato plants; these are SIX1 to SIX8 genes. Preliminary studies have revealed the presence of SIX7 and SIX8 genes in race 4 isolates of *Foc*, which are absent in races 1 and 2. This suggests that SIX7 and SIX8 genes are associated with pathogenicity in *Foc*, in particular host specificity.

About the author:

Rachel Meldrum is a PhD student with the Cooperative Research Centre for National Plant Biosecurity. She is enrolled at the University of Queensland and based in the Northern Territory with the Department of Resources. Her research project focuses on the epidemiology and biology of Fusarium wilt 'tropical' race 4, a disease which is currently exotic to the main banana growing regions in Australia.

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***Bactrocera tryoni* adult preference and larval performance on five citrus varieties**

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The Queensland fruit fly, *Bactrocera tryoni*, is the worst horticultural insect pest in Australia. *Bactrocera tryoni* is a highly polyphagous, tropical fruit fly which attacks a wide range of both commercial and native fruits. Despite its pest status, the host utilization behaviour of *B. tryoni* has not been thoroughly researched. Adult host preferences and immature stage survival of *B. tryoni* on many important commercial hosts are largely unknown, or at least unreported. The aim of this study is to investigate the oviposition preference, clutch size and immature stage survival of *B. tryoni* for five citrus types lemon (*Citrus limon*), murcott mandarine, valancia orange, naval orange and yellow grape-fruit. Oviposition preference was tested through choice and no choice tests and measured by the number of oviposition events, time taken until first visit, mean clutch size and total eggs laid per fruit.

Immature stage survival of *B. tryoni* in the same citrus varieties was examined by natural infestation and artificial inoculation methods. Host fruit parameters recorded were peel toughness, fruit diameter and brix value. All measures of adult oviposition preference varied significantly between the five citrus types in both choice- and no-choice tests. The fly exhibited clear oviposition preference for mandarins and grape-fruit over to naval oranges and lemon. None of the correlations between fruit parameters and oviposition preference measurements were significant except for the significant negative correlation between total eggs laid in lemon and lemon brix value. Immature survival rate in mandarins, lemon and naval oranges were lower than 30%. Immature survival was highest in mandarins and lowest in lemons. Overall results showed that *B. tryoni* exhibited a preference hierarchy among citrus varieties, but what fruit traits influenced this pattern was not identified in this study. When compared with studies on other fruit types, the results of this study indicate that citrus is a poor host for *B. tryoni* larvae.

About the author:

I am currently conducting my PhD study on Queensland fruit fly host utilization behaviour and how it affects on population dynamics of B. tryoni. One of my major objectives of this study is to investigate B. tryoni oviposition behaviour with different hosts, immature stage survival and its clutch size. I have completed masters research degree in which I have researched on B. tryoni population dynamics with yearly seasonal climatic variation across tropical and subtropical Queensland. In my masters study I specially focused on B. tryoni overwintering breeding in tropical and subtropical climate. I completed my Bachelor degree in Agriculture in which I majored in agricultural economics.

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Life outside the silo: stored grain pest ecology in the Riverina

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Lesser grain borer (*R.dominica*) and red flour beetle (*T.castaneum*) flight activity was monitored for two years in grain paddocks, areas adjacent to on-farm grain storages, and in remnant native vegetation near Leeton New South Wales (NSW) using Lindgren funnel traps and aggregation pheromones. Flight activity for both species was minimal between May and August of each year, however in 2009 severe heatwave conditions during February resulted in an early reduction in beetle activity that persisted until the following spring. Whilst *T.castaneum* was most abundant near silos, *R.dominica* was most abundant in areas of remnant native vegetation. This suggests that *R.dominica* may be utilising food sources other than cultivated grains, and we have shown that this species is capable of completing its entire life cycle on the seeds of Cootamundra Wattle (*A.baileyana*) and also on the fruit of at least one species of palm. In comparison to other hosts (wheat, maize, sorghum) development on these alternate hosts is slower, and fewer adults are produced. Good initial parental survival correlated to reproductive success, but the response of beetles in two-choice still-air olfactometer tests against a wheat standard provided inconsistent results; *R.dominica* is attracted to both Kurrajong (*B.populneus*) and Cootamundra Wattle seeds in preference to wheat, despite being unable to reproduce on Kurrajong. The existence of viable alternate food sources in non-crop environments suggests that refugia may exist where *R.dominica* is not subject to selection pressure for phosphine resistance, and this may have important implications for resistance management.

Field trials have shown that aggregation pheromones for both beetle species can be deployed on single traps without synergistic or antagonistic interactions, and this finding will improve the efficiency of future studies. Mass-marking techniques for *R.dominica* have also been developed that set the stage for mark-recapture studies looking at insect dispersal. Because stored grain beetles caught during ecological studies are potentially useful for population genetics research, we also investigated a range of different DNA preservation techniques for use in conjunction with funnel traps, and found that dry preservation using a section of dichlorvos pest strip as a killing agent is the best short-term option, particularly under conditions of low relative humidity. Absorption of atmospheric water by propylene glycol reduces its effectiveness as a DNA preservative.

About the author:

Mark Stevens joined Industry & Investment NSW in 1989 after completing his PhD at the University of Sydney. For the last 22 years he has worked on IPM and ecology projects, primarily for the rice and citrus industries. He has also published papers on ecotoxicology, biodiversity, biosecurity, and riparian zone rehabilitation. He is currently a Principal Research Scientist, Director of Yanco Agricultural Institute, the I&I NSW Team Leader for Broadacre Entomology, and an Adjunct Professor at Charles Sturt University.

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Investigating the receptors involved in chemical communication for the pest beetle *Tribolium castaneum*

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Providing fast and effective detection of pest insect infestation in food storage facilities is the foreseen outcome of an insect-based olfactory biosensor. Current visual methods for the detection of an infestation are not sensitive or reliable, so unless the produce has recently been fumigated with phosphine, pests are assumed to be present and the grain is re-treated. This leads to continued selection pressure for phosphine resistance and increases the costs of pest management in the grains industry. In the development of the detection technology, we are focussed on providing the biological recognition element for a biosensor platform capable of *in situ* measurement of insect produced volatiles.

We are taking two approaches to identify which of the many odorant receptors (ORs) annotated in the *T. castaneum* genome, can detect infestation odours. Here I will concentrate on an approach that focuses on sex pheromones; the other approach is outlined by Bradley Stevenson. Sequencing of the *T. castaneum* genome has recently been completed and revealed a large family of putative OR genes. It is within these genes that we are searching for one that encodes a target receptor. Determining which receptor gene sequences are potentially involved in pheromone communication involves quantification of gene transcript levels in the beetles. We hypothesise sex pheromone receptors will show sex-biased expression and are therefore examining OR expression in the heads of male or female beetles. Some differences in expression levels have been observed using real-time quantitative PCR and our search for a receptor solely expressed in one sex continues. Receptor function in the beetle will be confirmed using behavioural studies and RNA interference. RNA interference eliminates expression of a targeted gene, and if that gene is involved in a measurable behavioural response (such as attraction to the opposite sex), we can measure this in a test arena called an olfactometer.

It is envisioned that research into insect pheromone receptor systems will not only demonstrate the feasibility of using them as a potential bio-recognition element in a biosensor device, but would additionally aid in our overall understanding of the mechanisms involved in invertebrate olfaction.

About the author:

Kelly graduated from a Bachelor of Science, Nanotechnology (Hons) in 2004 from Flinders University in Bedford Park, South Australia. She then went on to do her PhD at CSIRO, Molecular and Health Technologies in Adelaide, in conjunction with the department of Biochemistry at The University of Adelaide. Her thesis was entitled: "Assay and Array technologies for G-protein coupled receptors". Her interests and expertise lie in molecular biology, protein expression and determining protein function. Her previous research interests involved membrane proteins, which are proteins that reside in the cellular membrane and are commonly important in extracellular communication. Specifically, she investigated the potential role of these proteins as biological recognition components for assay and array technologies, and this led her to take up a role in her current position as a postdoctoral researcher at South Australia's Research and Development Institute, working on the project "Biosensor-based detection of grain pests" for the CRC for National Plant Biosecurity team. Outside of work, Kelly likes her outdoor activities and spends her time down the beach in the summer and is a lifesaver for the local surf life saving club, and plays a bit of lacrosse in the winter.

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New recombinant antibodies for virus detection

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The use of serological assays in viral diagnostics is still the preferred method for robust detection assays. Nucleic acid-based detection is more sensitive and rapid, but the specificity of the reactions can limit detection, particularly within diverse virus species and those with high rates of recombination.

We are creating a system to generate recombinant single-chain variable fragment (scFv) antibodies, with properties that will allow their production and site-directed labeling. The specific chemistry used to label the scFvs should allow detection without alteration of the kinetics with which they bind to their antigen, an interaction that can be negatively affected by random crosslinking techniques that are currently employed in antibody-reporter linkage.

Two different vector systems, both based on the phage display library of pCANTAB-link (Sapats et al. 2003) have been constructed. One has the labeling site, and an immobilized metal ion affinity chromatography (IMAC) purification tag, and the second has both of these and the addition of the sequence for the human kappa light chain region. Expression of scFvs with the human kappa light chain have been shown to form dimers which increase target specificity, and will also allow detection using anti-human labeled antibodies.

For a test system, the use of Potato Virus Y (PVY) was chosen. Purified PVY was injected into chickens, and the spleens harvested for RNA extraction. An initial scFv library was created in pCANTAB-Link, screened and two binders to the purified virus were isolated. The scFvs developed will be tested for utility in traditional ELISA and microsphere assays.

About the author:

Paul obtained his PhD from the University of Queensland sometime in the last 10 years, and now works for the Queensland government in the Department of Employment, Economic Development & Innovation. He is a molecular biologist that happens to like working with plant viruses. He is slowly being seduced to the dark side of bio-informatics and database design, which everyone in his lab is happy about, because less things will probably get broken in the process of 'fixing' them. Outside work, he also enjoys the idea of long walks on the beach, but lives too far from the coast, doesn't like sand or salty water all that much, gets sunburnt really quickly, and therefore just stays at home.

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Dermestidae species differentiated using a novel approach to quantitative PCR

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Accurate identification of *T. granarium* is fundamentally important, however, morphology, DNA barcoding and traditional polymerase chain reaction has limitations in providing an accurate identification. To overcome the inherent limitations of these existing methods, a quantitative PCR multiplex test was designed using species specific primers and probes, an amplification control, followed by melt curve analysis. Each component of the multiplex reduced the incidence of both false positives and false negatives, therefore, increasing specificity and sensitivity of the test.

About the author:

*Mark Castalanelli is currently a PhD student with the Cooperative Research Centre for National Plant Biosecurity and is conducting research into molecular markers for Khapra Beetle, one of the worlds most serious pests of stored products. Mark is excited about his research into molecular understanding of the family Dermestidae as there is little published data on molecular markers for this family of beetles. Mark has previously worked on *Hulotrupes bajulus* (European House Borer, EHB) molecular diagnostics and gene flow population studies as part of an eradication program for the pest.*

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Systematics of the *Ustilago*, *Sporisorium* and *Macalpinomyces* complex of smut fungi

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Smut fungi are important pathogens of grasses, including the cultivated crops maize, sorghum and sugarcane. Typically smut fungi infect the inflorescence of their host plants. Three genera of smut fungi, *Ustilago*, *Sporisorium* and *Macalpinomyces*, form a complex with overlapping characters that makes species placement problematic. Previous attempts by others to more accurately define these genera using morphology and molecular phylogenetics have been unsuccessful and highlighted the polyphyletic nature of the genera.

A systematic analysis of 137 smut species in the *Ustilago*, *Sporisorium* and *Macalpinomyces* complex was completed. Morphological and molecular data from five loci were phylogenetically analysed by maximum likelihood and Bayesian analysis. The phylogenetic hypotheses generated were used to indicate morphological synapomorphies, which had previously been dismissed as homoplasious within the complex. These synapomorphic characters are the basis for a new taxonomic classification of the *Ustilago*, *Sporisorium* and *Macalpinomyces* complex, which takes into account their morphological diversity and coevolution with their grass hosts. The new classification is based on (i) a redescription of the type genus of *Sporisorium*, and (ii) the establishment of four new genera based on monophyletic groups to accommodate the species that are expelled from *Sporisorium*.

About the author:

Andrew Geering is a plant pathologist at the University of Queensland. His primary interest is plant virology although he has utilised the molecular skills he has acquired in this discipline to investigate the evolution and detection of other groups of pathogens. As part of the CRC for National Plant Biosecurity, Andrew has led projects looking at novel detection systems utilising nanotechnologies and recombinant antibodies. In his spare time, Andrew enjoys gardening, birdwatching, sport, tasting wine and listening to music. Andrew was also senior editor and coauthor of the book 'Shorebirds of Australia', winner of the 2007 Whitley Award for best field guide.

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Performance analysis of flying spores detection system for plant biosecurity management

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There is a global need to develop technologies for earlier detection and monitoring of spores of plant pathogens EPP incursions[1,4]. This paper presents the hardware development and testing of a new concept for air sampling via the integration of a prototype spore trap onboard Unmanned Aerial System (UAS). The paper describes the integration of a prototype spore trap onboard UAS to allow multiple capture of spore pathogens in multiple remote locations at high or low altitude; otherwise not possible with stationary sampling devices.

Existing spore sampling devices are stationary at the sampling location. Location is important due to prevailing climatic conditions, and use of sampling devices in remote locations and where topography is severe is almost impossible. In such scenarios, airborne sampling has been suggested as a viable alternative [2,3]. Thus a new solution is desired which capability present to take spore samples in multiple locations and in remote regions where access to local sampling is difficult.

There is some research previously conducted in the area of airborne sampling using remotely controlled manned and unmanned aircraft variants[2,3,4]. Dynamic sampling systems have the potential to improve upon current static ground based sampling methods.

During autonomous operations, the onboard autopilot commands the servomotor to rotate the sampling device to a new indexed location once the UAS vehicle reaches the predefined waypoint or set of waypoints (which represents the region of interest). Time stamped UAS data is continuously logged during the flight to assist with analysis of the particles collected. Testing and validation of the autopilot and spore trap integration, functionality and performance is described.

Wind tunnel testing was performed and highlighted several issues such as dispersion of larger particles (> 3microns) and analysis of particles under fluorescent microscopes. Flight testing was conducted to verify the spore traps capability to capture spores in real world conditions. The spore trap was integrated with the test platform and onboard autopilot systems. Flight experiments demonstrated that the spore trap was able to successfully capture and geo-locate simulated spore particles during autonomous missions. It was shown that sample contamination could be avoided through the inclusion of neutral locations on the tape. The tape rotation mechanism was programmed to automatically rotate the tape to the sampling location once the UAS entered the sampling region and shift the tape location to the neutral point once the UAS was outside the sampling region. Additionally all flight data was logged using the onboard autopilot data logger. A tape rotation algorithm was implemented to control the position of the drum to capture multiple samples without contamination. This allows for the geo-location of spores and for the characterisation of spores concentrations at discrete altitudes.

The sampling system has the ability to spatially monitor fungal spores, and protocols to interpret their spatial distribution. These tools greatly enhance the ability to detect new incursions of fungal pathogens and to enable more accurate delimiting of distribution. Overall, the use of this technology allows early detection of Emerging Plant Pest (EPP) incursions in remote or difficult areas.

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Dr Luis Felipe Gonzalez has a Ph.D. degree in aeronautical engineering from the University of Sydney, Sydney, Australia, in 2006. He is a Lecturer at Queensland University of Technology (QUT) and the Australian Research Centre for Aerospace Automation (ARCAA). Felipe joined ARCAA in 2006 and has directed his attention to enabling technologies for flight control and optimization of civilian UAVs systems. He has developed six operational UAVs and has written six journal papers, 35 refereed- conference papers and five book chapters.

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The description of three novel species of *Phytophthora* from native vegetation in Western Australia

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The *Phytophthora* culture collection of the Vegetation Health Service of the Department of Environment and Conservation of Western Australia (WA) has been re-evaluated using DNA sequencing (Burgess et al., 2009). This has revealed many undescribed taxa previously classified as known morpho-species, one of which has recently been described as *P. multivora* (Scott et al., 2009).

The aim of this study was to describe three of these taxa, all of which occur in WA native ecosystems. They were compared with both the morphological species to which they are most similar and their closest phylogenetic relatives. In addition, the pathogenicity of these taxa was assessed in glasshouse trials.

P. elongata (Rea et al. 2010) has been isolated from revegetated bauxite mine-pits and undisturbed sites in the jarrah (*Eucalyptus marginata*) forest. The distribution of this taxon appears to be restricted to this ecosystem. It belongs to ITS clade 2 of Cooke et al. (2000) and is most closely related to the nursery pathogens *P. bisheria*, *P. frigida*, and *P. mutlivesiculata*. This pathogen of *Eucalyptus* and *Banksia* appears to have been introduced to WA, as indicated by the *cox1* sequence data.

P. taxon constricta and *P. taxon arenaria* occur in the Kwongan vegetation of the sandplains to the north and south of Perth. They reside in clades 9 and 4 (Cooke et al., 2000), respectively. Both taxa are pathogens of proteaceous plant species, particularly *Banksias*.

All three taxa are homothallic with paragynous antheridia, and have a large oospore wall index possibly indicative of adaptation to the seasonal extreme heat experienced in the ecosystems in which they occur.

This study highlights the utility of DNA sequencing as a tool for delineating species where morphological identification is ambiguous, and indicates that both introduced and endemic *Phytophthora* species may be present in different ecosystems in the south-west of WA.

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About the author:

Alex Rea completed a B.Sc majoring in Molecular Biology and Biological Sciences, graduating with first class honours in molecular biology (molecular endocrinology) in 2004. Prior to undertaking his Ph.D with the CRCNPB in April 2007, Alex worked as a botanical consultant undertaking surveys of rare and endangered flora in the northern sandplains and goldfields of Western Australia.

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A learning method for emergency plant pest detection on hyperspectral image

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Emergency plant pests (EPPs) are one of the major problems in Australia's plant industry in particular causing productivity losses, incurring management costs, and restricting Australian trade opportunities, etc. Rising global food demand and the necessity of transportation have increased the potential for exotic plant pest incursion in the country. An emergency plant pest incursion can be eradicated through emergency response measures, but the chance of success and affordability in eradication depends on a surveillance system, which will reveal the occurrence of the pest while it is still confined in a small area. Such surveillance systems are essential as they are the first defensive array in place against incursions. Moreover, they are used for monitoring pest status during eradication programs.

Currently, plant pest surveillance relies on detection of exotic pest incursions by using insect trap grids. Since many plant pests are capable of spreading quickly, the network of traps must operate to reveal the presence of an insect target when just a few are present in a region. However, the operational expenditure for the existing systems is expensive, due to labour and travelling costs to access traps for inspection on a routine basis.

Recent developments in remote sensing and computer vision technology have opened-up the possibility of recovering spectral traces of insects for purposes of classification and recognition. This allows the development of tools and software for the automation of early warning trapping grids. This research focuses on the computational techniques in computer vision and machine learning required to recognise and identified emergency plant pests from hyperspectral imagery.

In this poster/or presentation, we present a method for object of interest detection, which forms part of the second phase of my PhD project. This method is statistical in nature and hinges in a model which combines salient features using a mixture of linear Support Vector Machines (SVMs). It exploits a divide-and-conquer strategy by partitioning the feature space into sub-regions of linearly separable data-points. The mixture weights and the feature combination coefficients are optimised using an Expectation-Maximisation (EM) algorithm. Thus, from this learning approach, a mixture of classifiers can be used to recover objects of interest, i.e. pests, in the image. The method provides results in the form of saliency map, in which each pixel is assigned with a measure of "relevance" to indicate the degree to which a region in the image is attractive to visual attention. An illustration of method utility by applying the method to a hyperspectral database (contains sets of Emergency Plant Pest images) will be provided as an application on pest detection and classification.

About the author:

Ms Pattaraporn Khuwuthyakorn is a PhD student with the Cooperative Research Centre for National Plant Biosecurity (CRCNPB). At present, Patt is studying at the Australian National University, Canberra under the supervision of Dr Antonio Robles-Kelly, Dr Jun Zhou and Dr Louise Morin. Her research interests are in the areas of computer vision and pattern recognition. She is working on the NICTA Smart Trap project, which is a joint project between CRCNPB and NICTA. It aims at developing algorithms to detect and classify pests based on hyperspectral imaging.

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Tools for Detection and Diagnostics

Chair: Rohan Rainbow



Evaluation of novel platforms for their ability to identify new biomarkers for bacterial pathovars

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Many of the biggest threats to the biosecurity of Australia's plant industries are bacterial. Difficulties in the identification of phytopathogenic bacteria to the subspecific, or 'pathovar', level is difficult and could seriously delay the management of major disease incursions and interfere with market access for plant produce. By definition, pathovars are distinguished by host specificity so bioassays on plants are the definitive means of identification. However, such bioassays require high level physical containment, are slow and subjective and often unreliable.

Rapid serological and molecular tests are available to rapidly and specifically identify some bacteria to pathovar level, but in reality, better diagnostic targets are required to differentiate many exotic pathovars from closely related, endemic organisms. The empirical search for robust markers to pathovar level using classical approaches such as the identification of DNA polymorphisms through sequencing or fingerprinting has been a slow and labour-intensive process and has a poor record of success. Practical limitations are often encountered where assays are based on proteins or genes of unknown function, or regions that are known not to be related to pathogenicity and/or are plasmid-borne.

This project has evaluated proteomic and metabolomic profiling techniques for their ability to fast-track the identification of biomarkers that reliably differentiate particular pathovars from each other. These platforms profile the functional molecules expressed by the organisms, molecules that may be associated with, or even determine, the plant-pathogen interaction. Our hypothesis was that the profiles of two pathovars from the same species would differ because they infect different host plants, and that, as potential determinants of pathogenicity, the differentially expressed functional molecules would translate to robust diagnostic markers. The project has used two *Xanthomonas* species as the model for the work.

The proteomics component of this project has focused on the two-dimensional gel electrophoresis and profiling of membrane-associated proteins extracted from selected bacterial isolates, either grown on media or after passage through sensitive or insensitive plant hosts. Results show that isolates of the same pathovar cluster together and can be differentiated from closely-related pathovars. Proteins that are differentially expressed between operative pairs of pathovars are evident and have been chosen for further analysis by mass spectrometry and peptide sequencing. Reference to genomic sequences has allowed us to identify the genes that encode the differentially expressed proteins. The project is currently developing DNA-based assays from these results and will go on to validate these and deliver the best as improved diagnostic tools for laboratory end-users.

The metabolomics component has analysed metabolite expression in selected bacterial pathovars and in whole plants artificially inoculated with *Xanthomonas campestris* pathovars. Results show separation between the different pathovars and differentially expressed metabolites, which have potential as new biomarkers, are evident and will be identified and assessed for their ability to provide differentiation at the pathovar level.

This project is the first application of these platforms to plant biosecurity, and the outputs of this project will guide decisions on their potential implementation in fast-tracking the identification of biomarkers to discriminate other species of biosecurity concern, where pathovar differentiation has been a problem.

About the author:

Dr Deb Hailstones joined I&I NSW late in 1997, following an early career spent in medical research. She now leads a range of research and diagnostic projects providing biosecurity for the horticultural industries of NSW through the development and implementation of DNA-based technologies. Recent activities include the development of national standards for the diagnosis of key exotic threats to Australia's plant industries, a leading role during the incursion of citrus canker in Queensland 2004/5, and the adaptation of biotechnologies to discriminate strains of fruit fly. Her current research projects include the evaluation of novel platforms to identify and deliver improved diagnostic methods for closely related pests and pathogens and studying the molecular basis of plant/pathogen interactions. In addition to her project activities, Deb is also the Research Leader for Plant Pathology in the Biosecurity Research Branch of I&I NSW and the Program Leader for Diagnostics Research in the CRC for National Plant Biosecurity.

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New technologies for the detection and monitoring of begomoviruses and their whitefly vectors

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Whitefly-transmitted begomoviruses (family Geminiviridae) cause economically important diseases of many dicotyledenous food and fibre crop plants worldwide. Epidemics of begomoviruses are increasing in frequency due to the capacity of these viruses to rapidly evolve, the globalisation of trade, and the worldwide dispersal and polyphagous nature of the efficient whitefly vector *Bemisia tabaci* (B biotype).

In 2006, the exotic begomovirus Tomato yellow leaf curl virus (TYLCV) was detected for the first time in Australia in commercial tomato plantings surrounding Brisbane, the Lockyer Valley and Bundaberg (Queensland). The introduction of TYLCV has had a significant economical impact on tomato production, with disease incidence in some areas reaching 100%.

To limit further spread of TYLCV within Australia and to detect new incursions of exotic begomovirus species, rapid, efficient and reliable diagnostic strategies are required. Multiplexed real-time PCR and novel microsphere-based suspension arrays are being investigated to improve the efficiency and accuracy of routine plant virus detection in Australia.

Multiplexed TaqMan™ real-time PCR diagnostic assays for the detection of the endemic begomovirus species Tomato yellow leaf curl virus and Tomato leaf curl virus, in addition to assays for the detection of genetic groups of the vector *B. tabaci* (specifically those known as the endemic "B" and exotic "Q" biotypes), have been developed. Together, these assays provide a flexible diagnostic toolkit for the detection and differentiation of begomoviruses and their vectors in Australia. These assays will facilitate monitoring of the spread of TYLCV and ToLCV, and the potential incursion of exotic begomoviruses and genotypes of *B. tabaci*.

The Luminex® xTAG™ microsphere platform is being investigated for high-throughput nucleic acid detection of plant viruses and vectors in Australia. This system utilises a proprietary universal tag system allowing the simultaneous analysis and reporting of up to 100 different reactions in a single reaction vessel. We propose using this technology for the detection of endemic and exotic begomovirus species and *B. tabaci* genetic groups, utilising a hierarchical assay design for the detection of DNA-A, DNA-B, DNA-α and DNA-β satellite molecules. This hierarchical assay design will facilitate the identification of both known and unknown (or newly evolved) begomovirus species and *B. tabaci* genetic groups.

About the author:

Sharon van Brunschot is a research PhD student supported by the Cooperative Research Centre for National Plant Biosecurity, Queensland Primary Industries and Fisheries (QPIF) and The University of Queensland (UQ). After completing her Science (Honours) degree in 2003, Sharon worked as a research assistant for the CRC for Tropical Plant Protection and QPIF. Her research was focused on the characterisation and development of diagnostic assays for a range of important fungal pathogens that affect horticultural industries in Australia. Sharon also recently developed and has lectured the postgraduate course "Molecular Diagnostics in Plant Protection" for the School of Biological Sciences (UQ).

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Project review: the development of new diagnostic platforms to assist post entry quarantine plant pathology laboratories

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The CRCNPB project 40035 concluded with the successful development of a range of diagnostic tools to support Post Entry Quarantine (PEQ) pathologists and include:

- Tests that can detect five genera of plant viruses that are biosecurity threats to the Australian grain industry.
- A diagnostic manual for the detection of potyviruses that has been submitted for inclusion in the Plant Health Diagnostic Standards. This manual is unique in that it has been validated to detect a defined group of potyvirus species. Other manuals developed in this project for the detection of groups of pathogens will also be submitted for review.
- A quantitative PCR test that determines the usefulness of FTA cards for storing virus RNA in crude plant extracts. Results from this study will benchmark the application of FTA cards for the storage of plant virus RNA and support active surveillance and incursion management programs. If feasible, this method could be used for the safe movement of plant virus RNA across quarantine borders.

A PEQ pathology workshop is being organised with QUADS partners to discuss these and other diagnostic techniques for use in a plant quarantine laboratory.

About the author:

Linda Zheng graduated from Bachelor of Biomedical Sciences with honors from the University of Melbourne in 2004. Her interest in genetics and functional genomics saw her undertake a doctor of philosophy program in Ecology, Evolution and Systematics from The Australian National University, Canberra. During her candidature, Miss Zheng investigated the implications of plant virus discovery in the genus Potyvirus on their detection and developed a novel method of designing group-specific universal primers for virus detection.

Her PhD studies also introduced her to the field of applied bioinformatics. Upon the completion of her PhD studies, Linda worked on a CRC funded project 'Post-Entry Quarantine' where she continued to explore the world of plant virus diagnostics. Linda is currently an employee of the Victorian Department of Primary Industries and her research interests include applied bioinformatics, virus detection and diagnostics, virus evolution and ecology.

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Sniffing out grain infestations with the Red Flour Beetle, *Tribolium castaneum*

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Stored product insect pests, such as the red flour beetle (*Tribolium castaneum*), produce pheromones and other volatile chemicals that can betray their presence. They also detect these odours with high sensitivity to find mates or suitable food sources. This sensitivity and specificity relies on odorant receptors (ORs) and would be ideal for detecting infestations for targeted pest management.

There are 259 potential OR genes annotated in the *T. castaneum* genome (Engsontia et al., 2008, Insect Biochem. Mol. Biol. 38: 387) and we aim to find one or more that can detect infestation odours. To improve our chances of finding a suitable OR, we are using two complementary approaches: one is presented at the 2011 Science Exchange by Kelly Bailey and the other is outlined here.

This approach is based on the observation that 35 OR genes are expressed in both adult and larvae heads (Engsontia et al., 2008). We hypothesised that both larvae and adults can detect infestation odours in order to find food or breeding sites. This hypothesis was confirmed by behavioural studies in an olfactometer with infestations of *T. castaneum* or two other grain pests: *Rhyzopertha dominica* or *Sitophilus granarius*. Therefore, this relatively small set of genes can be targeted.

To find a specific OR, we also need a specific odour. We are now testing several individual chemicals associated with infestation odours, such as aggregation pheromones. Chemicals that can be detected by both life stages are likely to be recognised by one or more of the 35 shared OR genes.

We aim to implicate OR genes in chemical detection by using RNA interference to attenuate the expression of each OR in turn. Without normal expression of the necessary OR, we hypothesise that beetles will lose their behavioural response to a chemical. In addition to these olfactometry studies, we are also investigating electroantennography as a method of discerning recognition. With these approaches we aim to identify ORs for application in protecting stored products, such as grain in silos or railcars, through early detection of infestation.

About the author:

After completing his Bachelor of Science (Hons) in 2001 at Lincoln University (Canterbury, New Zealand), Bradley moved to Canberra for his PhD at the Research School of Chemistry at the Australian National University. With the supervision of Professor David Ollis, Bradley completed his thesis entitled "Directed evolution of pyruvate decarboxylase for *in vitro* glycolysis" (2006). His interest and expertise in protein biochemistry, enzymology and molecular biology helped secure his post-doctoral appointment at the Liverpool School of Tropical Medicine (United Kingdom). In this position he isolated and tested many mosquito enzymes for their ability to metabolise insecticides as part of global efforts to control malaria and dengue fever.

At the end of 2009, Bradley joined the CRC research team and is based at CSIRO Ecosystem Sciences, Canberra. He is enjoying the challenge of working with integral membrane proteins: from their molecular details, biological implications, and potential biotechnological applications. Outside of the laboratory, Bradley spends time painting, mountain biking, hiking and generally being outdoors.

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Development of a smart spore trap

Les Zeller^{1,2} and Paul Kamel^{1,2}

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This project has evolved from a scoping study to determine the potential of a mobile geo-referenced spore trapping system into a hardware development project. CRCNPB project 30032 developed the technology for a sampling system that has the ability to spatially monitor fungal spores. This project extends on this development to incorporate different modes of operational functionality. This tool will greatly enhance the ability to detect new incursions of fungal pathogens and to enable more accurate knowledge of source and distribution. The technology will allow for earlier detection of emergency plant pest incursions in difficult areas and provide efficient and effective airborne surveillance.

The aim of this project is to modify an existing commercially available spore trap to include the developments of the mobile ground based spore trap to provide accurate information about the spore capture times and prevailing climatic conditions. Commercially available technology captures spores on a surface with the position of the spores on the surface being referenced by time. The proposed spore trap differs from this concept by allowing the ability to program the spore trap to reference the position of the spores on the surface to other parameters. For example, time of day, temperature, humidity, wind direction or location as for a mobile application. Therefore the population density of spores on the surface will produce a histogram which relates the programmed parameter with spore release. Also the smart spore trap will incorporate a data logging capability providing a multi-dimensional array of averages of all measured parameters for each programmable time interval during spore collection. This will improve the efficiency and accuracy for collecting data for researching the environmental conditions required for spore release.

Development of the smart spore trap involves modifying an existing spore trap to incorporate GPS, temperature sensor, humidity sensor, electronic compass and microcontroller PCB.

About the author:

Mr Les Zeller is a Senior Research Engineer, Food and Crop Science, Department of Employment, Economic Development and Innovation. He has almost 30 years experience in the design and development of electronic and mechanical equipment for agricultural research. A turf traction testing device he invented has been patented by the Queensland government. He has formal qualifications in applied physics and engineering. He enjoys a glass of wine and playing golf and tennis.

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Using CSI methods to detect fungal spores on clothing

Dominie Wright^{1,3}, David Berryman^{2,3}, Belinda Cox¹ and Mingpei You¹

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Picture this... Crime scene investigators walking into a room, using forensic tape on the victims clothing and personal belongings. The evidence is bagged and then transported carefully to the laboratory for processing. Chain of evidence is kept at all times, and all steps documented. Can we determine the perpetrator of this horrendous catastrophe? Can we prevent further damage? On TV, this evidence is bagged and then taken to a lab where it is processed, and inevitably there is a machine that goes 'ping' saying that the results are ready. Can we do this in the world of Plant Pathology? Do we need to do this? Why would we do this?

This project is investigating the use of CSI methods to determine the risk of spores entering Australia on travellers' clothing. Do fungal spores love to hitch a ride on our clothing? Can we determine if there are hitchhikers and what they are, and possibly where they come from?

This project has been able to demonstrate that clothing can be a donor or a recipient of these hitchhikers. The size of the fibers and the weave of the material influence the effectiveness in the collection and transfer of spores, as does the physical characteristics of the spores.

Meanwhile back in the lab... the evidence collected is being processed to remove the hitchhikers and identify those suspects using morphological techniques (microscopy), DNA techniques (Real-time PCR) and analysis using the mass spectrometer. Can the mass spec identify these hitchhikers reliably?

The project demonstrates the risk of spores travelling on clothing. More than 200 samples were processed using the above methods and the results will be very revealing. These results will demonstrate that further education is required for travellers to highlight the shared responsibility required for protecting Australia's agriculture and environment. The project will highlight the necessary strategies required to ensure that this risk is reduced when returning from field trips locally, nationally and internationally.

About the author:

*Ms Dominie Wright is a Plant Pathologist with the Department of Agriculture and Food, Western Australia. She has a broad background in plant pathology having worked in both the broadacre and vegetable sectors as a diagnostician for fungal and bacterial pathogens. Dominie has a strong interest in biosecurity having developed a national diagnostic protocol for *Tilletia indica*, and has recently completed the National and International Diagnostic Protocol for the identification of *T. indica*. She has also developed with colleagues two national contingency plans for *Tilletia indica* and *Tilletia contraversa*.*

Dominie's other main area of interest is training agronomists and farmers in disease identification in their crops. Dominie has just completed a Graduate Diploma in Education (Adults and Tertiary) through Murdoch University, and is also involved in the Scientist in Schools program where she is helping teach primary school children about growing plants. Dominie is excited to be investigating the use of forensic methods for plant pathology, and has thoroughly enjoyed this project and being able to think outside the square.

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Digital tools for diagnostics

Gary Kong¹, Amy Carmichael^{1,2}, Michael Thompson^{1,3}, Julianne Farrell^{1,4}, Ken Walker⁵, Dean Beasley^{1,4} and Joy Conroy⁴

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The way that we use the internet is evolving rapidly. It's no longer enough to simply access information – it now has to be personalised and shared. The ease of communication that the internet affords has given rise to faceted searching and social networking and these concepts are now key drivers in the way we collect, organise, preserve and disseminate information. Users of the internet want and need to be able to find their desired information quickly and easily – whether it's a car on e-bay, a fashion item, a book, an old high school buddy, the answer to a trivial pursuit question, a physics problem or political statistic, it doesn't matter – if it can't be found quickly and easily, if it can't be stored, edited, manipulated or shared, it will not attract users. Information that is not digital or is not organised for internet searching or compatible with social media, will become invisible.

This applies as much to scholarly information as any other and anybody considering the future of digital libraries, record databases, catalogues, etc must include these factors. This may seem like foreign ground for science, but the internet creates a unique opportunity for science communication, engagement with science communities and participation with the broader social milieu. If they say a 'rising tide floats all boats', then we need to make sure ours is at least in the water.

PaDIL, the Plant Biosecurity Toolbox and Remote Microscopy have been busy in the past year working on infrastructure, processes and products that consider the internet-user interface and the need for social networks, shared knowledge, shared workspaces, easy access and information output that fits the personal and social context of its users. To achieve this goal, we propose a conceptual framework based around a new web portal known as BowerBird.

About the author:

Gary's research with the CRCNPB will contribute to and improve the speed and accuracy of plant pest diagnostic procedures.

Gary has a background in Plant Pathology research and since 1987, has studied foliar diseases of field crops. In particular, he has investigated the genetics of resistance to biotrophic and necrotrophic pathogens of sunflower, studied the evolution and population dynamics of the sunflower rust pathogen and developed disease management strategies using marker assisted selection (MAS) as a breeding tool to pyramid disease resistance genes. In addition, he has managed a large research program within DEEDI consisting of plant breeders, genetic resources and post-entry quarantine facilities.

Gary's current interests include the development of electronic information systems such as databases, web-interfaces and remote diagnostic networks.

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Poster session 2:

- Predicting Incursions and Spread
- Sampling Design and Analysis
- Eradication and Control



A review of the climate change implications for the pest status and vectoring potential of the bird cherry-oat aphid, *Rhopalosiphum padi*

K.J. Finlay^{1,2}, J.P. Aurambout^{1,3}, P. De Barro^{1,4}, P. Trebicki⁵, W. Griffiths^{1,5}, D. Kriticos^{1,6}, H. Parry^{1,6} and J.E. Luck^{1,2}

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Aphids are likely to adapt to climate change given their short generation times, low developmental threshold temperatures and efficient dispersal capabilities. Surprisingly little is known however about their vectoring ability and the indirect effects to their hosts with climate change. In-depth analysis of the interactions of a single host-pest-pathosystem provides an exemplar system from which climate change effects can be elucidated. We have focused on the bird cherry-oat aphid (*Rhopalosiphum padi*); one of the major pests of temperate cereal crops worldwide, notable for its extensive Poaceae host range and as a prominent vector of the wide ranging highly destructive yellow dwarf virus (YDV). The two foremost factors influencing aphid vector population dynamics and the subsequent incidence and severity of YDV infection in host plants are the persistence (survival and abundance) of the vector and the timing, rate and extent of dispersal and migration events.

The main direct effects of climate change on *R. padi* persistence is elevated temperature leading to faster development rates and higher fecundities and reduction in winter mortalities at least up to an upper thermal threshold. Vector virus interactions were altered with greater virus inoculation and transmission efficiencies at higher temperatures. All effects were more pronounced on the apterae populations. The accompanying effects of elevated CO₂ are less clear but may cause reductions in population levels. Colonisation of wheat by aphid vectors is a direct consequence of aphid movement via dispersal or migration events, the magnitude of which can affect the occurrence of YDV infections in the crop. Elevated temperatures will shift timing and duration of lower and upper thermal thresholds that determine flight. Flight patterns will be disturbed by projected increases in wind strengths possibly leading to larger and longer range migration flights. Alternatively heavy precipitation will hamper aphid take-off and flight leading to poor colonisation by alates. Drought stressed plants encourage movement of *R. padi* nymphs and apterae. Finally, seasonal variation in precipitation will vary population dynamics. Late summer and early autumn rainfall, for example, is a determinant of population size colonising winter cereals in Australia.

The qualitative analysis of *R. padi* biology with the influence of climate change is being used to construct an integrated *R. padi*-virus-wheat model to quantitatively assess the yield impacts of YDV infections under future climates.

About the author:

Kyla Finlay is a Research Scientist in the Biosciences Research Division of the Department of Primary Industries, Victoria. She has worked as an entomologist with the Department for the past 10 years being involved in pest identifications, invasive species, plant health diagnostics, pest risk assessments and plant biosecurity. She completed her PhD in Entomology at Monash University in 2002. For the past five years, she has been involved in climate change research, particularly the direct impact of an altered climate on vector-borne diseases and the subsequent impact this may have on the interactions between the plant, vector, pathogens and environment and ultimately on plant health.

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A simulation technology approach to *Bactrocera* spp: lessons from a past incursion for improving future responses

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The Tephritidae family, and particularly *Bactrocera* spp., rank highly in economic importance for the AUD\$6.9 billion Australian horticultural industry. The major species in this group is *Bactrocera tryoni*, known as Queensland fruit fly (Qfly), which is the major pest of horticulture in eastern Australia. The Qfly is highly polyphagous and is also multivoltine, being able to exploit fruit and vegetables all year round. Increasing interstate trade and tourism, and therefore the movement of people and tourism will encourage the transport of commodities that are a fruit fly risk. This increases the long-distance dispersal, and thus the risk of incursion of Qfly into new areas. Qfly is native to Australia and was originally only found in tropical and subtropical rainforests of Queensland. It has now been found from Victoria to far north of Queensland and in New South Wales, but is absent from WA, where it is considered to be a high impact pest species. Qfly has hundreds of hosts, including most tropical and temperate commercial fruits and vegetables. Potential losses to the threatened horticultural industry have been estimated at AUD\$100 million a year, most attributable to Qfly.

In 1989, WA had its first incursion of Qfly and it spread rapidly throughout the Perth area. Although Qfly was eradicated, the historical event provided excellent data to allow a model of spread to be developed. Fruit surveillance at the time indicated that Perth had plenty of suitable fruit hosts available for Qfly and that the potential geographic distribution of *B. tryoni* would not be limited by temperature and rainfall. The Qfly flight range varies and its dispersal distance is debatable. The adults of Qfly are strong fliers but, in reality, most dispersal is over short distances within habitats, nevertheless, they can disperse between habitats separated by distances up to at least 90 km. Host availability for Qfly is a factor in determining dispersal flights between habitats. Clearly there is a need for an elegant approach to estimate and predict the worst case scenario for spread following an incursion. Such an approach will allow managers to simulate and predict the spread of any *Bactrocera* spp.

In this simulation project, we are focusing on population growth, time, host quality, seasonality, means of spread and the speed of spread of *Bactrocera* spp. after it is detected in a new habitat. Through the development of a simulator, rapid response and the selection a management strategy for containment/eradication can be developed. This project is developing methods for designing optimal surveillance strategies that quantitatively account for these factors. The product is a computer simulation model that provides decision-makers with more timely information to make decisions. The model has applicability for all levels of government within Australia allowing a national approach to any incursion. This simulation model has the potential to analyse and map many features of an eradication program.

About the author:

Dr Maria José (Mazé) de Sousa-Majer has a broad entomological background, having worked on bee diseases, microbial insects control, genetically modified crops and post-harvest disinfestations of native crops. She holds undergraduate and MSc degrees from the Federal University of Viçosa in Brazil and a doctorate from Curtin University of Technology, which was capped off by a postdoctoral fellowship at the same institution. She is currently working on the project Plant Biosecurity matters at DAFWA. They are also gathering information sets in support of improved strategies to prevent against the establishment and spread of Emergency Plant Pests (EPP) in Australia.

Dr Juan José García Adeva has a strong background in Software Engineering and has applied this in areas of building software frameworks for knowledge-based systems and text mining. He holds a Bachelor of Engineering degree from the University of the Basque Country UPV / EHU, an MSc from Essex in the UK, and a PhD from Sydney University. For the last few years he has been a Research Fellow in the computational modelling group in the School of Computer Science and Software Engineering at the University of Western Australia. With Professor Reynolds (UWA) and other members of the team from the WA state department of agriculture, he has been engaged in building a computer-based real-time simulator for modelling the spread of Emergency Plant Pests over time across a geographical region.

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Modelling the 1996 lupin anthracnose incursion in Western Australia

Michael Renton^{1,2,3}, James Bennett^{1,2} and David Savage^{1,2}

¹School of Plant Biology, University of Western Australia, ²Cooperative Research Centre for National Plant Biosecurity, ³CSIRO Ecosystem Sciences, WA

In this presentation I will explain how we used computational modelling to investigate the spread of lupin anthracnose over a spatially heterogeneous landscape. I will consider a situation analogous to the 1996 incursion in Western Australia which crippled the albus lupin industry, and address the question of whether the incursion could potentially have been eradicated. I will focus on several important factors that influence the likelihood of eradication: spatial characteristics of landscape suitability, organism detectability, surveillance effort and the type of management strategy applied.

For the purpose of this case study, a spatially heterogeneous suitability map that describes this landscape was created using a satellite image. I will discuss how the method used for creation of the suitability map has applications in a rapid response protocol and is part of the general system to rapidly classify potential spread of any new disease or insect invader that is being developed in CRCNPB project 10124. I will also demonstrate the effect that the spatial pattern of lupin paddocks has on disease progression and detection.

Within the simulation, we use a simple detection rule where the probability of detection is a function of the detectability of the organism and the search effort. Upon detection, control techniques are implemented. The predicted success of different control options and how this depends on organism detectability and surveillance effort under different scenarios will be discussed.

About the author:

Michael completed his Honours program at UWA in Maths, looking at control in chaotic systems, and his PhD at the University of Queensland in the Centre for Plant Architecture Informatics, looking at new approaches to modelling the interactions between plant form, function and environment. His post-doc in Montpellier, France, married stochastic models with structural models to create virtual apple trees and he then returned to Perth to teach applied maths at UWA, before spending a couple of years creating the Weed Seed Wizard (a model of seedbank dynamics) at the Department of Agriculture and Food. He started as a lecturer in computational agro-ecology in the School of Plant Biology in July 2007 and his current projects involve modelling of weeds, seedbank population dynamics, evolution of resistance to herbicides and pesticides, competition and interaction between plants in natural and managed systems, the role of new options (such as perennial pastures) in farming systems, optimal land use in agricultural systems and mixed-use landscapes, and dispersal of biological organisms.

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Can mechanistically parameterised, anisotropic dispersal kernels provide a reliable estimate of wind-assisted dispersal?

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The dispersal capabilities of invasive organisms plays an important role in defining their ability to colonise new areas, and to maintain populations in fragmented or dynamic environments. For invasive organisms that undergo passive, wind-assisted dispersal, the speed and spatial structure of unfolding epidemics is largely determined by wind conditions in the area under invasion.

As such, models of wind-assisted dispersal that capture the dynamics of local conditions and the effect of prevailing winds on resulting spread are required. We tested the ability of relatively simple two-dimensional kernels to encapsulate these dynamics, and to make accurate predictions of spread based only on wind data and the physical characteristics of the organism in question. The kernel uses a mixture of von Mises distributions to capture the anisotropic nature of local wind conditions and a mechanistically parameterised kernel to describe dispersal distance. Comparisons with a mechanistic model showed that this kernel was able to provide a good estimate of spread, and provide a far more informative and useful prediction than the isotropic equivalent commonly used in dispersal modelling.

About the author:

David Savage is a PhD student at the University of Western Australia. As part of his PhD David is investigating the use of simple models to describe wind-assisted dispersal of fungal pathogens. These models will then be used to drive regional scale simulations of population dynamics for fungal pathogens. David is also investigating the use of unpiloted aerial vehicles for surveillance of airborne fungal pathogens.

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The impact of elevated CO₂ on Barley yellow dwarf virus and its aphid vector *Rhopalosiphum padi*

P. Trebicki^{1,4}, A. Freeman¹, K. Powell², G. Fitzgerald¹ and J. Luck^{3,4}

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In a report released by the Intergovernmental Panel on Climate Change in 2007 it concluded that global warming is occurring and that changes in the global climate system will continue into the future. These changes including higher average temperatures and higher levels of carbon dioxide in the atmosphere which are expected to have a major impact on agricultural systems. However, there is a lack of empirical data on the effects of elevated CO₂ and temperature on agricultural pest and pathogen populations. Consequently, predictions on the future of our major crops such as wheat have not been fully explored.

The Department of Primary Industries Victoria, the University of Melbourne and the Department of Climate Change have established a Free-Air CO₂ Enrichment (FACE) research facility at Horsham, to study the effects of elevated CO₂ on wheat production in Australia. This facility is being used to study the effects of elevated CO₂ (550ppm) under field conditions on wheat, the Barley yellow dwarf virus (BYDV), as well as biology of its aphid vector *Rhopalosiphum padi* (Homoptera, Aphididae). Results from studies on wheat plants conducted at the FACE facility show changes in C:N ratio, increase in plant height, biomass, number of tillers, and surface area in response to elevated CO₂. However, variable field conditions have proved difficult for studying the impact of elevated CO₂ on BYDV and its vector, therefore in addition to the FACE facilities, controlled environment growth chambers are being used to study the physiology and feeding behaviour of *R. padi* and its ability to acquire and transmit BYDV under various climatic conditions and CO₂ concentrations. Results from the FACE facility and growth chambers will be described and presented. Potential ecological and epidemiological consequences will be discussed.

About the author:

Piotr Trebicki is a research scientist, working at the Department of Primary Industries (DPI) in the Biosciences Research Division in Horsham, Victoria.

Piotr completed his PhD at the Queensland University of Technology in Brisbane and DPI Rutherglen on tritrophic interactions between virus, leafhopper and host plants. He developed artificial feeding system and described probing behaviour of economically important leafhopper vector *Orosius orientalis* (Hemiptera, Cicadellidae). Currently, using Free Air Carbon Dioxide enrichment facility and growth chambers in DPI Horsham, he is investigating the impact of elevated carbon dioxide levels on insect/plant/pathogen interactions using wheat plant, Barley yellow dwarf virus and its aphid vector *Rhopalosiphum padi* (Hemiptera, Aphididae).

Piotr's research interests are: insect-host plant interactions, plant resistance to sap-sucking insects, insect feeding behaviour and pathogen transmission/acquisition, insect physiology and population dynamics, changes to plant physiology mainly due to elevated carbon dioxide and impact on insect vectors, epidemiology of plant viruses and role of ground beetles in field crop environment as a beneficials.

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Invasion genetics of Russian Wheat Aphid, *Diuraphis noxia*, in Western China and worldwide

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The Russian Wheat Aphid (*Diuraphis noxia*) is one of the greatest biosecurity threats to the grains industry in Australia. It is believed that *D. noxia* is endemic to western Asia, and has expanded its range to include southern Russia, the Middle East, Africa, Europe and the Americas. This species has become a major pest in grain production areas throughout the world, except for Australia.

The genetic relationships among endemic and invasive populations have not been examined previously. This study will use a unique combination of tools to study not only the background genetics of endemic and invasive populations (microsatellite and mitochondrial DNA markers), but also a group of genes known to influence feeding success and damage (salivary gland genes). These data will provide information on the invasion pathway of *D. noxia* and the mechanisms driving the colonization process i.e. have invasive clones arisen randomly from endemic populations, or have they arisen as a result of selection favouring a particular combination of traits (such as virulence).

Preliminary data are provided on the levels and patterns of genetic diversity in 18 endemic (Chinese) populations of *D. noxia* and the genetic relationships among invasive and endemic RWA lineages from around the world. Mitochondrial DNA of 1272bp in 124 individuals indicates low genetic variability, with 18 haplotypes unique to western China and one haplotype found in a range of sites throughout western China and worldwide. Nine microsatellite loci have been developed and screening of Chinese and worldwide populations will be undertaken to provide a pathway analysis of historical RWA invasions throughout the world.

About the author:

Ms Bo Zhang commenced her PhD research in January 2009 and has a scholarship from the CRCNPB. Ms Zhang is enrolled as an external student at QUT, and due to the nature of her project involving extensive field sampling in remote regions of western China; she is undertaking a significant proportion of her research at the Chinese Academy of Sciences, Beijing.

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Trapping to prove area freedom

Francis De Lima^{1,2}, Olivia Reynolds^{1,3}, Shirani Poogoda^{1,2}, Cathy Smallridge^{2,4}, David Madge⁵ and Jianhua Mo^{2,3}

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Methods of strategic deployment of traps in hosts at the time when they are most attractive to fruit flies (dynamic trapping) were tested against the standard methods where traps are placed in a grid system 0.4 - 1km apart (static trapping). The strategy utilised two data types: (1) trap data was collected over three seasons from fruit fly free areas, areas of low and very low pest prevalence in endemic areas for Queensland (QFF), *Bactrocera tryoni* (Froggatt) and Mediterranean fruit fly Mediterranean fruit fly (MFF), *Ceratitis capitata* (Wiedemann), and (2) mined incursion data from fruit fly free zones in NSW, VIC, SA and WA. All trial sites new and mined data sites were spatially mapped for host species.

In general, the grids are relatively effective when numbers are high, but are an inefficient strategy to detect early fruit fly incursions and are becoming increasingly expensive to deploy and maintain due to the prescribed fixed distances between traps. Research was conducted over three seasons from 2007 to 2010 in NSW and WA to determine if new methods termed 'dynamic trapping' methods would provide an equivalent proof of area freedom at lower cost.

The results show that in areas where populations are very low to zero:

- Dynamic trapping methods deploying traps in the most attractive hosts detect fruit fly infestations earlier than static traps.
- In areas where Mediterranean fruit fly occurs, the dynamic trapping method requires one-third to one-half the number of traps used in a static grid to obtain the equivalent information on detecting itinerant or established fly numbers required for the fruit fly code of practice.
- Adopting the dynamic trapping methods is based on good scientific principles and will benefit industry in reducing monitoring costs as well as in eradication costs through early detection of breeding populations.
- Environmental impacts of trap deployment and eradication of fruit fly outbreaks will be reduced.
- The results of this work are expected to be of considerable value for the quarantine requirements of overseas countries for trap placement in terms of early and effective detection of fruit fly incursions into area free zones.
- The results obtained in this project provide the scientific basis for quantifying Areas of Low Pest Prevalence thus enabling places that lose Area Freedom, or those places that cannot achieve area freedom to seek more favourable consideration for market access based on diminished fruit fly risk to trade.

About the author:

Dr Francis De Lima has worked at DAFWA for over 20 years on fruit fly ecology, IPM and disinfestation.

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Bayesian statistics for biosecurity

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A. Biosecurity challenge: Shed light on farm management practices to improve efficacy of methods and policies for ensuring post-harvest integrity of grains and better understand ecology of grain insects (CRC 5D151). **Statistical challenge:** Make the most of small intensive surveys.

Achievements: Farm management practices can be a highly sensitive topic, and eliciting an honest account of such information from farmers requires substantial preparation and time investment. Fifteen interviews on farm management practices were conducted over several months in the Condamine-Meandarra district of Queensland. We utilised an innovative Bayesian hierarchical model to make the most of this small yet valuable dataset: (i) eliciting regional demographics represented by annual wheat tonnage; (ii) harnessing this information to extrapolate survey results to the region; and (iii) estimating (with uncertainty) the prevalence of various farm management practices.

B. Biosecurity challenge: Designing surveillance for Myrtle Rust. **Statistical challenge:** Model-based surveillance design: aligning with client needs and accommodating uncertainty.

Achievements: Performance of biosecurity surveillance programs often depends on quantifying *sensitivity* and *specificity*. However end-users, such as farmers and plant nursery owners, need to know: *How sure can we be that the pest is absent when we've gone to all this effort and detected nothing?* This Negative Predictive Value (NPV) neatly corresponds to a Bayesian posterior probability. Moreover quantifying sensitivity is problematic since implementing controlled conditions, under which a new pest can be introduced, is difficult both practically and ethically. Alternatively, robust estimates of sensitivity can be obtained via structured elicitation of plausible values from experts. We used NPV and elicited sensitivity as the basis for a new fully Bayesian approach to designing surveillance to establish effective area freedom from Myrtle Rust. This work also contributes to design of a surveillance protocol for Russian wheat aphid, an exotic pest of grains (CRC 30009).

C. Biosecurity challenge: Combining Pest Risk Assessments (CRC 10068). **Statistical challenge:** Utilizing often-ignored information to help calibrate assessments by different experts, to provide a better basis for determining the overall consensus and diversity in expert assessments.

Achievements: Where multiple risk assessors have filled out a pest risk assessment questionnaire, results are typically collated question by question. However we can gain more insight by considering each risk assessor's responses in context: how that assessor has responded to other questions, and how they compare to other assessors. We developed a new Bayesian Expert Response Model to achieve this calibration. This highlighted experts who consistently provided conservative estimates, and changed the relative likelihood (accounting for diversity among assessors) for several factors affecting risk of entry of *Bactrocera* to the European Union.

These projects provide examples of working with local (A), national (B) or international biosecurity groups (C). They cover the spectrum of potential impacts from leveraging elicitation and Bayesian statistical methods: building new knowledge through pioneering scientific investigations (A); translating science into policy (B); and more effective use of information (C).

About the author:

Ph.D. in Spatial Statistics (Queensland University of Technology); then seven years as sole then lead environmetrician in State Government, two years statistical consulting and three years post doctoral research in Bayesian statistics. Since 2009 have been a Senior Research Fellow in biosecurity statistics within Cooperative Research Centre for National Plant Biosecurity. Previous experience includes teaching and statistical consulting in a variety of fields.

Expertise and current interests in tailoring Bayesian statistics to design and modelling in biosecurity, environment and ecology. Key problems addressed or being addressed include:

• modelling/prediction of presence of threatened or pest species • design and analysis of environmental monitoring • ecoregionalisation • ensuring early detection and area freedom from exotic pests/disease of plants • farm management practices and chemical resistance of grain insects • assessing ecological or health impacts • targeting & calibrating expert judgments in various contexts, from species detection and pest risk assessments to habitat modelling and marine taxonomy, as well as PhD durations. Co-developer of elicitation software tool "Elicitor".

Some recurring themes underlying my statistical consulting and research include:

• model-based design to support pioneering science • leveraging information, incl. expert knowledge, small datasets or large heterogeneous data warehouses • spatio-temporal variability • statistical methods and associated technology for capturing, encoding and combining expert knowledge • accounting for zeros in ecological data.

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Estimating time-varying components of Qfly dispersal in the benefit-cost analysis of a monitoring system

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A long time to detection from when a pest infestation arrives at a location and when it is detected can result in significant follow-on eradication costs as the infestation spreads out of hand. We consider explicitly the current costs of monitoring for Queensland fruit fly (Qfly) in fruit fly exclusion zone of eastern Australia in maintenance of pest area freedom. These costs are altered by varying the spatial density and frequency of monitoring. However, varying these monitoring parameters varies the risk of experiencing extensive and costly outbreaks. This risk depends directly on the ecology of Qfly, its pattern of outbreaks and its seasonal behaviour. In this talk we present our approach to estimating the distribution of detection and eradication times through applying time-varying parameters to a spatio-temporal population model.

This combines estimating seasonally dependent dispersal parameters from SIT release and recapture data, and growth parameters from the Climex and Dymex models. Success of this method will achieve a closer linkage between the ecology of Qfly and the economics of biosecurity. By specifically targeting the ecology of the Qfly this will potentially enable the design of “safer” market access rules that also lead to cost and risk minimising efficiencies. Further development includes identifying monitoring technologies that have greatest potential to return economic benefit.

About the author:

Rohan Sadler is a research assistant professor at the University of Western Australia with a background in dynamic ecological systems, statistical computing and remote sensing. Previous work has focused on the incorporation of remote sensing into optimal landscape planning for biodiversity and fire management, and in characterising fire regimes across ecological scales. Current research is looking at incorporating dynamic landscape ecological models into benefit-cost analysis and assessments of policy failure.

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Evaluating surveillance and control in benefit-cost analysis of area-wide management

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Benefit-cost analysis (BCA) of area wide management (AWM) strategies for Queensland fruit fly (Qfly; *Bactrocera tryoni*) began in earnest in with the PricewaterhouseCoopers evaluation of the Tri-State Strategy in 2001. Since then a number of BCAs have been undertaken by different jurisdictions as a policy tool to justify continued support of the Sunraysia pest-free area in eastern Victoria and NSW, and an evolution of the BCAs can be charted. The risks of policy failure are however driven by the seasonal dynamics of the Qfly's ecology, and in the pursuit of evidence-based policy we seek to integrate the ecology better into BCA methods. This means building direct linkages between the spatio-temporal distribution of outbreaks and the costs of consequent management. In our poster, we elaborate on how costs and production have been considered, and the costing detail required to build the requisite ecological linkages.

About the author:

Ben White graduated in agriculture from London University in 1981, and followed by a PhD from the University of Newcastle upon Tyne in 1989. He held lecturing positions at Newcastle University for 20 years first as a lecturer and in 1999 as a senior lecturer. Moving to The University of Western Australia (UWA) in 2001 to a senior lectureship and in 2007 became Head of School. Research interests are in environmental and agricultural economics with a particular interest in environmental contracts and incentives for farmers to provide environmental public goods. Recent involvement in the Auction for Landscape Recovery project which involved using auctions as a mechanism to increase landholder involvement in conservation. Mr White is also involved in the Institute for Agriculture at UWA.

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Sampling irrigation water for plant pathogens – coherently working together or organised chaos?

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Over the past 90 years the presence of plant pathogens in irrigation water has been documented in both natural and irrigation waterways as a significant issue for plant health. This is so, due to the ease of dispersion in which water provides to the pathogen - particularly in agricultural systems where there is a reliance on water for crop production. More importantly, with the decline in the available freshwater for use in agriculture, agricultural practices are being directed towards the use of recycled water, such as treated wastewater or recycled agricultural drainage water, and therefore this concern increases. In this instance, there is the potential for repeated inoculation of the plants with the pathogen if appropriate testing and subsequent management practices are not initiated.

A recent review of the literature regarding the presence of plant pathogens in irrigation water has highlighted several interesting points regarding the techniques being applied by Researchers to sample water. Quite evident though, was that no unified approach actually exists. So this draws into question, what techniques are being employed by Researchers globally? How sensitive are the methods? And are they addressing fundamental aspects such as Koch Postulates? A summary of the techniques being employed by Researchers for sampling water for the presence of plant pathogens will be discussed. As well as the gaps in knowledge that became apparent through the review of literature.

About the author:

In 2008 I completed a BSc (Hons) in Molecular Biology from the Centre for Rhizobium Studies at Murdoch University. My research focused on Plant Growth Promoting Rhizobacteria and the mechanisms they employ to enhance host plant root development.

Currently, I am enrolled as a PhD student with the Cooperative Research Centre for National Plant Biosecurity, due for completion in 2012. My project is assessing the risk of plant pathogens in the irrigation channels of the Ord River Irrigation Area located in the Kimberley region of northern Western Australia.

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Strong phosphine resistance eradication in Western Australia

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Phosphine resistance in grain pests is an escalating threat to the success of the Western Australian post-harvest grain storage system. Approximately 85% of annual grain yield is exported to trading partners whose demands are increasingly toward an insect and chemical residue-free product. Western Australia is well placed to meet demand from discerning customers because phosphine is widely used as the primary control agent. It is low cost, effective and easy to use. The lack of suitable alternatives has placed heavy reliance on phosphine throughout the export grain value chain and phosphine resistance in stored grain insects is a consequence of unrestricted use of the product in poorly sealed structures.

To extend the effectiveness of phosphine, monitoring is essential so that resistant insect populations can be eradicated before control failures occur. This has been conducted in Western Australia since 1984 along with a strong commitment towards effective management and control of resistance through sealed storage fumigation on farms, merchants and the central handling system. The Western Australian focus is on identification of resistance followed by effective treatment and eradication. Additional emphasis on IPM reduces the frequency of fumigations without the use of chemical grain protectants. All contact chemicals with the exception of Malathion have been banned on stored grain in Western Australia since the early 1980s and no contact insecticides have been used by the State's main grain handling cooperative since 1990.

In Western Australia weak resistance to phosphine has increased annually with the current average frequency at approximately 40 percent across all insect strains tested. However resistance frequency in a single species, for example the rust-red flour beetle, *Tribolium castaneum*, is approaching 70%. Research by the Queensland Department of Employment, Economic Development and Innovation (DEEDI) has shown that it is reasonable to expect strong resistance to develop once weak resistance frequency reaches 80% of strains tested.

Strong resistance has previously only been detected in Western Australia through quarantine incursions on import shipments of polished rice from China and personal effects from Oman. However there is also the risk of strong resistance being brought into Western Australia from the eastern states especially following dry winters when there is an increased need to import feed grain during the summer.

In Western Australia the onset of strong resistance has been delayed until 2007, when the first of three properties surveyed in the northern and central growing regions yielded strongly resistant strains of rust-red flour beetle, *Tribolium castaneum*. It is suspected these strains developed locally and an eradication program was put in place. Corrective action to control resistance on these properties involved improving hygiene standards, sealing storages, structural treatments with desiccant insecticides or contact insecticides followed by extended fumigations and gas monitoring.

Elevated sampling and resistance testing continues for a minimum of two years on affected properties to confirm that no strong resistance develops post-eradication. Landholder liaison and education is an integral part of this work to develop awareness and keep phosphine resistance manageable in Western Australia.

About the author:

Michelle Chami (BSc Biological Science and Conservation Biology) graduated from Murdoch University and commenced working as a Technical Officer in Entomology, Plant Biosecurity at the Department of Agriculture and Food in Western Australia in 2002. Michelle initially worked in Mediterranean Fruit Fly control and area-wide management. Further work within entomology included Social Insect Research on European Wasp eradication and Red Imported Fire Ant surveillance. Michelle also worked in the Insect Reference Collection contributing to the Insect Collection Database.

Over the last 6 years, Michelle has worked in the Grain Insect Resistance Monitoring Unit within Cooperative Research Centre for National Plant Biosecurity project 'CRC50116/CRC5D151 Management of resistance to phosphine in insect pests of stored grain'. Michelle's involvement in the Western Australian node of this national project serves to monitor and assess the Western Australian phosphine resistance situation for grain storage pests through regional sampling and laboratory bioassays following internationally agreed protocol. Michelle co-ordinates the associated data handling and management via the Australian Grain Insect Resistance Database to maintain this secure, central repository for national resistance data.

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Numerical study of wind induced pressure fluctuations on grain storage bunkers

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In Australia, grain storage bunkers fitted with covering tarpaulins are widely used. Tarpaulin billowing takes place when it is windy. It is well known that billowing has negative impacts on the life span of a tarpaulin, but also has positive effects on phosphine transport throughout the grain stack during fumigation. It is suspected that preventing billowing during fumigation would retard phosphine distribution to such an extent that contemporary phosphine dispensing protocols risk failure. Mathematically, a moving boundary condition that could represent wind induced tarpaulin billowing presents a challenging technical problem and has not been published.

In this study, three-dimensional wind flow around a grain storage bunker is investigated by numerical method based on finite element method (FEM), as the first step towards quantifying tarpaulin billowing. This study is focused on the wind induced pressure distribution and fluctuation of pressure on bunker surface at a relatively low Reynolds number. The applicability of simplification of flow from three-dimensional to two-dimensional at the mid span of the bunker was discussed with cross flow wind direction.

From the simulation results, it is observed that wind induced pressure on bunker surface fluctuates with time. Both mean value of pressure and root mean square (r.m.s.) value of pressure vary very much close to the two ends of the bunker. The Reynolds-averaged pressure on the windward surface is mainly determined by bunker's geometric form. However, on the leeward surface, it is also influenced by the near wake vortex, especially approaching to the two ends of the bunker in lateral directions. Three-dimensionality of the mean pressure and r.m.s. pressure are limited to two-ends of bunkers in the lateral direction. The wind flow within the mid span four times of bunker width away from each end is of two-dimensional. The tarpaulin billowing phenomenon is mostly affected by the pressure fluctuation on the roof of the bunker. It is estimated that the frequency and amplitude of fluctuations are largely related to bunkers' orientation, geometric configuration, and the turbulent intensity in the atmospheric boundary layer.

About the author:

Mr Wei He is currently a PhD candidate in the Civil and Resource Engineering School of UWA from 2009. His research topic is the numerical study of fumigant distribution in grain stores, with focusing on the computational fluid dynamics and fluid structure interactions. Before that, he was an engineer in the building consultancy since graduation with a BEng in 2003.

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Ensuring grain storage structural integrity for grain biosecurity

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Grain must be stored for relatively long periods of time to satisfy the need for it to be available throughout the year. During storage, grain is under severe threat from a range of organisms, particularly insects.

The major tool used by the grain industry to control insect infestations is fumigation with phosphine. To be effective, fumigation must be undertaken in well-sealed storages so that the gas has enough time to penetrate the grain and exert a toxic effect on target pests. Most existing grain storages, however, were not designed to the standard required for effective fumigation and this has resulted in serious threats to the biosecurity of the grain.

We are developing several cost-effective technologies that greatly enhance the integrity of grain storages and therefore biosecurity of stored grain:

- New plastic sheets and sealing materials for bunkers and horizontal storages.
- Polyvinyl alcohol (PVOH) as a flexible film for capping grain or as ground sealant.
- Powered and unpowered phosphine circulation systems and ground level application methods for farm storages.

These technologies need to be not only suitable for phosphine fumigation but also must meet the likely future requirements of a range of alternatives to phosphine.

About the author:

Dr YongLin Ren is employed as a permanent staff member within DAFWA. His appointment is initially to Murdoch University until 2012 as Associate Professor. YongLin's main areas of research include postharvest biosecurity, grain storage, fumigant and grain volatile chemistry, new fumigants and new applications (fruit, vegetable, grain, timber and soil), quarantine treatments and methyl bromide alternatives, and insect chemical ecology. He has 28 years research experience in grain storage and the development of quarantine treatments. Currently, he is a member of Controlled Atmosphere and Fumigation Permanent Committee and Australian representative for the Plant Health Quadrilaterals Scientific Collaboration Working Group.

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Fate of phosphine in grains

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The Australian grain industry relies heavily on phosphine to disinfest bulk grains and oil seeds (more than 85% grains are treated/re-treated with phosphine) in each of the linkages from on-farm storage to the grain terminal.

Phosphine has been scheduled for a toxicological and residue Re-Evaluation Review in 2014 by the FAO Codex Alimentarius Commission that sets internationally agreed maximum residue limits (MRLs) for pesticides. Despite the international importance of phosphine there is limited information on the physical and chemical behaviour of this fumigant in grain and its degradation. It is extremely important that the Australian grain industry has information on the fate of phosphine in grains so that breaches of MRLs do not occur as these could jeopardise market access.

Radioactively-labelled phosphine is useful for studies of the absorption, desorption and residue of phosphine in grains and their fractions. The radioactive label provides a sensitive means for following the fate of the absorbed phosphine. The research will guide industry in the conduct of good phosphine fumigation practice.

Five representative grains (wheat, barley, oats, canola and lupins) were fumigated with ³²P labelled phosphine at 700 ppm and 20°C for 2 weeks exposure. After 1 week aeration, the levels of ³²P radioactive residue in the grains and their fractions were analysed. The results show that:

- >85% absorbed ³²PH₃ can be removed after 1 week aeration
- ³²PH₃ converted to non-volatile ³²P compounds, eg., ³²P phosphate cannot be removed by aeration
- >90% ³²PH₃ + non-volatile ³²P residues were located or distributed in the embryo, testa, pericarp and husk of grain kernels

About the author:

Dr YongLin Ren is employed as a permanent staff member within DAFWA. His appointment is initially to Murdoch University until 2012 as Associate Professor. YongLin's main areas of research include postharvest biosecurity, grain storage, fumigant and grain volatile chemistry, new fumigants and new applications (fruit, vegetable, grain, timber and soil), quarantine treatments and methyl bromide alternatives, and insect chemical ecology. He has 28 years research experience in grain storage and the development of quarantine treatments. Currently, he is a member of Controlled Atmosphere and Fumigation Permanent Committee and Australian representative for the Plant Health Quadrilaterals Scientific Collaboration Working Group.

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Contingency plans for exotic pests of grain

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¹Plant Health Australia, ACT, ²Cooperative Research Centre for National Plant Biosecurity

Australia's geographic isolation and active quarantine systems have meant we have remained relatively free of many pests that affect production of grain crops overseas. To ensure that our high plant health status is maintained, activities that support biosecurity risk mitigation are essential. Preparation of contingency plans for key pest threats support risk mitigation through provision of detailed information on pest life cycles, potential for pest entry, establishment and spread, survival strategies and methods for surveillance and sampling.

In the event of an incursion of a pest, the collation of information within Contingency Plans assists with the development of response plans which results in more rapid and efficient decision making for eradication, containment or management options. Within this project, development of Contingency Plans for 14 priority pest threats and one pest weed species has been undertaken. These pests were selected based on the overall risk rating identified in the Grains Industry Biosecurity Plan and also on the value of crop production. Completion of these plans will provide information for all high priority and the majority of medium priority pests of major grain crops, ensuring the grains industry is prepared for potential incursions of a wide range of pest threats.

About the author:

Jo has a strong background in agricultural research and project management, working for many years with the Victorian Department of Primary Industries at Rutherglen and more recently with CSIRO Plant Industries in Canberra. She has more than 20 years experience in Rhizobium legume research working on grain, pasture and native legume projects across Australia, as well as joint projects with overseas collaborators.

For the past three years, Jo has been at Plant Health Australia working on projects involved in capturing information from industry-based surveillance activities for plant pests, developing and leading biosecurity preparedness activities for plant industries and supervising the Grains Farm Biosecurity Program.

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Widening the toolkit: Developing biosecurity solutions from chemical ecology

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Increasing volumes of tourists and cargo are generating unprecedented levels of alien invasive species establishment across the world, which can threaten productive and natural ecosystems. Invasive species are very difficult to eradicate. Government-sanctioned pest eradication programmes are increasingly being commenced worldwide in response, at a rate at least doubling each decade, with close to 100 programmes so far in Australia and New Zealand combined. Some programmes are more likely to succeed than others, based on the availability of suitable tools for delimitation and response.

Our CRC project has looked at combinations of tools for horticultural pests, and here we will also consider the importance of Allee effects in pest population dynamics, and how certain combinations of tactics can best be integrated to increase the likelihood of success.

About the author:

Max is the Biosecurity Science Group Leader for Plant and Food Research, and is also the Deputy Chair of The Environmental Risk Management Authority of New Zealand. His research focuses on developing new surveillance and response tools that can be used for incursion response and long-term pest management, and together with colleagues has commercialised six mating disruption products for controlling moths and more than 20 types of lures for surveillance. He is on the USDA Technical Working Group for the Light Brown Apple Moth, and is involved in projects at the National Center for Ecological Applications and Synthesis at Santa Barbara and an International Atomic Energy Agency cooperative research programme on the sterile insect technique. He was made a Fellow of the Royal Society of New Zealand in 2003.

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Sampling Design and Analysis

Chair: Phil Clamp



Sampling within heterogeneous systems: choosing the right model

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Developing effective methodologies for sampling pests within commodities is an essential component of any integrated pest management strategy. Sampling is undertaken so that pathogen or pests can be detected to minimise damage, determine when control strategies should be undertaken, or prior to commodities being distributed or exported. Grains sampling programmes have been developed based on underlying statistical distributions such as the Binomial, Poisson or Negative binomial distributions.

It is important to recognise however, that the appropriateness of the statistical distribution used for sampling will depend on the spatial distribution of target pests within the sampled commodity. In this paper we compare sampling models designed to deal with non-homogenous or aggregated distributions to determine their usefulness when sampling bulk grain commodities. Using both simulation and empirical data we demonstrate the importance of developing a sampling strategy based on a robust statistical framework and an understanding of pest species ecology.

About the author:

David Elmoultie is a Research Fellow in the discipline of Biogeosciences at QUT. Currently, David's research is focused on the development of a flexible statistically based sampling strategy for the detection of post harvest grain storage pests for the Australian grains industry.

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'Alluring appeal' – evaluation and development of female fruit fly lures for improved market access

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Fruit fly monitoring programs are vital to protect Australian horticultural industries from exotic fruit fly incursions and to maintain market access for producers within Pest Free Areas of production. Traps containing lures specific to male fruit flies generally predominate in these programs due to the impracticality of existing female fruit fly lures. However, the supplementary use of female fruit fly lures in monitoring programs could greatly improve the chances of detecting an incursion, particularly of some exotic species where male flies are not responsive to lures.

Fruit flies require dietary protein to become sexually mature. Therefore, most existing female fruit fly lures are food-based attractants such as proteins or products of protein degradation. The most common female lure used in Australia consists of 2% aqueous yeast autolysate deployed in a McPhail trap. This lure has a number of disadvantages: it needs to be replaced weekly; it's unpleasant to handle; attractive to non-target insects; and causes deterioration of fruit fly specimens drowned in the liquid. Alternative lures for female fruit flies that could overcome these shortfalls were developed and/or evaluated during this project.

Two prototype food-based lures were developed at the beginning of the project. One was a gel lure with the consistency of agar; the other a dry lure made by applying a liquid lure to vermiculite. These lures were tested in series of laboratory, outdoor cage and field trials on a range of *Bactrocera* sp. and *Ceratitis capitata*. In NSW, the prototype lures were compared to yeast autolysate lure (standard female lure for *Bactrocera* sp.), whereas in WA, the lures were compared to 3-component Biolure (standard female lure for *C. capitata*).

Controlled laboratory data demonstrated that only a small proportion (~20%) of female *Bactrocera tryoni* are attracted to proteinaceous lures. Observational field data also suggested that all the female lures tested attracted only a small proportion of the predicted *B. tryoni* and *C. capitata* populations, as indicated by captures of flies in traps charged with male lures. Similar observations have been reported for other fruit fly species, but in the absence of more reliable cues for female fruit flies, the current project aimed to overcome the disadvantages of the current yeast autolysate lure, while maintaining a similar level of attractiveness.

In all field tests, the dry lure performed very poorly compared to other lures, capturing significantly lower numbers of flies under all environmental conditions. The standard lures (yeast autolysate or Biolure) also outperformed the gel lure in terms of the number of captures in most, but not all, field tests. The real advantages of the gel lure compared to the yeast autolysate lure was evident in the longevity of the lure (lasting up to 12 weeks), the reduced captures of non-target insects such as blowflies and moths, and the improved quality of fruit fly specimens captured due to reduced humidity and decomposition within the trap. Because of the importance of these advantages, it may be worthwhile to invest in the enhancement of the gel lure chemistry and/or trap technology in the future.

About the author:

Katina is a researcher with the Industry & Investment NSW Market Access group based in Gosford. Katina specialises in market access entomology, her primary roles include the development of quarantine treatments for horticultural products and field experimentation of new fruit fly lures and baits.

Katina completed her Bachelor of Science with Honours in plant pathology at The University of Queensland in 2001. She then went on to complete a PhD, researching the physiological basis of chilling injury in navel oranges with La Trobe University and CSIRO in 2007. Once completing her PhD Katina was employed by Industry & Investment NSW, working in citrus and vegetable research. She has been in her current role as Market Access Entomologist since April 2008.

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Evidence for area freedom: prospects for Bayesian modelling in plant biosecurity

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Most plant biosecurity pest management decisions are underpinned by inference on the extent of an invading pest. As a pest incursion unfolds, hierarchical Bayesian modelling approaches can assimilate evidence for pest absence from surveillance data and ecological knowledge to answer a number of pest management questions. Models were developed at several spatial scales to analyse a large data set for the spiralling whitefly (*Aleurodicus dispersus*) invasion of Queensland. At a local scale, models estimated spread rates and variability in detectability by different inspectors on different host types.

The analytical methods developed can be adopted during the early stages of an invasion to improve surveillance operations and strategies. At broader scales, management of human-mediated dispersal is a key component for containing pests. A novel hierarchical Bayesian model set in a reliability analysis framework has been developed to accommodate pests with multiple dispersal modes. Its use is demonstrated by implementing a gravity model to estimate human-mediated dispersal parameters for spread between towns of different sizes. The model is then extended to a state-wide scale to estimate the climatic limits of the pest and the probability of area freedom over time.

The future development of hierarchical Bayesian models will undoubtedly provide greater ecological insight into invasion processes. They have the potential to play a pivotal role in both the technical development of biosecurity programs and provide inference for making sound risk management decisions. However, it is necessary to temper this potential with the reality of what is predictable about invasions. While models may provide useful inference at some spatio-temporal scales, ecological complexity and uncertainty may prevent their use at the scales for which management decisions are desired. Perhaps the greatest benefit they offer to biosecurity is as a heuristic framework for planning and evaluating surveillance data. They encourage the valuation of surveillance data and the ecological investigation of uncertainty for more focussed risk management decision making.

About the author:

Mr Mark Stanaway has recently submitted his PhD at QUT on hierarchical Bayesian models for estimating the extent of plant pest invasions. He has worked with Biosecurity Queensland for twelve years on a range of surveillance and risk analysis activities. Prior to joining Biosecurity Queensland, he worked at the University of Queensland's Entomology Department on several biosecurity projects for ACIAR, Biosecurity Australia and the CRC for Tropical Pest Management.

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The statistical analysis of rare events

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When detecting low density or invasive species, the majority of observations are non-detections or 'zeros'. Confidence intervals around a parameter of interest, for example, the probability of detection are usually based on a normal approximation to the binomial distribution. A problem arises when the event is rare (ie, when the number of detections is small) as the data is composed of too many zero observations or non-detections. In this case we need to identify at what point an excess of zeros (non-detections) becomes nearly all zeros. In addition, and in the surveillance area, the observed data (detections and non-detections or presence and absences) are not actually analysed; decisions and actions are made simply when species are detected. Thus, the data is not utilised to its fullest.

We explore various techniques to analyse such low incidence data. We aim to demonstrate the use of these non-detections to quantify, in the case of invasive species; *How confident are we that the data observed are consistent with species absence*, ie probability of presence is zero in the sampling frame.

As a simple exploratory tool we show how the likelihood function (binomial, negative binomial etc.) can be used to answer the question, *What is the likelihood that a detected individual is an invasive species?* A likelihood function concentrated very close to zero provides stronger evidence that the data could have arisen from a binomial distribution where the probability of detection is close to zero. This in turn provides greater confidence that the probability that a detected species is invasive could in fact be exactly zero.

Various approaches have been taken to address the issue of calculating confidence intervals that do not use a normal approximation to the binomial. A simple approach is the Rule of Three where a 95% confidence interval for a binomial probability of zero occurrences of the event is $3/n$. Moreover, use of $3/(n+1)$ is more appropriate when the number of detections is ≤ 20 .

In addition to the binomial we consider the use of other distributions such as the negative binomial and the hypergeometric to obtain confidence intervals for the probability of detection.

To illustrate these techniques we use detection data from the pilot surveillance on Barrow Island, WA.

About the author:

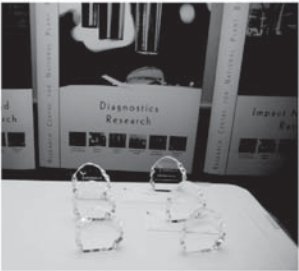
Susan is a Research Fellow in the School of Mathematical Sciences at Queensland University of Technology, Brisbane, Australia and received her PhD at Griffith University in 2007. She has a broad range of experience in statistical consulting and applied statistics.

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Eradication and Control

Chair: Kathy Ophel-Keller



Eradication of black rot from vineyards using a drastic pruning protocol

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Eradication of exotic grapevine diseases can incur significant costs to growers and the industry using current strategies, which include complete removal of affected and surrounding vines. Alternative strategies need to be developed that optimise efficiency of the eradication process and minimise the economic cost of returning the crop to its previous quality and production levels. The endemic disease of grapevine, black spot (*Elsinoe ampelina*), was used as a model to evaluate a drastic pruning eradication protocol for the exotic disease black rot (*Guignardia bidwellii*). These pathogens have similar biology and epidemiology, as they infect fruit, leaves and shoots of grapevines; overwinter in infected wood and debris on and beneath the vines; and are mainly spread by rain splash.

The following protocol was developed based on knowledge from previous eradication campaigns and literature. Vines are cut off at the crown with a chainsaw and the excised material placed in an excavated pit. Then, the vineyard floor beneath the treated vines is raked and the debris placed in the pit is burnt and buried. Finally, the area between rows is cultivated to bury any remaining debris.

A trial was established in the Sunraysia district of Victoria to evaluate and fine-tune the eradication protocol. Vines inoculated in spring 2007 developed black spot leaf lesions and stem cankers that season. In July 2008, a simulated eradication was conducted using the proposed protocol on selected vines, leaving untreated vines as controls. Leaf and fruit infections were recorded on 4 of the 36 treated vines in December 2008. On treated vines, each symptomatic shoot grew from the trunk within 20 cm of the ground. A bioassay conducted on vine debris sieved from the soil below vines indicated that symptoms on treated vines were most likely caused by inoculum present in the debris. Monitoring of potted sentinel vines placed strategically within and around the trial site during spring and early summer revealed that there was no spread of disease between plots or from external sources.

As a result, the protocol was modified to include removal of lower shoots and the use of straw mulch on the vineyard floor to act as a barrier to the spread of inoculum and to accelerate the decomposition of debris. Furthermore, a foliar spray program using the fungicides mancozeb and myclobutanil was also incorporated into the protocol.

A trial was established in May 2009 on black rot infected vines on a Cornell University research station in New York State, USA to validate the modified protocol. Vines were assessed over two seasons, in August 2009 and July 2010. No black rot symptoms were detected on vines treated with the pruning protocol, whereas leaf and fruit infections developed on untreated control vines. The results confirmed the efficacy of the drastic pruning protocol as a means of eradicating black rot from grapevines.

This protocol could save millions of dollars in lost production and vineyard re-establishment if an incursion of black rot occurs and it also has potential to be used for other exotic diseases of grapevines and other perennial crops.

About the author:

After graduating with a B. Ag. Sc. from the University of Adelaide, Dr Sosnowski commenced working for SARDI in 1997 and went on to complete a PhD in 2002, studying the epidemiology and management of blackleg disease of canola at the Uni of Adelaide. Since 2003, he has been responsible for research on managing eutypa dieback disease in grapevines at SARDI as part of the CRC for Viticulture and remains responsible for supervision of current GWRDC funded research of eutypa dieback. Currently managing a national CRCNPB project aiming to optimise eradication strategies for exotic plant pathogen incursions on perennial crops, Dr Sosnowski is concentrating his own research on the eradication of grapevine pathogens.

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Achieving successful impact management of invasive plant pests using sterile insect release and mating disruption

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The Australian leaf roller light brown apple moth (LBAM) is a pest in Australia, New Zealand and now California. In stage 1 of this CRCNPB project trials were carried out in Australia and New Zealand on the irradiation biology of the moth to determine the appropriate irradiation dose to induce sterility. Competitiveness and flightability of irradiated moths was studied in wind tunnels, flight tubes and field cages.

In stage 2 mating disruption was investigated in trials in Perth and Adelaide. Two trials in Perth successfully used sterile Medfly as pheromone carriers to disrupt mating of LBAM in urban areas. Two trials in South Australia demonstrated that new pheromone application technologies were as effective as current labour intensive approaches for mating disruption in vineyards.

Stage 3 of the project will integrate these two technologies in trials in urban/peri urban areas in Perth and vineyards in South Australia to determine if eradication or area wide management can be achieved using an integrated approach. Issues with phased application and interaction of the two technologies will need to be resolved. Application of the technique to two potential threats to Australian horticulture, False Codling moth and European Vine moth, will be discussed.

About the author:

From the cotton fields of Kununurra to the orchards of south Western Australia Bill has worked as an applied entomologist for almost 40 years. Currently he works on area wide management of fruit flies and on eradication of moth pests. He still enjoys the new discoveries that entomology brings and the pleasure of being part of a great team but dislikes the bureaucracy and regulation that are increasingly part of a scientists life.

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Alternative to phosphine – nitrogen storage

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The Australian grain industry relies heavily on the internationally accepted treatment of fumigation with phosphine to maintain freedom from insect infestation. The efficacy of this material is now seriously threatened by the development of resistance in many target pests. Continued broad-scale use of this fumigant appears to be unsustainable in the long term. There is a need to develop cost-effective, readily adoptable alternatives that will reduce selection pressure for resistance, control resistant insects and comply with industry and market standards. The potential of using nitrogen to produce a low oxygen atmosphere to disinfest stored grain is being evaluated in collaboration with grain industry partners and growers.

Laboratory bioassays conducted on mixed-age cultures of *Tribolium castaneum* (Herbst) and *Sitophilus oryzae* (L.) in wheat, barley, oats, canola and lupin at 98-99.5% nitrogen and 20-25°C determined that 100% control of adults could be achieved after only one week and complete control of all life stages was achieved after 3 weeks exposure. It was also established that there was no effect on grain quality including germination, colour, protein, α -amylase activity (falling number), oil content and moisture content.

The new protocols were trialled on farm at Lake Grace, WA. Nitrogen was applied to wheat and canola held in 75 ton storage using a pressure swing adsorption (PSA) nitrogen generator (capacity: 30m³ of 99.5% per hour). At nitrogen concentration of 97-98% and 20°C all adults of *T. castaneum* were killed after one week and complete extinction of all life stages occurred after 3 weeks exposure as predicted from our laboratory study. The treatment also significantly contributed to the safe storage of canola by inhibiting the respiration process that can lead to rapid build up of moisture and mould growth which causes heating of the grain mass and severe deterioration of the product.

About the author:

Dr YongLin Ren is employed as a permanent staff member within DAFWA. His appointment is initially to Murdoch University until 2012 as Associate Professor. YongLin's main areas of research include postharvest biosecurity, grain storage, fumigant and grain volatile chemistry, new fumigants and new applications (fruit, vegetable, grain, timber and soil), quarantine treatments and methyl bromide alternatives, and insect chemical ecology. He has 28 years research experience in grain storage and the development of quarantine treatments. Currently, he is a member of Controlled Atmosphere and Fumigation Permanent Committee and Australian representative for the Plant Health Quadrilaterals Scientific Collaboration Working Group.

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Three-dimensional Computational Fluid Dynamics Model for forced convective flow in grain storages

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A finite element model (FEM) is established for simulating fan forced fumigation inside a grain silo with a headspace. The Navier-Stokes equations and the extended Darcy's equation are solved to simulate the flow in the headspace and the flow in grains respectively. The continuity conditions of fluid mass and pressure are applied at the interface between the grains and the headspace. The effects of silo filling extent, the position of the aeration duct, and the size of the fumigation system exhaust outlet on the air flow inside the silo were studied initially. The parameters for the resistance to interstitial airflow of the bulk grain, the dimensions of the inlet aeration duct and the static pressure throughout the aeration duct is kept constant in the study.

It was found that the presence of a headspace affects total flowrates through the stored grain substantially, with flows curtailed in a silo without a complete headspace. Flow rates decrease with increases in silo filling extent, but not linearly. As air (with fumigant) flows through the grain for practical fumigation settings, pressure drop was predominantly controlled by filling extent and the size of the exhaust outlet. The exhaust outlet restricts flow for small diameters only, but these diameters were the preferred commercial options.

Numerical results of fan forced fumigation inside a silo were compared with the trial results and good agreement is obtained. The effects of other parameters on the fumigation effectiveness that are often reported, such as molecular diffusion, have been included in the numerical model.

About the author:

Dr. Ming Zhao is a research assistant professor at The University of Western Australia. He was awarded his PhD degree at Faculty of Civil and Hydraulic Engineering, Dalian University of Technology, China. His research interests are Fluid Engineering, Computational Fluid Dynamics, Fumigation of grain storages, etc.

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Development of a fumigant monitoring system for stored grain

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In Australia fumigation of stored grain is a common practice. We have rigorous grain quality standards, including nil tolerance of live insects. Our export customers expect us to maintain the quality of our product.

The widespread current practice during fumigation periods is that a storage site is periodically checked by use of a handheld instrument and the measured concentration of fumigant is manually recorded. This practice has several shortcomings.

Fumigation is usually undertaken a short time after harvest. Thus a bulk handler is often under time pressure during this phase especially when attempting to effectively manage the monitoring of possibly dozens of sites during the same period. In addition to this, storage sites are typically located away from major population centres. Hence these sites are often visited infrequently and irregularly by fumigant monitoring staff. Therefore for any given site the readings of fumigant levels will typically be sporadic and may be several days or even weeks apart. On this basis it is difficult to construct a data set indicating the continuous levels of fumigant during the fumigation period. As a result it is challenging to prove with a high level of certainty that the stored grain was in fact fumigated at the correct concentration for the required time interval especially when unsealed storages are employed.

In addition, the cost associated with requiring monitoring staff to frequently travel to remote storage sites is not insignificant. Besides wages there are also the costs of transportation, meals and overnight accommodation.

The goal of this project is to develop and demonstrate a remote fumigant monitoring system which will provide bulk handler staff the ability to remotely monitor the fumigant levels at a storage site and to access a record of the continuous levels of fumigant during the entire fumigation period.

About the author:

Paul Kamel holds a Bachelor of Engineering Technology and a Master of Engineering Practice. Both awards were undertaken with a major in Electrical & Electronic Engineering. He has over 12 years experience in developing product both for research and industry. His emphasis has predominantly been on the use and application of microcontroller based systems for monitoring, recording and control functions.

In recent years he has worked on various projects, such as a machine vision based weed spot sprayer, remote water asset monitoring for irrigators, a generic wireless sensor network system and a system for remote condition monitoring of ore vibrating screens used in the mining industry. He has also in the past had a close association with the development of automatic aeration management systems for stored grain.

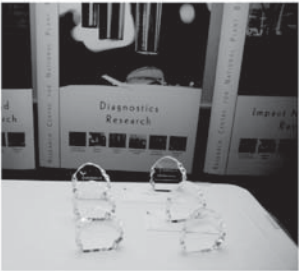
Paul was employed by the Queensland Department of Employment, Economic Development and Innovation in December 2009. His primary roles have been in the development of a mobile spore trap and of a remote stored grain fumigant monitoring system.

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Predicting Incursions and Spread

Chair: Rod Turner



Targeting detection and risk assessment capability for exotic plant parasitic nematodes

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Plant parasitic nematodes cause documented losses of over AU\$600 million annually to the Australian agriculture. Australia is fortunate in lacking many of the known damaging species of nematodes, but with increasing volumes and sources of traded goods there is increased risk of these species gaining entry to Australia. In addition, newly-described and poorly-known nematode species have recently emerged as pests. This project is to assess the risk of invasive nematodes to Australia, and develop a standard methodology for this risk assessment.

So far, nematode species of biosecurity significance have been identified from published literature and international quarantine lists. Over 200 nematode species of quarantine significance have been found, with 9.5% of the species currently present in Australia, compared to 18.5% present in USA, 10% in China, 8.5% in UK and 8% in New Zealand. We have identified various levels of threat from plant parasitic nematode species and subspecific groups, and have created a preliminary framework for prioritising them. This framework will be discussed, including the use of global distribution data on economically important species and analysis using Self Organising Maps (SOM) to determine potential invasives. The SOM analysis has identified species for more detailed analysis. The predictive modelling software Climex can also contribute in predicting climatic suitability for invasive species.

About the author:

Sunil is a PhD student working on risk assessment of exotic pest nematodes. Sunil completed his Masters of Science in Biology in 2009 from the University of the South Pacific, Fiji. For his Masters of Science thesis, he studied the diversity and distribution of root-knot nematodes in agricultural areas of Fiji. His research interests include nematode diagnostics, biosecurity risk assessment and nematode management.

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Meta modelling of biological invasion for rapid response

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When a new pathogen or insect pest is detected, rapid response is critical to maximise the chance of containment and eradication and minimise the threat to relevant industries. However, inappropriate response can be extremely costly. For example, we might waste resources on trying to eradicate a pest that has already spread too far to be contained or use a management strategy that has a lower chance of success than another possibility and thus allow the pest to escape and become permanently established. Simulation modelling is a tool that can be used to evaluate different management options in light of available knowledge about the pest's dispersal and population dynamics and its new environment. However, simulation models typically take a long time to develop, parameterise, test, run and analyse. How then can modelling be used to provide valuable predictions when rapid response is critical?

We present an approach for meta-modelling of biological invasions. Meta-models, or emulators, are relatively simple and empirical models that capture the important characteristics of more complex and realistic process-based simulation models, and thus 'emulate' their predictions. However, the meta-model is much simpler than the simulation model being emulated, making it much quicker to run and analyse. It can also be used to make predictions for a wide range of organisms, environments, and management options, and to evaluate which characteristics of these organisms and environments are most important to the final outcome. This allows expensive and time-consuming collection of new data to be focussed on areas where it is most needed.

About the author:

Michael completed his Honours program at UWA in Maths, looking at control in chaotic systems, and his PhD at the University of Queensland in the Centre for Plant Architecture Informatics, looking at new approaches to modelling the interactions between plant form, function and environment. His post-doc in Montpellier, France, married stochastic models with structural models to create virtual apple trees and he then returned to Perth to teach applied maths at UWA, before spending a couple of years creating the Weed Seed Wizard (a model of seedbank dynamics) at the Department of Agriculture and Food.

He started as a lecturer in computational agro-ecology in the School of Plant Biology in July 2007 and his current projects involve modelling of weeds, seedbank population dynamics, evolution of resistance to herbicides and pesticides, competition and interaction between plants in natural and managed systems, the role of new options (such as perennial pastures) in farming systems, optimal land use in agricultural systems and mixed-use landscapes, and dispersal of biological organisms.

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Using TOPS to identify host hot spots for rust incursion management: Lessons learnt

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Rust fungi are important pathogen of plants, causing environmental and economic impacts. In addition to the current distribution of rusts, knowing likely sources and potential changes in distribution is important for managing rust incursions. We used NASA's Terrestrial Observation Prediction System - Gross Primary Production model (TOPS GPP) to model daily photosynthetic rates, to gauge the suitability or susceptibility to rusts in vegetation types for South Eastern Australia. Using TOPS one can use weekly composite data of GPP at a one km spatial resolution to indicate susceptibility of vegetation to rust infection.

Combining these data with meteorological climate data and a rust sporulation model, we predicted areas susceptible to rust infection, areas suitable for sporulation, and the direction that the spores may disperse. The change in vegetation suitability was also used to aid the location of traps for monitoring for presence of rusts. Simulations can be used to forecast pest outbreaks and potentially identify feasible and effective containment or management options.

After involvement in a preliminary monitoring process for myrtle rust in NSW in July, we reviewed the predictive capability of the process and identify some areas for improvement. The main shortfall in trying to predict potential origins of the rust is due to the inherent variability of wind direction and speed. Wind direction during the possible initial infection period (one week in mid February) was highly variable and came from all major directions.

Initial sporulation models based on laboratory studies of the rust were improved although this would have had insignificant impact on the location of the spore monitoring points. However the process and the illustrative output maps was found to be advantageous in assisting decision making in the spore monitoring program.

About the author:

John Weiss is a PhD student with the Cooperative Research Centre for National Plant Biosecurity and the Victorian Department of Primary Industries.

He has been working on and researching invasive species for nearly 20 years. He investigated the biological control and integrated management of the invasive weed, Horehound for nine years and more recently worked on weed risk analysis and predictive modelling of potential weed impacts. At present he is enjoying working with NASA to see if we can use dynamic environmental layers to improve predictions for pest incursions.

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Factors affecting the dispersal of fungal pathogens: Chickpea ascochyta blight as a model

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⁴Department of Agriculture and Food Western Australia

Exotic fungal plant pathogens pose a threat to Australian agriculture. Some of the most devastating fungal pathogens are transported by rain splash, wind dispersal or a combination of both. The transport of fungal pathogens via rain and wind makes containment and eradication difficult. *Ascochyta rabiei*, causal agent of ascochyta blight of chickpea, is a wind/rain borne pathogen already present in Australia. *A. rabiei*, therefore, provides a suitable pathogen for modelling the potential spread of an exotic fungal pathogen dispersed by wind and rain.

Field trials and laboratory studies were conducted to examine key environmental factors influencing the short distance (rain splashed) and long distance (wind borne) distribution of spores.

Laboratory experiments were conducted to investigate the effect of wind speed (m/s), rain splash (ml/m) and a combination of the two factors on the dispersal of conidia in a purpose-built wind and rain tunnel.

A model for determining the spread of rain and wind-borne pathogens was developed for ascochyta blight based on the spatiotemporal model for simulating the spread of anthracnose in lupin fields. The data collected from the field trials and laboratory experiments were entered as the model parameters. The adjusted parameters produced a model output in Mathematica™ that best fit field disease observations.

The outcome of this work is a model calibrated with experimental data and tested with field observations for accuracy. Weather data are entered into the model and pathogen spread is predicted by graphical output showing disease occurrence in the field. The model developed now provides a basis for future predictive models for exotic plant pathogens. It will also facilitate improved management of disease through forecasting, and more precise application of fungicide and timing of crop sowing.

About the author:

Steve Coventry is a PhD candidate who is studying the factors affecting the dispersal of fungal pests using chickpea ascochyta blight as a model. He is based and conducts his studies at the University of Adelaide where he received his honours degree in agricultural science, majoring in integrated pest management. His PhD project has been supported by the CRC for National Plant Biosecurity.

Steve has a broad range of experience in plant pathology, modelling, entomology and plant breeding through study and work placements. Steve is in the final stages of writing his PhD thesis and intends to complete in early 2011.

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Sudden Eucalypt death? Australian native plant susceptibility to *Phytophthora ramorum*, and its potential global distribution

Kylie Ireland^{1,2}, Daniel Hüberli^{2,3}, Bernard Dell², Ian Smith⁴, David Rizzo⁵, Darren Kriticos^{1,6} and Giles Hardy^{1,2}

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Phytophthora ramorum causes considerable and widespread damage in nurseries, gardens and natural woodland ecosystems of the USA and Europe, and is classified as a Category 1 plant pest in Australia. It is of particular interest to Australian plant biosecurity as, like *P. cinnamomi*, it has the potential to become a major economic and ecological threat in areas with susceptible hosts and conducive climates.

Research was undertaken in California to assess the pathogenicity of *P. ramorum* on Australian native plants. Seventy plant species within 24 families were sourced from established gardens and arboretums, and selected based upon provenance from areas of climatic suitability for *P. ramorum* as well as ecological and economical importance. Foliar, branch and log susceptibility were tested using detached leaf, branch and log inoculations.

Sporulation potential and chlamydospore production was also tested on detached foliage of a select mid to upper storey species. Potentially highly susceptible foliar Australian host species included *Eucalyptus regnans*, *Isopogon cuneatus*, *I. formosus*, *Leptospermum lanigerum*, *L. scoparium*, and *Melaleuca squamea*, while potentially resistant hosts included *Hedycarya angustifolia*, *Olearia argophylla*, *Phyllocladus aspleniifolius*, *Pittosporum undulatum*, and *Podocarpus lawrencei*.

Disease incidence and severity were greater during the summer, and when the leaves were wounded. Putative sporulating hosts included *Agonis flexuosa*, *C. ficifolia*, *Eucalyptus delegatensis*, and *E. viminalis*. Susceptible branch hosts included *E. denticulata*, *E. sideroxylon*, *E. viminalis*, *Hardenbergia violaceae*, *I. formosus* and *N. cunninghamii*, and potential bole canker hosts included *E. delegatensis* and *E. regnans*.

A simulation model developed using CLIMEX suggests a high likelihood of potential distribution in Australia along coastal NSW, and in cooler, wetter regions of Victoria and Tasmania. These results extend the known potential host range for *P. ramorum*, confirming it as a potential threat to Australian plant industries and ecosystems, and highlighting additional potential hosts prevalent in global horticultural trade. Results of the studies will be discussed in relation to their implications for disease entry, spread and development of an epiphytotic within an Australian biosecurity framework.

About the author:

Kylie Ireland is a PhD student with the Cooperative Research Centre for National Plant Biosecurity at Murdoch University, Perth, Western Australia. Hailing from the east coast of Australia, she has a Bachelor of Science majoring in Ecology, with Honours in Botany, as well as a Bachelor of Arts majoring in Political Science and Spanish, from the University of Queensland.

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Climate change, biosecurity and migratory insect pests: integrating population dynamics with 'over the horizon' invasion ecology

Hazel R. Parry^{1,2}, Darren J. Kriticos^{1,2}, Jean-Philippe Auranboud³, Wendy Griffiths^{2,3}, Kyla Finlay³, Paul De Barro^{1,2} and Jo Luck^{2,3}

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Migratory insect pests can pose recurrent biosecurity risks as pests disperse from source areas into seasonally vulnerable regions. Under a changing global climate, pest risks may alter as migration patterns shift; for example changes in the timing of migration events to higher latitudes. Future pest impacts are likely to be influenced by a combination of both direct and indirect factors, such as changes in pest demography, geographical ranges and host growing conditions. Understanding such complex future scenarios requires a simulation approach to project the implications for biosecurity.

The CRCNPB 10071 project has focused on the case study of the population dynamics of the aphid *Rhopalosiphum padi* in several agricultural landscapes of Australia. The spatially-explicit aphid-wheat-CYDV model demonstrates a novel integration of (1) a coupled spatial population dynamics model of host-disease-vector; (2) airborne pest dispersal simulation; (3) climate change scenarios to estimate future risk from existing pest species in the Australian agricultural environment. Here we present successful simulation results from the coupled model in Spatial Dymex to examine impacts of BYDV and changing CO₂ levels on the aphid-wheat-virus system, as well as the spatial simulation of aphid dispersal across the landscape into wheat crops from their over-summer grassland hosts.

This work carried out by the CRCNPB 10071 project has been an important precursor to the development of a bid for future CRC work on biosecurity threats in Australia via wind-borne dispersal.

About the author:

Hazel joined CSIRO/CRCNPB to work on this CRCNPB project in August 2009, having moved from the Food and Environment Research Agency (Fera), formerly Central Science Laboratory, in the UK. Hazel completed her PhD at the University of Leeds, UK, in late 2006, entitled 'Effects of Land Management upon Species Population Dynamics: A Spatially Explicit, Individual-based Model'. Her research interests include: agent-based and individual-based modelling, computer simulation of crop pest population dynamics and dispersal, grid computing, geographical information systems, environmentally sensitive farming and predicting the implications of policy and environmental change for agricultural landscapes.

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The CUBAn Crisis: The story of how prophet can triumph over evil

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The air was dank and cold. The prophet stared blankly at the empty consultation room. The halcyon days when industry had sought him out in his hilltop retreat to advise them of their biosecurity risks were far behind him. In the three productive years he had spent preparing pest impact simulation models and communicating the results to industry audiences eager to listen, he had sown the seeds of his own demise. Now that they had all the materials and knew how to use them to manage their biosecurity risks, there was no need for the industries to consult the prophet any more. Little by little, the torrent of business activity had slowed to a trickle and finally stopped.

The prophet now sat in his chair a shadow of his former self, frail and prematurely aged. He sighed aloud as he fondly recalled working with wonderful folk like the apple and pear growers. His personal assistant, Flora McKitchen, interrupted her game of Medal of Honour to enquire as to the source of his distress. "What troubles you, oh wise one?", she enquired as she sauntered into his office.

"Oh, my dear Flora", he laboured, "Long has it been since someone has sought my advice on biosecurity matters, and since I have felt the warmth and excitement of dispensing that advice. You know, a lesser prophet once said 'pride goeth before destruction, and a haughty spirit before a fall'. I fear my spirit is ebbing away".

Flora despaired at the broken man who slouched before her. She needed to inspire him and give him back the pride that once filled him so entirely. She stood there in the doorway, staring in to the same piece of nothingness as the prophet, when suddenly she hit upon an idea.

"Why don't you go spatial?", she suggested, excitedly.

"You mean like Michael Jackson in Moonwalker?", replied the prophet.

"Not exactly", replied Flora, "I mean rather than handing industry aggregated indications of potential pest impacts as you've done in the past, why not present a similar set of information on a finer spatial resolution, thereby making it more relevant to policy-makers operating at regional or sub-regional scales". Heavily inspired by the computer game she had just been playing, she continued. "You could then encourage industry representatives to play war games in which a pest arrives in a region, and they have to work together to formulate the best way of managing it. Do you remember that Jolly Apple Farmer with the crazy dog, Erat? Why not talk to her about the idea?"

At this suggestion, it was as if a fire had been reignited within the old prophet. The sparkle returned to his eye and his back straightened, as he suddenly rose and declared, "Flora, you are almost as amazing as I! What a truly splendid idea. I was a little uncertain about the process of aggregation anyway. Hey, we could incorporate uncertainty into the information we provide too so that growers know when we're not so sure about our predictions, as when we are. We shall call our new venture 'Communicating Uncertainties in Biosecurity for Agriculture', or CUBA for short. Summon the Jolly Apple Farmer at once. Only, tell her to leave that meddlesome pooch of hers at home, would you? Quickly now, we've much to do".

And with that, the prophet embarked on what would later become his crowning achievement, including all the magic and inspiration of his first research project with the added bonus of spatial relevance. Little did he know what adventure and mirth it would bring not just to the apple and pear producers, but to the banana growers too.

About the author:

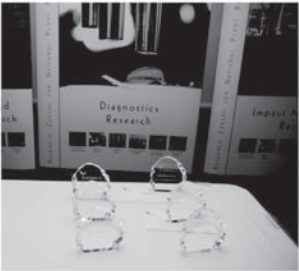
David Cook is from the Great Southern region of WA. He completed a BSc(Hons.) degree at Murdoch University in 1995, and between 1996 and 2004 worked as a Regional Economist for the Department of Agriculture Western Australia in Bunbury. There he researched a wide range of issues related to biosecurity economics, from incursion response and impact assessment to trade modelling and quarantine. During this period David received an ARC-SPIRT grant to complete a PhD with UWA's School of Agricultural and Resource Economics (1999-2001). David returned to the Department of Agriculture for a period before taking up a postdoctoral position at Imperial College London's Wye Campus (2003-2004) profiling UK Biosecurity risks. He then headed back to Australia to take up a Research Economist position with CSIRO Entomology (now Ecosystem Sciences). David has successfully managed two CRCNPB projects to completion (CRC10001 and CRC10010), and is currently leading the CRC10162 Communicating Uncertainties in Biosecurity for Agriculture project.

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Decision Making

Chair: Shashi Sharma



AQIS Operational Science Program and R&D challenges for CRC

Mark Whattam¹

¹*AQIS Science Program (South East Region)*

The AQIS Operational Science Program (OSP) is a national network of Entomologists and Plant Pathologists who are responsible for providing timely identifications of pests and diseases intercepted by AQIS Officers from imported goods. In addition OSP develop and deliver technical training to AQIS Officers and provide risk management advice at the border.

More than 20,000 pest identifications are performed by OSP annually and this number continues to increase in line with increasing cargo, animal, plant, mail volumes and passenger movements. With the increasing globalisation of trade combined with climate change, the range of pests and pathogens is likely to expand and the threat of pests crossing international borders will continue to present challenges for regulatory authorities. The demand for rapid, robust and reliable pest and disease detections will continue to intensify. Research and development is needed to produce validated and cost effective diagnostic protocols to identify emergency plant pests as well as the 'unknown' risks. This presentation will identify some research and development ideas that may be of interest for CRC project collaborators.

About the author:

Mark Whattam is the Senior Manager of the Australian Quarantine and Inspection Services (AQIS) Operational Science Program (OSP) in the South East Region (Victoria/Tasmania). I started working with AQIS in 1996 as a Plant Pathologist delivering diagnostic services, advice and disease training to AQIS Operational programs in particular the Post Entry Plant Quarantine program which facilitates the entry of high risk planting stock into Australia. I have a Bachelors Degree in Science (Biology) with Honours, Advanced Diploma in Environmental Management and Graduate Diploma in Business Management. I am currently located at the AQIS Regional Office (Tullamarine) two days a week and three days a week at the AQIS Plant Quarantine Nursery (Knoxfield).

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Biosecurity risk assessment systems: an international comparison

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How do biosecurity risk assessment systems differ around the world? What qualitative or quantitative approaches are taken, and how do these compare with respect to important issues such as consistency and uncertainty? This presentation describes the outcomes of a recently concluded CRCNPB project that aimed to address these questions. The project was a collaboration between the CRCNPB, ACERA, CSIRO and DAFF, with international engagement by FERA (UK) and Pratique (UK). The outputs of the project were twofold. The first was a report co authored with Professor Mark Burgman (ACERA Project 0709) that reviewed the frameworks used by Australia, the USA, Canada and New Zealand to assess the biosecurity risks associated with importation of animals, plants or their derivatives, including compliance with relevant international standards, expression of appropriate level of protection, methods for assessing risk and evaluating risk management options, and ways in which risk was communicated. The results of the review suggested a broad framework for IRAs, with 15 recommended properties.

The second output was a set of five papers that investigated particular aspects of the quantitative approaches adopted in these frameworks. These papers addressed the following issues: ways in which uncertainty is defined, acknowledged and used in PRAs; new approaches to assessing the homogeneity of expert scores for PRAs and how this can be used to improve the PRA questionnaires; and a new unifying 'expert response' framework for calibration and combination of expert opinions in plant pest risk assessment. These papers were co authored with Dr Sama Low Choy and Dr Grant Hamilton (QUT), Dr Alan MacLeod (FERA) and members of Pratique.

About the author:

Kerrie is a statistician with a research interest in evidence-based modelling of complex systems, Bayesian models and Bayesian networks. She has a strong focus on collaborative, multi-disciplinary projects and leads a Collaborative Centre in Data Analysis, Modelling and Computation at QUT. She is part of a number of CRC projects, and a PhD supervisor, in cool new statistical approaches to plant biosecurity.

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Economic analysis of surveillance and quality assurance as strategies to maintain grain market access

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The aim of the project is to analyse the economics of insect pest biosecurity in the Cooperative Bulk Handling (CBH) grain storage and transport network in Western Australia (WA) using a system-based modelling approach. To date, a transport model has been constructed based on linear programming. The model includes transport costs for rail and road transport of grain from farms to Kwinana port within the Kwinana region. As grain may need to be stored at farms, receival points, at CBH or even at port, the model has included the storage costs of grain at these different storage nodes. Estimates have been included for biosecurity costs that accompany storage for grains until accurate figures are reached. The model assumes three periods of time (harvest, post-harvest, and clearance) and produces results for the efficient transport and storage costs of grain. To calculate the most efficient distances and costs between farms and different receival points as well as to port, a GIS map was constructed. The GIS map includes all farms (~13000), and all receival sites (~114) within the Kwinana region.

The results of this research will allow the grain industry in Western Australia to account for the costs, benefits and risks associated with different spatial patterns of grain movements between farms and port in the Kwinana region.

About the author:

Hoda graduated from the University of Commerce (Egypt) with a degree in Accounting. Then, he completed a diploma in Environmental Economics and his master thesis was on how Economic Instruments can be used to address agricultural externality problems. Now, he is studying his PhD at the University of Western Australia, School of Agriculture and Resource Economics (SARE). In his research, he is trying to improve the efficiency of the grain network by looking at costs of transportation, storage, and biosecurity issues accompanied in an attempt to optimize these involved costs.

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Towards a new framework for the appraisal of R&D investments to safeguard biosecurity within pest management systems

Veronique Florec^{1,2}, Rohan Sadler^{1,2}, Ben White^{1,2} and Bernie Dominiak^{1,3}

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Investment in research and development (R&D) on biosecurity has become increasingly important as the growing intercontinental movement of people and goods continues to raise concern about threats from invasive organisms affecting human and animal health, agriculture and natural environments.

These R&D investments may result in the development of new technologies that increase the accuracy or reduce the cost of surveillance, provide evidence to export markets to secure market access, improve the timeliness of eradication efforts and provide improved tools to farmers and regulators.

The allocation of funding between R&D possibilities should be objectively based on expected welfare gains to consumers and producers. However, R&D projects have complex, long term and uncertain net benefits. Within a limited budget, R&D projects need to be prioritised in order to efficiently allocate scarce resources.

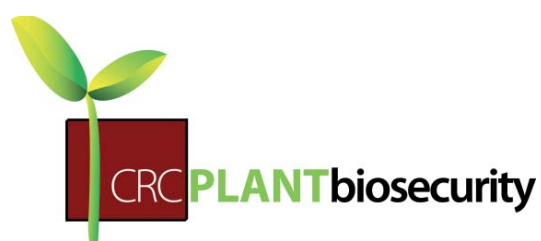
In this talk we present our approach towards developing a new framework for the appraisal of R&D investments on biosecurity. The objective is to assist decision making in the prioritisation and selection of competing project proposals. Improved methods of evaluating biosecurity R&D can potentially lead to biosecurity research investments that achieve greater net benefits for society.

About the author:

Veronique Florec comes from the second-largest producer of coffee in the world on the other side of the Pacific Ocean: Colombia. With not quite a typical Colombian name, she is also French. She completed a Bachelor of Economics degree with Honours between France (Université Pierre Mendès France, Grenoble) and the United Kingdom (University of Sussex, Brighton) in 2005 and a Masters in Development Economics (Université Panthéon-Sorbonne, Paris) in 2006. Veronique is now a research assistant at the School of Agricultural and Resource Economics, The University of Western Australia, looking at the economics of biosecurity in the establishment and maintenance of fruit fly area freedom through surveillance and control.

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Core Participants



Supporting Participants



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