2013 BSPP Presidential Meeting
17th and 18 December

University of Aston in Birmingham

"Arcadia, utopia or dystopia? Visions of plant disease management in 2050"

As well as invited speakers and contributing posters, there will be opportunities for group discussion and brainstorming of the issues involved, looking to the future of applied plant pathology.

Mike Shaw,
President-elect

British Society for Plant Pathology
BSPP

Fitness Costs and Trade-offs in Plant-Parasite Interactions

Notes

We are grateful for the financial support of Illumina, and their sponsorship of Sophien Kamoun's talk.

Notes

President's Welcome

Welcome to Norwich - "A Fine City". One of England's oldest cities, Norwich combines ancient and modern in a uniquely attractive fashion: more mediaeval churches than any other city in Europe but also some of the best shopping of anywhere in Britain. If you have time to look around, don't miss the 12th-century cathedral, the market, the Norman castle (now a museum), and the historic streets around Elm Hill, dating back hundreds of years. Norwich has many excellent restaurants while Norfolk is England's leading county for independent beer production.

The Assembly House, where BSPP's 2012 Presidential Meeting is held, has a chequered history as a hospital, a monastery, a private house, a school and a place of entertainment for the Norfolk gentry. After a major fire in 1995, it was restored to the way it would have looked in its hey-day in the early 19th century.

More recently, Norwich has become renowned for research on plants, microbes and agriculture, while Norfolk is one of Britain's most productive farming regions. It is appropriate, then, that our conference on costs and trade-offs in plant disease focuses on a topic which is not only scientifically fascinating but also highly relevant to sustainable and productive agriculture. We have brought together an excellent selection of speakers on diverse aspects of fitness costs, from molecular genetics through plant biology to ecology and agriculture. We also look forward to stimulating talks and posters from a new generation of plant pathologists.

We hope you enjoy your visit to Norwich and this BSPP conference.

Organising committee:
James Brown, Chris Ridout and Steve Whisson

We wish to thank Sarah Maxwell and Julie Ellwood at the John Innes Centre, Georgina Postlethwaite and the staff of the Assembly House for all their help in organising this conference, Carol Jenner for proofreading the abstracts and Sarah de Vos for design and artwork. We also thank BASF for use of the *Ramularia collo-cygni* image on the front cover.

16th December – 18:30 to 20:00: Opening reception (drinks and snacks), The Assembly House. Delegates to make their own arrangements for evening dining.

17th December

Session 1 Chair: Michael Shaw (University of Reading, UK)

09:00-09:45 **Meeting opening and Presidential Address: James Brown** (John Innes Centre, UK) "Fitness costs in plant disease and their roles in agriculture and nature"

09:45-10:15 **Hans Cools** (Rothamsted Research, UK) "Resistance to azole fungicides in plant pathogenic fungi: cost and adaptation"

10:15-10:45 **Mogens Hovmøller** (Aarhus University, Denmark) "The role of increased pathogen fitness in yellow rust epidemiology"

COFFEE

Session 2 Chair: James Brown (John Innes Centre, UK)

11:15-12:00 **Garrett Memorial Lecture: Tom Mitchell-Olds** (Duke University, USA) "A novel gain-of-function polymorphism controlling complex traits and fitness in nature"

12:00-12:30 **Fernando Garcia-Arenal** (Polytechnic University of Madrid, Spain) "Virulence and defence in a plant-virus systems: costs of different fitness components"

12:30-13:00 **Anna-Liisa Laine** (University of Helsinki, Finland) "Pathogen life-history trade-offs revealed in allopatry"

LUNCH

Session 3 PH Gregory Prize Competition Chair: Gary Foster (University of Bristol, UK)

14:00-14:15 **Timothy Miles** (Michigan State University, USA) "Blueberry fruit infection by *Colletotrichum acutatum*: host defence mechanisms and screening methods"

14:15-14:30 **Kaneez Fatema** (University of Hertfordshire, UK) "The effect of silicon on strawberry plants and its role in reducing infection by *Podosphaera aphanis*"

14:30-14:45 **Ruth Bryant** (John Innes Centre, UK) "Effect of temperature on wheat resistance to yellow rust"

Notes

General Poster

War between plant and insect: local victory but systemic loss?

Irene A. Vos, Andriaan Verhage, Corné M. J. Pieterse and Saskia C. M. van Wees
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Jasmonic acid (JA) is an important defence-related phytohormone. In Arabidopsis, JA-dependent resistance against herbivorous insects and necrotrophic pathogens is mediated by distinct branches of the JA signalling pathway, which act antagonistically to each other. The phytohormone abscisic acid (ABA) co-regulates defence against herbivorous insects via activation of the JA-signalling branch that is controlled by the transcription factor MYC2, leading to expression of the marker gene *VSP2*. On the other hand, the phytohormone ethylene (ET) steers defence against necrotrophic pathogens via activation of the JA-signalling branch that is under control of ERF1/ORA59 transcription factors, leading to *PDF1.2* gene expression. Recently, we revealed that oral secretions of the caterpillar *Pieris rapae* directs JA signalling to the ERF-branch. However, the plant was found to rewire JA signalling, resulting in activation of the MYC-branch and suppression of the ERF-branch, thereby becoming less attractive to the attacker. We now investigate whether the effect on plant responses by *P. rapae* feeding extend to systemic tissue and what the role of ABA is in the induction of systemic responses.

14:45-15:00 **Emmanuel Ogwok** (National Crops Resources Research Institute, Uganda) “RNAi-mediated control of cassava brown streak disease in field grown cassava”

15:00-15:15 **Camilla Korner** (University of Basel, Switzerland) “Role of plant RNA-silencing pathways in recovery from viral disease symptoms”

15:15-15:30 **Remco Stam** (University of Dundee, UK) “Characterisation of Crinkler (CRN) effector proteins from *Phytophthora capsici* and their putative host targets”

15:30-15:45 **Pernille Roelsgaard** (University of Copenhagen, Denmark) “Barley: the correlation between powdery mildew infection and leucine-derived hydroxy nitrile glucosides”

15:45-16:00 **Dominik Klauser** (University of Basel, Switzerland) “The anticipation of danger: MAMP perception enhances *At*Pep-triggered oxidative burst”

TEA

Session 4 Chair: Cyril Zipfel (The Sainsbury Laboratory, UK)

16:30-17:00 **Ralph Hückelhoven** (Technical University of Munich, Germany) “ Loss of susceptibility: a costly way to resist powdery mildew?”

17:00-17:30 **Luis Mur** (Aberystwyth University, UK) “ Stomatal lock-up contributes to the cost of resistance to foliar fungal pathogens”

17:30-18:00 **Corné Pieterse** (Utrecht University, The Netherlands) “Trade-offs and benefits of hormonal modulation of plant immunity”

18:00-20:00 **Poster Session**, including judging for the **J Colhoun poster prize**

18:00-18:30 (concurrent with poster session) Annual General Meeting of the British Society for Plant Pathology.

20:00- **Presidential Dinner**, The Assembly House

18th December

Session 1 Chair: Murray Grant (University of Exeter, UK)

09:00-09:30 **Jonathan Jones** (The Sainsbury Laboratory, UK) "How plant pathogenic oomycetes cause or fail to cause disease"

09:30-10:00 **Didier Andrivon** (INRA, France)"The hard life of *Phytophthora infestans*: when trade-offs shape evolution in a biotrophic plant pathogen"

10:00-10:30 **Gail Preston** (University of Oxford, UK) "Uncoupling of defence signalling in the metal hyperaccumulator *Noccaea caerulescens*"

10:30-11:00 **Bruce McDonald (**ETH Zürich, Switzerland) "Fitness costs associated with horizontal acquisition of host-specific toxins"

COFFEE

Session 2 Chair: Mari-Anne Newman (Copenhagen University, Denmark)

11:30-12:00 **Angus Buckling** (University of Exeter, UK) "Costs and coevolutionary dynamics: Insights from bacteria-virus interactions"

12:00-12:30 **Aurélien Tellier** (Technical University of Munich, Germany) "Costs in plant-parasite coevolution: bridging the gap between ecology and population genetics"

12:30-13:00 **Santiago Elena** (CSIC-UPV, Spain) "The genetic architecture of RNA virus fitness"

LUNCH

Session 3 Chair: Fiona Doohan (University College Dublin, Ireland)

14:00-14:30 **Richard Summers** (RAGT Seeds Ltd, Essex, UK) "Breeding Wheat Varieties Fit to Fight Disease"

14:30-15:00 **Paul Nicholson** (John Innes Centre, UK) "Trade-offs: the need for compromise in breeding for disease resistance in wheat and barley"

15:00-15:30 **Sophien Kamoun** (The Sainsbury Laboratory, UK) "Genome evolution in filamentous plant pathogens: the bigger the better?"

15:30 **Close of meeting.**

General Poster

Auxin Response Factor 2* enhances susceptibility to the hemibiotrophic plant pathogens *Fusarium culmorum, Magnaporthe oryzae* and *Ramularia collo-cygni* in *Hordeum vulgare

Andrew Steed, Martha Clark, Graham McGrann, Xinwei Chen, Christopher Burt and Paul Nicholson
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T-DNA tagged insertion mutants of *Arabidopsis thaliana* were screened for resistance to the hemibiotrophic pathogens *Fusarium graminearum* and *F. culmorum*. One mutant identified "fgr1" exhibited enhanced resistance in detached leaf bioassays. The mutant is disrupted in the gene *Auxin Response Factor 2* (*ARF2*), one member of a gene family of 22 ARFs that regulate auxin mediated transcription activities. This gene acts as a central component in the crosstalk between the auxin, brassinosteroid and abscisic acid signalling pathways. The orthologous gene in *Hordeum vulgare* (barley) *HvARF2* was identified and the sequence used to generate RNAi lines in the two-row barley variety Golden Promise (GP). *ARF2* is a negative regulator of auxin signalling that has pleiotropic effects on many aspects of plant development. However, the role of *ARF2* in disease resistance is less well characterised. The role of *HvARF2* in disease resistance to barley pathogens with differing lifestyles was assessed in the *HvARF2* silenced lines. The *HvARF2* silenced lines showed a significant reduction in disease caused by the hemibiotrophic pathogens *F. culmorum, Magnaporthe oryzae* and *Ramularia collo-cygni* compared to GP and null transformed lines, but showed no significant effect on disease development caused by the biotrophic pathogen *Blumeria graminis* f. sp. *hordei*. The result indicates a positive role for auxin signalling in disease resistance to these hemibiotrophic pathogens and demonstrates that manipulating a member of the ARF gene family can have a positive effect on enhancing disease resistance against hemibiotrophic pathogens without the negative trade-off of increasing susceptibility to biotrophs.

General Poster

Host cell modulation by aphid effector proteins

Patricia A. Rodriguez[1], Tim Warbroek[1], Camille Lenoir[1,2] and Jorunn Bos[1]
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Like most plant parasites, aphids require intimate associations with their hosts to gain access to nutrients. Aphids predominantly feed from the phloem, and have stylets that navigate through different layers of leaf tissue to form an interface with the host where signals are exchanged. Indeed, aphid feeding induces clogging of phloem sieve elements, which is suppressed by the aphid in successful host interactions. In addition, aphids can alter host plant phenotypes by, for example, inducing the formation of galls or causing leaf curling. Suppression of host defences and altering plant physiology is common among phytopathogens and involves secretion of effectors. Recent evidence suggests that aphids, like other plant parasites, secrete effectors that share functional features with plant pathogen effectors. The identification and characterization of such aphid proteins is crucial to gain insight into the molecular mechanisms underlying plant resistance and susceptibility to aphids. Our research aims to identify aphid effectors and their host targets to understand their involvement in host cell manipulation. In the long term, our findings will provide new knowledge on plant–aphid interactions that is crucial to develop effective and sustainable aphid control strategies. As part of our work, we have screened a set of candidate effectors from the broad host range aphid *M. persicae* using yeast two-hybrid assays. Here, we will report our progress on identifying and characterizing effector–target interactions and describe the interaction between the aphid effector Mp1 with a putative host target protein in mainly pre-vacuolar compartments.

Awards

The Board of BSPP wishes to encourage young plant pathologists to talk about their work. There are two prizes awarded at the presidential meeting:

The P. H. Gregory prize, awarded for the presentation of an oral paper. The competition is open to (a) members of BSPP who have not previously presented a paper to a meeting of a learned society and (b) to all registered postgraduate students, whether or not they are members of the society, or have presented a paper before to a meeting of a learned society. Contestants should not have entered the P.H. Gregory competition previously. The winner receives a certificate and a cheque for £250

Philip Gregory (1907–1986) pioneered aerobiology as a topic for research, combining many disciplines to contribute to better understanding of fungal spore dispersal and plant disease epidemiology. He developed theories of spore dispersal, which was published in his classic paper on the dispersion of airborne spores (Gregory PH. 1945. Trans. Br. Mycol. Soc. 28:26–72). He became Head of the Plant Pathology Department at Rothamsted in 1958 where he further developed his research on spore dispersal and sedimentation velocities. In his retirement, Philip Gregory, continued work on elucidating the epidemiology of black pod disease of cocoa in Nigeria, and maintained enthusiasm for his wide range of scientific interests. He proudly and enthusiastically showed his garden to visitors and they often regarded this as the highlight of their visit to Harpenden (Source: Lacey et al (1997) Annual Review of Phytopathology Vol. 35: 1-14).

The John Colhoun Prize, awarded for a poster. The work presented in the poster must form part of a research project conducted by the entrant in support of a PhD or Masters degree, and the entrant must not have been awarded the degree prior to the deadline for abstracts date. Students need not be members of BSPP. The winner receives a certificate and a cheque for £100.

John Colhoun (1913–2002): cryptogamist and plant pathologist. John Colhoun was awarded a MAgr in 1937 at Queens University, Belfast, and then moved to Imperial College, London, working on fungal pathogens

of apples for his PhD, awarded in 1940. He returned to Northern Ireland where he worked on flax, an important crop in the province during World War II, leading to a definitive text (Muskett, A. E. & Colhoun, J. (1947): The Diseases of the Flax Plant.). He became reader at Queens University in 1954. Subsequently, he took up the Chair of Cryptogamic Botany at the University of Manchester in 1960, where he worked on *Fusaria*, *Phytophthoras*, *Septoria* and *Phoma*, with hosts ranging from cereals to Chrysanthemum, Yam, Oil Palm, and Banana. In 1968 he was elected Chairman of the Federation of British Plant Pathologists, forerunner of the British Society for Plant Pathology. He retired from Manchester University in 1980 as Professor Emeritus, having occupied the Barker Chair of Cryptogamic Botany for 20 years. (Source, Epton H (2003). Mycol. Res. 107 (3): 377–381).

General Poster

Compromised photosynthetic electron flow and stomatal locking prove to be an important cultivar-specific component of a cost of resistance against biotrophic fungi in oats

Javier Sánchez-Martín[1], Luis A. J. Mur[2], Diego Rubiales[1] and Elena Prats[1]
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Genetic resistance is the most cost effective and environment-friendly approach to fight pathogens. However, evidence show that disease resistance may affect crop performance. Particularly, recent work in barley demonstrated that elicitation of hypersensitive response (HR) provokes stomatal dysfunctions known as locking, which could be an important component of the disease resistance cost. We here assessed how spatial and temporal patterns of HR in oat (*Avena sativa*) influence stomatal and photosynthetic parameters. To this aim 9 oat cultivars with different resistance responses (i.e. penetration resistance, early and late HR) to powdery mildew (*Blumeria graminis* f. sp. *avenae*; *Bga*) and rust (*Puccinia coronata* f. sp. *avenae*, *Pca*) were used. Results demonstrated that stomatal dysfunctions were genotype but not response-type dependent since genotypes with similar histological characterization showed very different locking patterns. This trend was observed following either inoculation with *Bga* or *Pca* inoculation, albeit resistance responses of epidermal cells to *Bga* attack lead to stronger stomatal dysfunctions than those observed following mesophyll attack by *Pca*. Maximum quantum yield (Fv/Fm) and operating efficiency (ØPSII) of photosystem II was compromised in most *Bga/Pca*–oat interactions and photoinhibition increased. However, the extent of the photosynthetic alterations was not directly related to the extent of HR. Increase of light rates during plant growth reduced further Fv/Fm ratios and augmented the patterns of stomatal dysfunctions previously observed. Thus, stomatal dysfunction and disruption of photosynthetic electron flow appears to be genotype-specific. Further, a cost of resistance may be tightly linked with coping with oxidative stress occurring during defence induced photoynsthetic disruption.

General Poster

Characterization of an orphan nuclear wheat gene

Alexandre Perochon, Guillaume Erard and Fiona Doohan

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Orphan genes are genes of limited phylogenetic distribution. In general these genes either present no homolog in other organisms or homologous genes are restricted to closely related organism. Emergence of these genes may reflect evolutionary processes which allow plants to adapt in the best way to changing environmental conditions. We have discovered a wheat orphan gene restricted to cold tolerant grasses. This gene encodes a small intrinsically disordered protein with both a nuclear localisation and a nuclear export signal. Studies showed that fluorescently tagged protein localised within punctate areas of the nucleus of wheat cells. Yeast two-hybrid studies suggest that this protein interacts with SnRK1 (SNF1-related kinase 1), a NAC transcription factor and a Plant Homeo Domain (PHD) finger-containing protein; thus it is likely that this novel protein is involved in genes expression regulation. We are currently characterising these interactions and the role of this protein in stress adaptation.

Presidential Address

Fitness costs in plant disease and their roles in agriculture and nature

James K. M. Brown
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Interest in fitness costs in plant disease goes back to the 1960s, to the work of Vanderplank on late blight resistance in potato and Leonard on virulence in oat stem rust. While early work on costs of resistance concerned their effects on reproductive fitness, it is now apparent that they are diverse and involve much of a plant's structure, metabolism and physiology. There is increasing evidence that genes with large effects on resistance to one disease may have trade-offs with responses to other diseases. By contrast, costs which are too small to estimate experimentally may be large enough to have significant impacts on breeding for resistance or on the dynamics of host and parasite populations in nature. Research on fitness costs in plant disease is made more complex (and even more interesting!) by genotype-by-environment effects on the size and even the existence of costs and by epistatic effects on costs as plants or parasites accumulate genes for resistance or virulence. Fitness costs and trade-offs imply that plant breeders need to balance increasing disease resistance with improving commercially important traits such as yield and quality, while costly pathogen virulences may point to candidates for sources of durable resistance. In natural populations, fitness costs interact with the ecology and epidemiology of disease to generate balanced polymorphism in host and parasite genes. A challenge for plant pathologists is to exploit our increasing understanding of fitness costs in plants and parasites and their interaction with the wider environment to find ways of making farming both more productive and more sustainable.

Invited Speaker

Resistance to azole fungicides in plant pathogenic fungi: cost and adaptation

Hans J. Cools, Nichola J. Hawkins and Bart A. Fraaije
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The development of resistance to fungicides is a consequence of a basic evolutionary process. Application of a fungicide selects a proportion of the population that are able to resist the compound and pass this characteristic to their offspring. Modern, highly efficacious systemic fungicides that have a single biochemical target are acutely affected by this phenomenon as mutation in a single gene can be sufficient to confer a highly resistant phenotype. However, field resistance to the azole class of fungicides is rare, despite a single-site mode of action. More commonly, gradual reductions in sensitivity are reported, with cross resistance within the azole class often incomplete. As a consequence, azoles have remained the leading agents for control of fungal pathogens for over 30 years. Here we describe the evolution of the azole target protein, sterol 14a-demethylase (CYP51), in fungal pathogens of arable crops targeted by azole fungicide sprays. We provide evidence for constraints on CYP51 structural changes that affect azole binding and confer resistance. We hypothesise that these constraints on CYP51 evolution are responsible for the longevity of azole fungicides, and speculate whether this will enable the continued use of azoles in the future.

General Poster

Identifying sources of genetic resistance to *M. graminicola* in wheat

Aoife O' Driscoll[1], Fiona Doohan[2], John Spink[1] and Ewen Mullins[1]
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M. graminicola is the most important disease of winter wheat in Ireland with Irish farmers solely reliant on fungicides to preserve yields. The problem is compounded by the emergence of fungicide resistant isolates of *M. graminicola* (Beyer *et al.*, 2011). We are following three parallel research initiatives, with the overarching goal of enhancing current levels of durable resistance to STB.

Field trials, now in their third successive year, have seen up to 34 varieties and breeding lines being screened for STB resistance. Current data indicates varieties Stigg, Avatar and Invicta to have particularly high levels of durable resistance with varieties Torch and Oakley exhibiting high susceptibility under Irish STB pressures.

The role of ethylene in promoting resistance and/or susceptibility to *M. graminicola* is also being investigated. In glasshouse screens, ethylene increases susceptibility to *M. graminicola*. This response is dependent on timing of ethylene application (from 4 days pre- to 14 days post-inoculation (dpi)) and is host-genotype dependent. The strength of the effect varied within the 5 dates on which disease assessments are conducted (from 17 dpi to 31 dpi). VIGS of the primary genes (*ACC*, *ACS*, *ERF1* and *EIN2*) in the ethylene pathway is now underway to investigate these responses.

Finally, using the Affymetrix array the transcriptional response of variety Stigg in contrast to the susceptible variety Gallant is being examined at 0, 1 and 14 dpi with *M. graminicola*. The results from this work, combined with field and glasshouse research will go towards achieving the overall goal of identifying candidate genes which may provide effective resistance to STB.

General Poster

Characterization of *Rhizoctonia solani* anastomosis groups on potato in the Pacific Northwest of the United States

Timothy D. Miles[1], James W. Woodhall[2], Laura A. Miles[1], Philip B. Hamm[3] and Phillip S. Wharton[1]
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Rhizoctonia solani is an important pathogen of potato, causing both qualitative and quantitative losses. It has been associated with black scurf, elephant hide and stem canker. *Rhizoctonia solani* isolates are assigned to one of 13 anastomosis groups (AGs), of which AG3 is most commonly associated with potato disease. Knowledge of the AG present is important as AGs can differ in aggressiveness to potato, host range, symptoms and fungicide sensitivity. In August 2011, isolates of *R. solani* were collected from diseased potato plants grown in Idaho. The majority of isolates were identified as AG3 by real-time PCR, but sequencing confirmed that two were AG2-2IIIB and another was AG4 HG-II. Koch's postulates confirmed the pathogenicity of these three isolates on potato. In spring 2012, seed lot tubers were collected from seed lots throughout the Pacific Northwest, including Idaho, Montana, Oregon, and Washington. 192 *R. solani* isolates were recovered from 102 tuber samples. Direct screening of tubers showed 64% were positive for AG3. In summer 2012, stem canker samples were collected from potatoes and soil samples were collected from 7 different crops grown in rotation with potatoes throughout Idaho. Seventy-one stem canker isolates were screened for their AG using real-time PCR and 60 isolates tested positive for AG3. Further research is required to determine the AG of the remaining 11 isolates as well as their pathogenicity on potato. However, results from this study show the importance of AG screening, and could have implications on the crop rotation practices in Idaho.

Invited Speaker

The role of increased pathogen fitness in yellow rust epidemiology

Mogens Støvring Hovmøller and Chris Sørensen
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Yellow rust on wheat is caused by *Puccinia striiformis* (Pst), a biotrophic pathogen specialised at host species as well as host variety levels. The pathogen is spreading by airborne spores potentially across long distances, which may contribute to a sudden and sometimes unexpected spread of the disease to new areas. While shifts in pathogen virulence may render resistant host varieties susceptible, solid evidence of a fitness trade-off for isolates possessing virulence alleles, which are not essential for infecting a specific host variety is lacking. In contrast, large differences in fitness have been observed for Pst isolates of distant geographical and evolutionary origin when infecting a susceptible host plant. The consequences of recent exotic incursions of Pst isolates into Europe and North America, which were superior to isolates of the existing Pst population in these areas, will be presented. One example deals with a global spread of isolates of two aggressive strains, which were also tolerant to warmer temperatures, and another examples is the recent the spread of races, which gave rise to large scale epidemics in triticale in Scandinavia in 2009-2010.

Hovmøller MS, Sørensen CK, Walter S, Justesen AF (2011). Diversity of *Puccinia striiformis* on Cereals and Grasses. *Annual Review of Phytopathology* 49: 197–217.

Hovmøller MS, Walter S, Justesen AF (2010). Escalating threat of wheat rusts. *Science* 329: 369.

The Garret Memorial Lecture

A gain-of-function polymorphism controlling complex traits and fitness in nature

K. V. S. Prasad[1], B.-H. Song[1], C. Olson-Manning[1], J. T. Anderson[1], C.-R. Lee[1], M. A. Schuler[2] and T. Mitchell-Olds[1]
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Identification of the causal genes that control complex trait variation remains challenging, limiting our appreciation of the evolutionary processes that influence polymorphisms in nature. In *Boechera stricta* (a close relative of *Arabidopsis*) we cloned a quantitative trait locus that controls plant defensive chemistry, damage by insect herbivores, survival, and reproduction in the natural environments where this polymorphism evolved. These ecological effects are driven by duplications in the *BCMA* (branched-chain methionine allocation) loci controlling this variation and by two selectively favored amino acid changes in the glucosinolate-biosynthetic cytochrome P450 proteins that they encode. These changes cause a gain of novel enzyme function, modulated by allelic differences in catalytic rate and gene copy number.

Next, we expanded these analyses to a pathway level in *Arabidopsis*. Theoretical analyses suggest that adaptive substitutions should be concentrated in the enzymes that exert the greatest control over flux. Although several studies have found a correlation between position in a pathway and evolutionary rate, these investigations have not examined the relationship between evolutionary rate and flux control. Here we perturbed the enzymes in the glucosinolate pathway with gene insertion lines, and showed that flux control is focused in the first enzyme in the pathway. Next, by analyzing signatures of selection, we showed that this enzyme is the only one in the pathway that shows convincing evidence of selection. Our results support the hypothesis that natural selection preferentially acts on enzymes with high flux control – as suggested by non-neutral evolution at orthologous genes in *Boechera* and *Arabidopsis*.

General Poster

How to prevent selection for fungicide resistance when using mixtures of high risk fungicides with low risk fungicides?

Alexey Mikaberidze, Bruce A. McDonald and Sebastian Bonhoeffer
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Fungicide mixtures produced by the agrochemical industry often contain low risk fungicides, to which fungal pathogens are fully sensitive together with high risk fungicides known to be prone to fungicide resistance. Can these mixtures provide adequate disease control while minimizing the risk for the development of resistance? We present a simple population dynamics model to address this question. We found that the fitness cost of resistance is a crucial parameter to determine the outcome of competition between the sensitive and resistant pathogen strains and, thus, to assess the usefulness of a fungicide mixture. Furthermore, for any known cost of resistance, an optimal ratio of fungicides in the mixture can be found, at which further selection for resistance is expected to vanish and the level of disease control can be optimized.

General Poster

Oops! … I did it again … – disease resistance trade-off between the *mlo* locus and Ramularia leaf spot in barley

Graham R. D. McGrann[1], Anna Stavrinides[1], Laetitia Chartrain[1], William T. B. Thomas[2], Joanne Russell[2], Allan Booth[2], Margaret Corbitt[1] and James K. M. Brown[1]
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Ramularia leaf spot (RLS) is an emerging threat to barley cultivation across Northern Europe. To advance our understanding of the genetics of resistance to RLS a doubled haploid population was produced from the *Ramularia* resistant barley variety Power and the susceptible variety Braemar. Disease development was scored at both adult and seedling stages and the resulting data was used to identify two QTL associated with reduced Ramularia leaf spot. One of these QTL, from the resistant parent Power, was located on the long arm of chromosome 4H. In the susceptible parent Braemar, this region contains *mlo11*, the recessive broad-spectrum powdery mildew resistance gene, suggesting that mutations associated with mildew resistance at the *Mlo* locus enhance susceptibility to RLS. To further characterise the role of *mlo* mutations in RLS susceptibility a set of near isogenic barley lines containing different *mlo* mutations were inoculated. In all cases mutation at the *Mlo* locus increased susceptibility to RLS. Two additional genes (*Ror1* and *Ror2*) are required for *mlo* resistance against powdery mildew to be effective. Mutations at either the *Ror1* or *Ror2* locus, which increase susceptibility to mildew, reduced RLS symptom development. These results indicate a true trade-off between *mlo*-mediated resistance to powdery mildew and susceptibility to RLS. We speculate that the widespread use of *mlo11* in European spring barley to control powdery mildew may have been a contributing factor in the elevation of Ramularia leaf spot to a major disease of barley.

Invited Speaker

Virulence and defence in a plant–virus system: costs in different fitness components

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Despite that plant viruses are virulent crop parasites, and that resistance in crops selects for increased pathogenicity in viruses, virus evolution in crops is poorly understood, and there is no clear demonstration of plant –virus co-evolution. We have analysed the reciprocal effects of virulence and defence of viruses and plants on plant and virus fitness, and on whether they lead to co-evolution. Results derive from analyses of tobamovirus infection of pepper (*Capsicum annuum*) crops and wild relatives. Increased pathogenicity (i.e. the ability to overcome resistance factors in a gene-for-gene interaction) results in decreased virulence (i.e. reduction of host fitness upon infection). Moreover, pathogenicity has associated penalties on different components of the virus' fitness, not all related to its interaction with the host plant, revealing new effects of plant defence on virus fitness through associated trade-offs. On the plant side, we have made a detailed analysis of the evolution of the *L* resistance alleles to tobamoviruses in wild *Capsicum* populations, to our knowledge the first such analysis in a wild plant. Results strongly suggest that *L* alleles are under adaptive selection, which is compatible with a negative effect of infection in the host plant under natural conditions. Taken together, our results support that there is plant–virus co-evolution resulting from reciprocal negative effects of virulence and defence in the plant and virus, respectively. Results also show that evolution to overcome these effects may be associated with complex trade-offs, affecting different fitness components.

Invited Speaker

Pathogen life-history trade-offs revealed in allopatry

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Trade-offs in life-history traits is a central tenet in evolutionary biology, yet their ubiquity and relevance to realized fitness of natural populations remains questioned. Trade-offs in pathogens are of particular interest because they may constrain pathogen evolution and impact risks of disease. Here, we studied life-history traits determining transmission in obligate fungal pathogen, *Podosphaera plantaginis*, infecting *Plantago lanceolata*. We find that while traits are positively correlated on sympatric host genotypes, on allopatric host genotypes correlations between infectivity and subsequent transmission traits change, becoming even negative. This supports the paradigm that life-history trade-offs are only expressed under stressful conditions. Based on our results, we would expect to see a reduction in growth rate of newly established pathogen populations (i.e. allopatry) compared to older pathogen populations. In an analysis of the natural *Po. plantaginis* metapopulation, we find that newly colonized host populations by the pathogen are smaller and more likely to go extinct during the first winter than older pathogen populations. This finding is consistent with our laboratory results, and suggests that trade-offs mediated by pathogen local adaptation could strongly influence epidemiological dynamics both at the population and metapopulation levels.

General Poster

Blackleg of canola displays a 'Boom and Bust' cycle

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Blackleg, caused by *Leptosphaeria maculans,* is the most important disease of oilseed rape (canola) worldwide. Field populations rapidly adapt to selection pressure from sowing of varieties with major gene resistance and can 'overcome' resistance. For the last decade we have monitored virulence of blackleg populations and disease severity of varieties in field trials across Australia. In 2003 after two seasons of extensive sowing, blackleg resistance of a set of varieties broke down in the Eyre Peninsula, South Australia, causing 90% yield losses and withdrawal of these varieties from sale. By 2005, virulence of populations towards these varieties declined appreciably. Thus the blackleg–canola interaction behaves in a 'Boom and Bust' manner. Extensive sowing in recent years on the Eyre Peninsula of a variety with a different source of resistance led to a warning in February that this variety should not be sown. This advice was heeded by growers and has been vindicated, as our recent field trial data showed high disease levels in this variety on Eyre Peninsula.

This high evolutionary potential of the blackleg fungus is reflected in its genome structure. Effector genes are embedded in AT-rich, gene-poor regions with transposable elements degenerated by Repeat Induced Point (RIP) mutations. Thus genes are easily gained, lost or inactivated. Analysis of isolates collected before and after the resistance breakdown in 2003 showed that deletions, RIP mutations and amino acid substitutions accounted for rapid evolution of four linked effectors, including the avirulence gene complementary to the resistance gene that had been overcome.

General Poster

Susceptibility of vining pea varieties to downy mildew in the UK

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Downy mildew caused by *Peronospora viciae* is a major problem of vining and fresh peas in the UK. The disease begins with the infection of young seedlings soon after germination. From these initial plants the disease spreads to neighbouring plants. Infected plants become stunted and early infection may result in the death of the plant. Late infection often results in the pods becoming infected. This reduces the quality and the yield of the crop. Disease pressure can be lowered by growing peas on a long rotation (1 year in 5) and using a seed dressing to reduce the primary infection. Control of the disease once in the crop is limited.

There are some varietal differences to downy mildew; however over the recent dry summers, it has been problematic to assess the new varieties for disease susceptibility. Two parallel field trials were set up in the 2012 season to test the resistance of these varieties to downy mildew. The results illustrate that there are some varieties with field resistance to the races of downy mildew they were exposed to this season but further trials are needed to expose these varieties to other races of the pathogen.

PH Gregory Prize Speaker

Blueberry fruit infection by *Colletotrichum acutatum*: host defence mechanisms and screening methods

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Anthracnose fruit rot of blueberries caused by *Colletotrichum acutatum* is a serious problem in humid blueberry-growing regions of North America. Most cultivars are susceptible but ‘Elliott’ is resistant. In order to investigate host resistance mechanisms in blueberry, ripe fruit of ‘Elliott’ was compared to that of the susceptible cultivar Jersey. Defence-related genes were differentially expressed in ‘Elliott’ compared to ‘Jersey’ after inoculation. Furthermore, higher levels of hydrogen peroxide, anthocyanins and flavonols were observed in ‘Elliott’ than ’Jersey’ fruit. Flavonols in ‘Elliott’ fruit, including two distinctive compounds, had antifungal properties. Inoculation techniques were evaluated on ripe fruit in order to develop efficient resistance screening assays: spray, droplet, and injection inoculation of a conidial suspension on whole fruit; and droplet inoculation of the open surface of cut fruit. The cut-fruit assay required substantially less time and half the amount of fruit to accomplish compared to whole-fruit assays. Detached ripe fruit from a range of blueberry cultivars were screened using various assays. Results from the cut-fruit assay correlated best with previously published resistance ratings. Of the following fruit characteristics measured (pH, titratable acidity, sugar content and firmness), sugar content was found to be positively correlated with resistance. On defined media, mycelial growth was restricted as sugar concentration increased and pH decreased. The results from these studies show that multiple mechanisms contribute to anthracnose fruit rot resistance in ripe blueberry fruit and can facilitate future fruit rot resistance breeding efforts in blueberry.

PH Gregory Prize Speaker

The effect of silicon on strawberry plants and its role in reducing infection by *Podosphaera aphanis*

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Podosphaera aphanis, which causes powdery mildew of strawberry, has a major impact on strawberry production, requiring extensive use of fungicides to control this disease. Anecdotal observations suggested that a foliar application of a silicon-based wetter, Omex SW7, had a synergistic effect with potassium carbonate in controlling *P. aphanis* on strawberries. The work reported here aimed to quantify this effect and explore possible explanations. The effect of foliar applications of silicon and potassium carbonate to limit *P. aphanis* infection was examined in a field trial under a polythene tunnel at Wisbech. Treatments were arranged in a randomised block design of 3 replicates. Results showed that germinating ascospores and colonies were present in all plots before the trial was sprayed. The results indicated that application of Standard and High concentrations of Omex SW7 on to the strawberry plants significantly ($P < 0.05$) reduced the number of germinating ascospores and the number of colonies. The results also indicated that potassium carbonate alone gave some reduction in the number of germinating ascospores and number of colonies. Potassium carbonate mixed with Omex SW7 significantly ($P < 0.05$) reduced the number of germinating ascospores and number of colonies. The present study showed that silicon levels were increased by the foliar application of Omex SW7, and in addition there were changes in the physical properties of the leaves, including increased number of leaf hairs and increased length of leaf hairs and this may assist the plants to resist fungal infection.

General Poster

Profiling conditionally dispensable chromosomes of the plant-biotrophic fungus *Zymoseptoria tritici* (syn. *Mycosphaerella graminicola*)

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Conditionally dispensable chromosomes (cDCs) are common genomic features in many parasitic ascomycetes. The presence of cDCs entails a high amount of intraspecific genomic variation that is inherited in a non-Mendelian manner. Because genes located on cDCs have in some species been shown to play a role in pathogenicity cDCs may promote rapid adaptive evolution in response to host defenses.

With up to eight cDCs the genome of the wheat pathogen *Zymoseptoria tritici* (synonym *Mycosphaerella graminicola*) contains by far the largest known proportion of dispensable elements among all ascomycetes. In comparison to the core chromosomes, cDCs of *Z. tritici* are smaller, have on average less and shorter genes with a lower GC content and a higher amount of paralogous sequences and repetitive elements. Hitherto, the functional relevance of cDCs for *Z. tritici* remains unclear. In this study we elucidate the relevance of cDCs in *Z. tritici* by assessing expression profiles during *in planta* and axenic growth. We demonstrate an overall significantly lower transcription of genes located on cDCs relative to genes located on core chromosomes. In addition, cDCs encode several unique genes that are expressed. Furthermore, we focus on duplicated genes and show differential gene expression of paralogs on core and dispensable chromosomes. In summary, our study suggests the relevance of cDCs for gene innovation and adaptive evolution in *Z. tritici*.

General Poster

Characterisation of a novel wheat NAC transcription factor

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The plant-specific NAC domain transcription factors are proteins that play important roles in different stress responses and/or diverse developmental processes. Our laboratory investigates the effect of the *Fusarium* mycotoxin deoxynivalenol (DON) on the wheat transcriptome, and through those studies identified several DON-responsive genes including a novel wheat gene. Yeast two-hybrid (Y2H) analysis, conducted using a cDNA library from DON-treated wheat, identified a NAC protein as an interactor of the protein encoded by the novel DON-responsive wheat gene, designated *Ta*NAC1-2. *TaNAC1-2* sequence was BLASTed against wheat 61k microarray data, and it showed 94.5% homology with the probe TaAffx.86847.1.S1_at which was up-regulated by *Fusarium graminearum*. Domain analysis of *Ta*NAC1-2 protein revealed a NAC domain at the N-terminus and low complexity regions in the C-terminus. The NAC domain has five conserved subdomains A–E that serve as a DNA-binding domain (BD). The C-terminus is more divergent and serves as a potential transcription domain with either activator or repressor function and also possess protein binding activity. Further Y2H confirmed that *Ta*NAC1-2 is a functional transcription factor and that it can form a homodimer. Y2H studies also confirmed that *Ta*NAC1-2 can interact with a SNRK1a protein that was also identified as being an interactor of the DON-responsive novel wheat gene.

PH Gregory Prize Speaker

Effect of temperature on wheat resistance to yellow rust

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Environmental effect on performance of wheat defence is poorly understood. We have shown that a change in day temperature affects wheat resistance to *Puccinia striiformis* f. sp *tritici* (*Pst*), the causative agent of yellow rust. In UC1041 there was no significant difference in leaf pustule cover between plants kept in controlled environment facilities with day temperatures of 18°C and plants at 25°C. However when plants were shifted, following infection with *Pst* to the cooler day temperature, resistance was notably compromised. In contrast, plants shifted from 18° C to 25°C were effectively resistant. A comparable trend is seen in young UC1041 plants and UK varieties, Shamrock and Solstice, yet leaf pustule cover in other varieties does not appear to follow this trend when plants undergo a temperature shift in either direction. To investigate this, pathogen development was followed using microscopy and experiments were performed to see how temperature changes could affect resistance both directly and indirectly. We hypothesise that temperature fluctuations in the field may compromise resistance in some wheat varieties, whereas resistance in other varieties is more stable. This research has potential to identify vulnerable periods for yellow rust susceptibility in crops and to inform breeding to develop wheat varieties with more environmentally stable resistance.

PH Gregory Prize Speaker **J Colhoun Poster**

RNAi-mediated control of cassava brown streak disease in field grown cassava

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Cassava brown steak disease (CBSD) is caused by *Cassava brown streak virus* (CBSV) and *Uganda cassava brown streak virus* (UCBSV). Due to its impact on root quality, CBSD is now considered the most important biotic threat to cassava production in East and Central Africa. In this study, transgenic resistance mechanisms were explored for management of CBSD. Two RNAi constructs, pILTAB718 (DFull Length-CP) and pILTAB719 (N-terminal CP), were generated from coat protein (CP) sequence of UCBSV, and transgenic cassava produced in CBSD susceptible cultivar 60444. Transgenic lines expressing high CP specific siRNAs were challenged by grafting to UCBSV-infected rootstocks in the greenhouse. Plants for both constructs proved to be highly resistant to UCBSV. Seven lines each of pILTAB718 and pILTAB719 were planted under confined field trial conditions at Namulonge, Uganda. CBSD leaf symptoms development was delayed in transgenic lines compared to non-transgenic controls, but reached 100% of plants in all lines except those of pILTAB718-005 and pILTAB718-001, in which 50% and 95% (n=60) remained symptom-free respectively. RT-PCR analysis of leaf samples showed presence of CBSV in 13 of the 14 lines tested but no detectable UCBSV, while plants of line pILTAB718-001 proved to be free of both CBSV and UCBSV. At harvest, incidence and severity of root damage was significantly reduced in lines pILTAB718-005 and pILTAB718-001 compared to controls, with 109 out of 116 (95%) roots remaining symptom-free in plants of pILTAB718-001. Data from greenhouse and field studies demonstrate proof of concept for control of CBSD by RNAi technology.

General Poster

Escaping the trade-off between yield and Septoria tritici blotch

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Septoria tritici blotch is the most important foliar fungal disease of wheat in the UK. With insensitivity to fungicides increasing, breeding for *Septoria* resistance is becoming a key concern for the farming industry. There is a trade-off, however, between disease resistance and yield. Snape *et al.* (2007) identified a QTL on chromosome 6A for increased yield and 1000 grain weight. The same region of the genome was found to be associated with disease susceptibility in an association genetics study. The possibility of a trade-off between increased yield and greater susceptibility to disease is being studied using near-isogenic lines (NILs) for this region. We are investigating whether this trade-off is due to linkage between yield genes and susceptibility genes in this region, or if the effect is pleiotropic. The NILs do not differ significantly in seedling resistance to Septoria tritici blotch, nor in a number of morphological traits but they do differ in their rate of senescence. This may affect the amount of *Septoria* on upper leaves if a shorter lower leaf lifetime reduces splash-borne dispersal of spores up the plant. Thus the yield and *Septoria* trade-off may be explained by high-yielding ideotypes favouring pathogen movement and reducing disease escape.

General Poster

Guardee evolution: trade-off between improved defence activation and avoidance of auto-immune responses?

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Host–pathogen coevolutionary dynamics can be dominated by balancing selection, leading to the maintenance of allelic diversity at genes involved in interactions between hosts and pathogens. In plants, balancing selection is a major force affecting *R* genes, which are directly involved in pathogen recognition. However, little is known about the evolutionary mechanisms shaping the targets of pathogen effectors in the host. The 'Guard-Hypothesis' proposes that modification of those targets ('guardees') by pathogen effectors is sensed by R proteins ('guards') triggering the defence response. Due to its connectivity, the guardee is expected to be subject to contrasting evolutionary forces. We show that the evolution of the guardee *RCR3* is characterized by gene duplication, gene conversion and balancing selection in the wild tomato species *Solanum peruvianum*. Investigating the functional characteristics of 54 natural variants through *in vitro* and *in planta* assays, we found differences in the interaction of the guardee with fungal and oomycete effectors, and substantial variation in the strength of the defence response. This variation is maintained by balancing selection at each copy of the *RCR3* gene. Our analyses pinpoint amino acid polymorphisms with key functional consequences for the coevolution between the guardee (*RCR3*) and its guard (*Cf-2*). We conclude that in addition to coevolution at the 'guardee–effector' interface for pathogen recognition, natural selection acts on the 'guard–guardee' interface. Guardee evolution may be governed by a counterbalance between activation in the presence and prevention of auto-immune responses in the absence of the pathogen.

PH Gregory Prize Speaker **J Colhoun Poster**

Role of plant RNA-silencing pathways in recovery from viral disease symptoms

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Virus-infected plants that initially show disease symptoms may start to develop new symptom-free leaves, a phenomenon known as recovery. Studies in *Nicotiana benthamiana* have indirectly linked recovery to anti-viral RNA silencing, but the proteins involved remain unknown. Here we present a system to study recovery from RNA viral disease in *Arabidopsis thaliana.* This system allows us to investigate the role of specific RNA-silencing pathways in onset and maintenance of recovery. Upon infection with the tobamovirus *Oilseed rape mosaic virus* (ORMV), *Arabidopsis* plants develop severe symptoms, but at about 25 dpi non-symptomatic leaves appear. Recovered leaves still contain virus but viral silencing suppression activity is absent or only detected in the mid-rib. To identify pathways involved, we infected different silencing-deficient *Arabidopsis* mutants with ORMV. As anticipated, mutant plants impaired in 21 nt siRNA-mediated post-transcriptional gene silencing (PTGS) (*rdr6, dcl2, dcl4, ago1, hen1, sgs3*) showed delayed or no recovery from symptoms, while mutant plants with defects in miRNA pathways (*hyl1, dcl1*) recovered as wild type. Interestingly, mutants of 5'–3' exoribonuclease XRN4 (*xrn4-3*, *ein5*), a known endogenous RNA silencing suppressor, recovered faster than wild type. Together these observations emphasize the importance of PTGS not only in maintenance but also in the onset of recovery. Finally, we will present data indicating that proteins belonging to other silencing pathways are also involved in recovery.

PH Gregory Prize Speaker

Characterisation of Crinkler (CRN) effector proteins from *Phytophthora capsici* and their putative host targets

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The oomycete pathogen *Phytophthora capsici* is a pathogen of crops including pepper, tomato and cucumber. Upon infection, *P. capsic*i secretes a diverse array of proteins that modify host cell processes and enable infection (effectors). The Crinkler (CRN) gene family encodes a large and complex family of intracellular proteins. CRN proteins feature conserved N-termini and a highly conserved LFLAK motif that is required for translocation. Although CRN C-termini have been hypothesized to specify effector activity, and over 30 domains have been identified in the oomycetes, functions carried by C-termini remain largely unknown. We identified 85 putative full length CRNs that can be classified in conserved domains. We can confirm the genes by RT-PCR and sequencing. Micro-array data of a time series of *P. capsici* infection on tomato leaves shows differential expression patterns.

To elucidate the function conferred by CRN C-termini, we selected and cloned a diverse array of effector domains. Transient expression of GFP tagged C-termini shows that all CRNs localise to the nucleus. Interestingly, we see differential subnuclear localisation patterns for different CRNs, suggesting diverse functions in nuclear compartments. To further study effector function, (co-)immunoprecipitation experiments are performed. Here we will present the latest result emanating from these experiments. CRN effectors are evolutionary ancient. Insight into CRN targets will give us a better understanding of the mode of action of this abundant class and may aid towards enhancing disease resistance in general.

General Poster

Trading age for specific resistance: influence of plant senescence on the epidemiology of the fungus *Ramularia collo-cygni*

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Being hardly recognized until only 10 years ago the as necrotroph classified fungus *Ramularia collo-cygni* has become a major pathogen in barley production of temperate climates. Its epidemic shows some particularities which can explain why its presence in the crop has been overlooked for a long time. Typically epidemic starts with unspecific spotting leading to rapid loss of green leaf area and heavy sporulation on upper leaves. Unlike the epidemic of most necrotrophic fungi this phenomenon is decoupled from the general plant maturity moving upwards from in the lower canopy. Still it appears only late in the growing season, not until past flowering. The effect of plant age dominates differences in tolerance. Sporadic sporulation on senescent leaves and molecular detection from asymptomatic leaves early in the season give evidence of endophytic stages and a hemibiotrophic life style.

The present study uses real-time PCR to quantify fungal DNA in different plant parts throughout the growing season and compares them to the visually and microscopically assessed disease development. The influence of plant senescence is observed in field plots of the same spring barley variety differing in plant development due to different sowing dates. While DNA quantities generally correlate with the observed symptoms and sporulation on the leaves contradictive contents can appear in other parts of the plant.

The influence of senescence on epidemics will be discussed in respect to the conclusions on the life cycle of *Ramularia collo-cygni* and the consequences for the resistance breeding.

General Poster

Understanding the complex relationship between barley and the fungus *Ramularia collo-cygni*

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Ramularia collo-cygni is now one of the major economic fungal pathogens which attack barley (*Hordeum vulgare*) crops in temperate countries. Ramularia leaf spot (RLS) symptoms appear primarily on the upper leaves in the crop canopy post-flowering. However, DNA analysis has revealed much higher fungal levels in the symptomless lower leaves. This observation combined with spore capture data suggests seedborne infection may be the primary source of early *R. collo-cygni* infection in crops. Fungal movement and symptom expression are strongly influenced by environmental factors e.g. periods of sustained crop wetness and light interception. The asymptomatic growth of the fungus in the host plant, the lack of host response and the association with barley seed suggests that an endophytic or even mutualistic relationship may exist during the vegetative stage of crop growth. Symptom development in the crop post-flowering is related to the production of light activated anthraquinones by the fungus although the trigger for this production is not fully known. As symptoms develop in the host plant spore supporting bodies emerge from stomata and produce swan necked shaped conidiophores. The release of conidia has been shown to be related to periods of prolonged leaf surface wetness. A prediction scheme for RLS severity in a cropping season based on surface wetness at GS 31 has been devised and in addition the impact of RLS on yield has been established.

PH Gregory Prize Speaker **J Colhoun Poster**

Barley: the correlation between powdery mildew infection and leucine-derived hydroxy nitrile glucosides

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Cyanogenic glucosides are well-known defence compounds in plants. Barley produces five hydroxy nitrile glucosides (HNGs), which accumulate in the epidermis and account for 90% of the soluble carbohydrates in this tissue. Only one of them, Epiheterodendrin, is a cyanogenic glucoside, hence having the potential to release cyanide upon β-glucosidase degradation. Barley powdery mildew (Bgh) is an obligate biotrophic fungus specialised to infect and feed on barley epidermal cells. It is speculated that the fungus exploits the HNGs as a glucose and nitrogen source. The relationship between Bgh susceptibility and leaf cyanide potential is unclear. Cyanide is not liberated during powdery mildew infection, and no β-glucosidase able to cleave Epiheterodendrin is known in barley leaves. Epiheterodendrin is also known to stimulate fungal appressoria formation *in vitro*, suggesting that Bgh uses Epiheterodendrin in host recognition[1].

To investigate the proposed link between Bgh susceptibility and HNGs, we are currently measuring HNG levels +/– Bgh. Preliminary results indicate that after fungal infection HNG levels increase and the relative HNG distribution changes in susceptible barley leaves. Additionally, we found that HNGs are transported to the wax layer. The route of transport has not been elucidated. Apart from functioning as a structural barrier between the plant and the environment, the wax layer may be more dynamic taking direct, chemical action in defence. Also, the bioactive compounds encountered in the wax can, upon degradation, take part in plant-to-plant signalling and/or be used as fungal host recognition factors.

1. Nielsen *et al.,* 2002. *Plant Physiology* 129: 1066–75.

PH Gregory Prize Speaker **J Colhoun Poster**

The anticipation of danger: MAMP perception enhances *At*Pep-triggered oxidative burst

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The endogenous Arabidopsis peptides *At*Peps elicit an innate immune response reminiscent of PTI (PAMP-triggered immunity). Moreover, detection of various danger signals, including microbe-associated molecular patterns (MAMPs) like flg22 leads to elevated transcription of both, *At*Pep precursors (*PROPEPS*), and *At*Pep-receptors (*PEPRs*). Therefore, it has been hypothesized that *At*Peps are involved in enhancing PTI. Following this idea we analysed the relationship between MAMP- and *At*Pep-elicited signalling. We found that the perception of MAMPs enhanced a subsequent *At*Pep-triggered production of reactive oxygen species (ROS). Intriguingly, other components of *At*Pep-triggered immunity remained unchanged.

In contrast, treatment with MeJA promotes a general increase of subsequent *At*Pep-triggered responses. We positively correlated the intensities of generic *At*Pep-triggered responses with the abundance of the two *At*Pep-receptors by generating constitutively expressing PEPR1 and PEPR2 transgenic lines and by analyzing *pepr1* and *pepr2* mutants.

Further we show that enhanced as well as basal ROS production triggered by *At*Peps is absent in the *rbohD rbohF* double mutant. We present evidence that the enhancement of *At*Pep-triggered ROS is not based on changes in the ROS detoxification machinery and is independent of MAP kinase and Ca^{2+} signaling pathways.

Taken together these results indicate an additional level of regulation beside receptor abundance for the RbohD/F-dependent production of *At*Pep-elicited ROS, which is specifically operated by MAMP-triggered pathways.

General Poster

Molecular identification of four *Botrytis* species three of them associated with neck rot and blasting diseases of onion with special reference of two, *Aclada* and *Byssoidae*

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Botrytis aclada and other *Botrytis* spp. can cause neck rot, a storage disease and blasting diseases on onions. Twenty fungal *Botrytis* isolates were isolated from infected onion, strawberry and broad bean. The fungal isolates of causal pathogens obtained from different hosts were identified as *Botrytis* spp. based on morphological, microscopical and cultural characteristics of mycelia, conidiophores and conidiospores. Moreover for molecular identification primers BA2f and BA1r were used to amplify the specific region belonging to *Botrytis* spp. A PCR product with molecular size 413 bp was obtained with the examined *Botrytis*-infected plant tissues different hosts. The 413 bp DNA fragment obtained was subjected to DNA sequencing. Partial DNA sequences and phylogenetic analysis distinguished the isolates obtained into four groups: *Botrytis aclada* types AI and AII (*B. allii*), *B. byssoidea*, and *B. cinerea*. The major dominant species associated with onion neck rot and blasting was type AI (*B. aclada*). *Botrytis byssoidea* is investigated and recorded for the first time in Egypt on onion plants associated with seeds and bulb neck rot. Furthermore, the specificity of the primer was examined on another fungal genera and the results revealed that only the *Botrytis* spp. gave a specific band. No amplified products were obtained with the other tested genera and species isolated from onion or healthy tissues of onion bulbs.

General Poster

Pectobacterium atrosepticum: pros and cons on non-host crop

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The plant microbiome is colonised by a large variety of benign microorganisms, which roles and functions are mostly unknown. Characterisation of the barley bacteriome of field-grown leaves was initially undertaken using culturable and molecular techniques. T-RFLP profiles demonstrated a significantly higher diversity than results from culturable isolation.

One of the molecularly detected bacteria, *Pectobacterium atrosepticum* (*Pba*), is a well-known potato pathogen, causing black leg on stem and soft rot on tubers. The presence of this bacterium was correlated in the field with significant variation in disease symptoms on non-host crop. *Pba* could actively colonise barley leaves under controlled conditions. *In vitro* assay showed biological control activity against *Rhynchosporium commune* (*Rc*), causal agent of leaf blotch on barley, whereas a significant increase of powdery mildew symptoms, caused by *Blumeria graminis* f. sp. *hordei* (*Bgh*), was observed on barley leaves. The biocontrol mechanism against *Rc* could involve the type IV secretion system of the bacterium, under quorum sensing control. The mechanism involved in hyper-susceptibility against *Bgh* remains unknown.

As a conclusion non-pathogenic microorganisms can have significant positive and negative effects on disease development. Studying the effects of current crop protection practices on these microorganisms could be very valuable for the development of future integrated disease control methods.

Invited Speaker

Loss of susceptibility: a costly way to resist powdery mildew?

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Plant immunity to adapted microbial pathogens is a result of pathogen recognition and subsequent pathogen-induced defence. Vice versa, susceptibility to diseases involves molecular interaction of microbial effectors and host targets. In most cases, pathogen effectors prevent recognition or suppress host defence. However, successful pathogenesis of fungal biotrophs requires also host structural and metabolic components, which fulfil the demands of pathogen accommodation. This explains why, besides negative regulators of defence, metabolic host enzymes or regulators of the host cytoskeleton are required for susceptibility. Among them are plant RAC/ROP GTPases such as barley RACB. The physiological function of powdery mildew susceptibility factor RACB is pivotal for normal development of root hairs, such that loss of RACB is accompanied by severe trade-off. Molecular dissection of RACB signalling revealed a role of RACB-interacting proteins in the organization of cortical microtubules. RACB-interacting MICROTUBULE-ASSOCIATED GAP1 and ROP BINDING KINASE1 appear to antagonize RACB and might be useful in molecular breeding or engineering of powdery mildew resistance. Hence, understanding of susceptibility might pave the way for new strategies in genetic plant protection.

Invited Speaker

Stomatal lock-up contributes to the cost of resistance to foliar fungal pathogens

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Pathogen attack can reduce yield in plants with effective major gene resistance. In barley genotypes Pallas (susceptible) and P01 (with *Mla1*) attacked by *Blumeria graminis* f. sp. *hordei* (*Bgh*) stomatal behaviour was disrupted. In *Bgh* infected Pallas, stomata exhibited a "lazy" phenotype where only opening in the light was restricted but in P01, stomata were "locked" open in both dark and light and failed to respond to drought or the exogenous application of ABA (1). Pallas genotypes with *Mla1*, *Mla3*, or *MlLa R* genes conferred distinctive spatiotemporal patterns of HR following challenge with *Bgh* and which correlated between the speed of cell death and stomatal locking. Locking occurred at inoculation rates of ~ 10 conidia/mm^2 and in response to the non-host pathogen *B. graminis* f. sp. *avenae* (*Bga*) (2). Examining rust pathogens, in barley genotypes exhibiting major gene resistance against brown rust (*Puccinia hordei*), stomata locked shut. This was also the case in a wheat cultivar expressing *R* gene *Lr24* following inoculation with *Puccina triticina* (3). NO plays a role in bacterial effects on stomata but analysis of transgenic lines of barley cultivar Golden Promise over-expressing a non-symbiotic form of haemoglobin (catalysing the oxidation of NO; NO + $O_2 \rightarrow NO_3$), suggested a negligible role for NO in *Bga*-induced lock-open. Metabolomic and photosynthetic analysis suggests that stomatal locking may be symptomatic of wider-ranging effects on primary metabolism which are likely to contribute to a cost of resistance.

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General Poster

Uzu: an alternative to *Rht*

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Semi-dwarfing genes played a vital role in the Green Revolution period of crop improvement. They confer a favourable shorter stem phenotype leading to reduced lodging and therefore increased yield. They have also been shown to have a pleiotropic effect on plant immunity. A resistance trade-off between biotrophic and nectrotrophic fungi is evident in semi-dwarf cultivars possessing gibberellin insensitive alleles. *Rht* (*Reduced height*) in wheat and *Sln1* (*Slender 1*) in barley confer susceptibility to biotrophic stages of fungal infection, but resistance to nectrotrophic stages. Identification of semi-dwarfing genes in other phytohormone pathways which do not produce a pleiotropic effect on disease resistance is therefore important when aiming to further improve crop varieties. Barley near-isogenic lines showing a semi-dwarf phenotype caused by the '*uzu*' mutation in the *BRI1* (*brassinsteroid insensitive 1*) gene was used to determine if a similar resistance trade-off occurred in the brassinosteroid pathway. In response to infection with biotrophic, hemibiotrophic and nectrotrophic fungi, the *uzu* mutation did not have a significant effect on disease resistance when compared to the wild-type barley lines. However, *uzu* lines were significantly more resistant to stem base infection by the hemibiotroph *Fusarium culmorum* and also to the bleaching effects caused by the mycotoxin deoxynivalenol (DON). Results suggest that whilst the barley semi-dwarf brassinosteroid insensitive *uzu* mutation does not seem to produce a resistance trade-off similar to that seen with the barley *Sln1* gibberellic acid insensitive alleles, it may play a role in specific resistance to *Fusarium* and DON.

General Poster

Developing understanding of *Ramularia collo-cygni* at the sequence level

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The fungus *Ramularia collo-cygni* is the major biotic agent involved in Ramularia leaf spot (RLS). It was first identified as a pathogen of spring barley in Scotland in 1998 and since then has increased in its importance throughout the whole of the UK. Results from testing of the Rothamsted Hoosfield spring barley archive using quantitative real-time PCR indicated a significant increase in pathogen levels since the 1990s. *R. collo-cygni* is currently classified as a member of the *Mycosphaerella* genera and sequence data derived at SRUC suggests a genetic similarity between *R. collo-cygni, Mycosphaerella graminicola* and *M. fijiensis*. These sequences focus primarily on the genes associated with the target sites for fungicides, such as b-tubulin, cytochrome b, succinate dehydrogenase and eburicol 14a-demethylase (*CYP51*) genes.

This poster will highlight previous sequence work and newly obtained genome and transcriptomic data generated by the combined approach of Illumina/Solexa and Roche/454 sequencing. This combined approach has enabled the assembly of a complete genome sequence. The finished assembled genome of *R. collo-cygni* is 30.2 Mb and is currently to be found in 355 contigs. The complete annotation of this genome is currently underway using the FGENESH 2.6 software to generate first consensus gene calls. This approach will allow for comparative genome analysis in related genomes which will help to address the biology of *R. collo-cygni* in areas such as population genetics, fungicide resistance and pathogenicity. These advances should assist in the development of environmentally sound strategies to control this important disease of barley production systems.

Invited Speaker

Trade-offs and benefits of hormonal modulation of plant immunity

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In nature, plants live in complex environments in which they are attacked by a multitude of pathogens and pests. In agriculture this leads to tremendous annual crop losses, representing a total value of over €450 billion worldwide. Beneficial associations between plants and mutualistic microbes are abundant in nature as well, improving plant growth or aiding plants to overcome stress. In the past years, we investigated the complexity of the natural plant immune system and discovered that plant defence signalling networks finely balance plant responses to beneficial microbes, pathogens, and insects to maximize both profitable and protective functions. Signalling networks that are recruited in response to parasitic and beneficial organisms can overlap, indicating that the regulation of the plant's adaptive response to its biotic environment is finely balanced between protection against aggressors and acquisition of benefits. Plant hormones play pivotal roles in the regulation of the defence signalling network. Their signalling pathways interact, providing the plant with a powerful capacity to tailor its immune response to the attacker encountered. As plants co-evolved with an enormous variety of alien organisms, they harbour a fantastic reservoir of natural adaptive mechanisms. We study natural plant defence signalling networks and focus on the question: how are plants capable of integrating microbial- and insect-induced signals into defences that are specifically directed against the attacker? And how do beneficial microbes help the plant to protect itself? By placing molecular mechanisms into an evolutionary and ecological context we try to make sense out of signalling during plant defence.

Invited Speaker

Breeding Wheat Varieties Fit to Fight Disease

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Breeding for disease resistance in wheat has a long and by and large successful history. In western Europe the development of highly effective systemic fungicides and a continued breeding emphasis on selection for adequate disease resistance has led to remarkable productivity gains in wheat production. The challenge to maintain and increase genetic yield gain in new varieties requires that any interaction between disease resistance genes and plant productivity is well understood. Examples of disease resistances that have been detrimental to yield performance have been documented and often include genetic elements introduced from exotic sources and wild wheat relatives. Pleiotropic and epistatic effects have been cited and may be relevant. However parental founder effects, breeding inefficiencies and close genetic linkages to deficiencies in the physiology of yield are likely to be at least as important. Conversely some resistance genes appear to have a neutral effect on yield in the absence of disease, although systematic evaluation of such genes is lacking.

To ensure that wheat breeders producing commercial varieties can continue to select higher yielding material whilst maintaining and enhancing disease resistance, research into resistance genes and their efficient selection is essential. Objectives should include:

- Validation of fitness effects associated with important resistance genes
- Development of molecular markers to trace durable sources of resistance
- Identification of new derivatives of resistance genes
- Resistance to intransigent problems such as take-all and BYDV

General Poster

Cross-talk between 'nutritional stress' and plant defence signalling

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It is understood that plant defences may be primed or altered by exposure to abiotic factors such as temperature and water availability acting prior to, or concurrent with, biotic stress. These cross-talk effects often occur due to shared signalling components such as ROS, kinase cascades and plant hormones. I am currently investigating the possibility that nutritional stress may be capable of influencing plant defences *via* such cross-talk. The nutrients under consideration are zinc and nitrogen. Zinc is an important trace element which can interact with many proteins. It can also be an indirect inducer of ROS. Mildly stressful high zinc concentrations (200 µL) have be found to promote the growth of *Pseudomonas syringae* pv. *tomato* DC3000 in *Arabidopsis thaliana*, and data indicate that plants grown with this zinc concentration have reduced signalling through the calcium-dependent protein kinase CPK5 and through H_2O_2, possibly due to an effect of zinc or zinc stress upon the NADPH oxidase, RBOHD. Nitrogen stress produces a more complex picture, due to the importance of nutritional effects for bacterial pathogens. Nevertheless, comparison of *Arabidopsis* provided with high concentrations of ammonium nitrate (20 mM) with plants provided with the same nitrogen concentration composed of 3:1 nitrate:ammonium shows that ammonium has a negative effect upon *P. syringae in planta* growth, and is capable of altering ROS signalling, as well as MAPK4 activity and the expression of the defence marker gene, *PR1*.

General Poster

Developing site-specific advisories for agricultural producers

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Weather INnovations Incorporated (WIN) provides information and decision support tools that improve the sustainability, consistency and profitability of agricultural production. WIN specialises in providing turnkey weather-based monitoring and modelling solutions for agribusinesses, producer organisations, government agencies, researchers and others. WIN makes models easy to use at the farm level by providing a connection to innovative research with site-specific applications. Client requests encourage a multi-disciplined approach to providing custom solutions. WIN produces programs for disease, insects, frost mitigation, soil moisture, harvest timing and insurance; and also provides solutions for research, marketing and consulting requirements. The poster provides background information on WIN and the range of activities the company is involved in and focuses on a number of advisory solutions specific to the arable or horticultural industry both in North America and throughout Europe.

Invited Speaker

The hard life of *Phytophthora infestans*: when trade-offs shape evolution in a biotrophic plant pathogen

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Their strict dependency upon living host tissue for multiplication and survival makes biotrophic pathogens particularly exposed to evolutionary trade-offs. Such trade-offs can occur both between life history traits directly involved in pathogenicity (e.g. fitness costs to unnecessary virulence factors), or between traits involved in either pathogenicity (within season fitness) or survival (between-season fitness). Both types of trade-offs should result in the limitation of maximum pathogenicity, and shape the invasive potential of pathogen genotypes. While their evolutionary consequences are subject to strong theoretical developments, including recent work taking seasonality into account (e.g. periodic host absence and/or periodic sexual/asexual reproduction), experimental evidence to confirm theoretical predictions are still scarce. This paper will therefore attempt to illustrate the different kinds of trade-offs that can be measured, and their likely consequences, taking the biotrophic pathogen *Phytophthora infestans* (cause of potato and tomato late blight) as a case study.

Invited Speaker

Uncoupling of defence signalling in the metal hyperaccumulator *Noccaea caerulescens*

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The metal hyperaccumulator plant *Noccaea caerulescens* is protected from disease by the accumulation of toxic concentrations of metals such as zinc, nickel and cadmium in its aerial tissues. Since these metals can lead to the production of damaging reactive oxygen species (ROS), metal hyperaccumulator plants have developed highly effective ROS tolerance mechanisms. We have observed that accumulation of zinc can cause increased superoxide production in *N. caerulescens*, but that inoculation with a bacterial pathogen does not elicit the defensive ROS burst normally associated with plant responses to infection. Downstream defences dependent upon signalling through ROS are also modified or absent in *N. caerulescens*. Nevertheless, the plant retains the ability to produce the defence signal salicylic acid in response to infection. Collectively, our observations suggest that metal hyperaccumulation is incompatible with defence signalling through ROS. We propose an evolutionary scenario that explains how fundamental changes in defence signalling in *N. caerulescens* may have accompanied the evolution of metal hyperaccumulation as a defensive trait.

General Poster

Phenotypic changes in oak seedlings infected by powdery mildew: host tolerance response or host manipulation by the parasite?

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Plant parasites negatively affect their host fitness by deriving their nutrition from their host. Infection also often affects the physiology of the host leading to changes in morphology, timing of development or fecundity. Plant pathologists have paid much less attention to these life-history changes which could be seen either as tolerance response of the host or as manipulation by the parasite to enhance its transmission, than to resistance mechanisms preventing infection, thus yield loss. We studied the phenotypic changes induced by the oak powdery mildew on its host, *Quercus robur*, in order to assess the effect of infection on host growth pattern. Fifteen half-sib families of oak (2595 individuals) were exposed to three different levels of powdery mildew: low (with fungicides), medium (natural infection) and high (natural infection supplemented by inoculations). Fine monitoring of host growth, phenology and leaf infection were performed over three years. As expected, increasing infection resulted in increasing growth losses in seedlings. More surprisingly, it also had a dramatic effect on seedling phenotypes by causing an accelerated shoot flushing both between and within years. This increased polycyclism provided benefits for both host and parasite: partial compensation of growth losses and extension of the availability of receptive tissues along the season, respectively. Nevertheless, increasing the number of flushes in a season may expose seedlings to higher damage by winter frost. Altogether, these observations are suggestive of both host tolerance and parasite manipulation responses in the “complex phenotype” resulting from the interplay of host and parasite genes.

General Poster

Evolution of recognition specificity in a cluster of soybean disease resistance genes

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Effector triggered immunity in plants involves highly specific recognition events in which plant resistance (R) proteins either detect pathogen effector proteins directly, or alternatively, the modifications of effector targets. Detection of modified effector targets is thought to provide more durable resistance as effector recognition and virulence activity are linked. How R proteins detect effector-induced modification of host proteins, and how new specificities evolve, remain important questions. We are addressing these questions by studying two closely linked soybean genes, *Rpg1b* and *Rpg1r*, which mediate detection of the *Pseudomonas syringae* effector proteins, AvrB and AvrRpm1, respectively. We have previously cloned *Rpg1b,* and have now identified *Rpg1r,* both of which are CC-NB-LRR type genes. The *R* genes share a close evolutionary relationship, with *Rpg1b* containing a gene conversion event that combined an *Rpg1r*-like NB-ARC with CC and LRR domains from a more distantly related NB-LRR gene. Interestingly, by mapping polymorphisms between the *Rpg1b/Rpg1r* sequences onto models of the R proteins' tertiary structures we have identified highly polymorphic surfaces within both the CC and LRR domains. This raises the possibility that both these regions have a role in determining recognition specificity for these genes. As in *Arabidopsis*, the *P. syringae* protease AvrRpt2 partially blocks recognition of both AvrB and AvrRpm1 in soybean. Furthermore, preliminary results indicate that the CC domains from both Rpg1 proteins interact with at least one soybean RIN4 homologue in yeast. These observations suggest that while Rpg1b and Rpg1r can distinguish between AvrB and AvrRpm1, they may use related recognition strategies.

Invited Speaker

Fitness costs associated with horizontal acquisition of host-specific toxins

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Population genetic and phylogenetic studies indicated that *Phaeosphaeria nodorum* (aka *Stagonospora nodorum*) is a member of a species complex that shares its center of origin with wheat. We investigated the evolutionary history of three necrotrophic effectors (NEs) produced by *P. nodorum*. We screened over 1000 global strains across seven major regions, including North America, Europe, Iran, Central Asia, China, South Africa and Australia for the presence/absence of each effector and assigned each individual to a multi-effector genotype. Diversity at each NE locus was determined by sequencing ~200 individuals. We found significant differences in effector frequency among populations and regions. We hypothesize that these differences reflect the presence/absence of the corresponding susceptibility gene in wheat cultivars. The population with the highest sequence diversity was different for each effector locus and never coincided with Fertile Crescent populations having the highest diversity at neutral loci. Coalescent analyses indicated that *P. nodorum* did not inherit NEs from a common ancestor. Interspecific hybridization likely occurred between *P. nodorum* and its sister species, *P. avenaria tritici 1*, leading to a second horizontal transfer of all three NEs from *P. nodorum* to *Pat1*. We hypothesize that the horizontal acquisition of NEs was an important innovation that enabled the emergence of *P. nodorum* and *Pat1* as globally important wheat pathogens. But there was no evidence for a fitness cost associated with the acquisition of these NEs.

Invited Speaker

Costs and coevolutionary dynamics: insights from bacteria–virus interactions

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Bacteria and lytic viruses (phages) undergo extensive real-time antagonistic coevolution in the laboratory. The dynamics of coevolution during early stages follow an arms race dynamic (ARD), with both bacteria and viruses evolving increasing resistance and infectivity ranges through time. However, both resistance and infectivity ranges are associated with growth rate costs, and theory suggests that the range evolution may then be constrained. Consistent with this view, the ARD switches to a fluctuating selection dynamic (FSD) as coevolution progresses. Moreover, in soil, where costs of resistance ranges are greatly elevated, coevolution primarily follows FSD, with ARD only observed when bacteria–phage encounter rates are high as a result of extensive population mixing. Existing models of coevolution do not fully capture these environment-dependent coevolutionary dynamics, in part because the genetic bases of bacteria–virus specificity are different to that assumed in existing coevolutionary models. Specifically, virus infectivity is consistent with a multilocus gene-for-gene type interaction, with increased infectivity range associated with increased number of "infectivity alleles", while bacteria resistance range does not correlate with the number of "resistance alleles". Given the relative simplicity of bacteria–phage interactions, it seems likely that plant–pathogen systems will undergo even more complex coevolutionary dynamics.

J Colhoun Poster

Allele mining for *Resistance to Phytophthora infestans (Rpi) vnt1*-like genes in *Solanum okadae* accessions

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The biggest threat to potato production worldwide is late blight disease caused by the oomycete pathogen *Phytophthora infestans*. Resistances found in some wild Solanaceae species provide environmentally benign means of restricting late blight infections. The Commonwealth Potato Collection (CPC) is hosted at the JHI and contains more than 1800 accessions from 80 different wild potato species. This collection represents a unique resource for identifying and cloning novel resistances.

The resistance gene *Rpi-vnt1* from the wild potato species *Solanum venturii* recognises the cognate *P. infestans* effector *Avr-vnt1* and provides broad-spectrum resistance against various late blight isolates. Three functionally equivalent alleles of *Rpi-vnt1 (Rpi-vnt1.1, Rpi-vnt1.2* and *Rpi-vnt1.3)* have been identified and share more than 98% sequence identity.

Some late blight resistant *S. okadae* accessions recognize *Avr-vnt1* following transient expression via *Agrobacterium tumefaciens* and yield a hypersensitive-like response. The aim of this study is to assess the presence of functional *Rpi-vnt1*-like genes within these CPC accessions. A two-pronged approach is used to assess functionality: (a) cloning and sequencing of *Rpi-vnt1*-like genes; and (b) *Avr-vnt1* recognition studies following transient co-expression of candidate *Rpi-vnt1*-like genes in *Nicotiana benthamiana*. So far, functional *Rpi-vnt1.1* genes have been identified in two different accessions of *S. okadae*. Moreover, 11 different *Rpi-vnt1* variances with unknown functions have been amplified.

J Colhoun Poster

The impact of elevated CO_2 on crop productivity and disease resistance

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Wheat productivity is highly dependent on environmental factors and the presence of pathogens. Evidence to date suggests that the higher level of carbon dioxide (CO_2) predicted in future climate estimations will positively influence disease development. The aim of this study is to determine the effect of plant and pathogen adaptation to high CO_2 on the severity of Fusarium head blight (FHB) disease. The disease resistant/ susceptible cultivars CM82036/Remus were grown in walk-in growth chambers adapted to normal (390 ppm) and high (780 ppm) CO_2 concentrations. The pathogen *Fusarium graminearum* GZ3639 strain was grown and subcultured over 20 generations under normal and high CO_2 concentrations. The adapted pathogen and plants were used for FHB experiments. Plants were grown under normal or high CO_2 and were inoculated with spores from either ambient or high CO_2-adapted pathogen. Preliminary results indicate that pathogen adaptation to high CO_2 leads to higher disease levels and that it compromises the FHB resistance innate to cultivar CM82036.

Invited Speaker

Costs in plant–parasite coevolution: bridging the gap between ecology and population genetics

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A recent goal in host–parasite studies is to reveal genes underlying coevolution and changes of alleles for resistance or virulence in the populations over time, using genomic data. Three types of coevolutionary dynamics are predicted: (1) the so called “trench warfare” dynamics with cycles of host and parasite allele frequencies, (2) a stable maintenance of alleles in host and parasite populations at fixed frequencies, and (3) the “arms race“ dynamics with recurrent fixation of alleles in hosts and parasites. These dynamics are expected to occur over different time scales and to generate different polymorphism signatures at the genomic level. We study by simulations a gene-for-gene model of finite host and parasite population sizes with genetic drift, including fitness costs of resistance and virulence and costs of disease. Our aim is to quantify differences in the speed of evolution between these dynamics and to predict observable genomic signatures. We separate the effect of genetic drift and mutation on polymorphism maintenance for the different dynamics, and show that allele frequencies changes are not necessarily faster under the trench warfare model than under the arms race. In addition, fixation of resistance alleles in the host population could only occur in small populations. We then use a coalescent simulator to generate observable genomic signatures for each model. We show how to distinguish statistically between different coevolutionary scenarios and the neutral genomic background based on the observable polymorphism data. These results suggest new methods of analysis of hosts and parasite genomic data from population samples.

Invited Speaker

The genetic architecture of RNA virus fitness

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To forecast emergence we must identify the factors determining the distribution of genetic variants within the reservoir host as well as across potential new ones. To this end, it is crucial (*i*) what is the distribution of mutational fitness effects (DMFE) on the reservoir, (*ii*) how it changes on different hosts (*G´E*), (*iii*) the way in which multiple mutations interact (*G´G*) in the reservoir, and (*iv*) how different hosts may affect the form of epistasis (*G´G´E*).

We characterized the DMFE for *Tobacco etch potyvirus* (TEV) genotypes carrying single substitutions across a set of hosts. We found a significant *G´E* component, sustained by differences in genetic variance for fitness and the pleiotropic effect of mutations among hosts. DMFEs were markedly different between natural and non-natural hosts and the fraction of possible beneficial mutations was larger in the latter.

Second, we generated random pairs of mutations and observed significant epistasis for many, including both positive and negative. A large fraction consisted of cases where the sign of the effect of mutations at two loci are dependent on each other.

Finally, we provide first evidence that the distribution of epistatic interactions significantly varied among hosts, and that average epistasis was stronger in the primary host but became more multiplicative as host's genetic relatedness decreased.

The existence of significant *G´E*, *G´G* and *G´G´E* imply that no precise predictions on fitness effect of individual mutations can be made since it will depend on the genetic background but also in the host wherein the virus replicates.

J Colhoun Poster

Phytophthora infestans effector Avr2 and the brassinosteroid pathway in potato

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Phytophthora infestans is the causal agent of late blight; the most devastating disease of potato crops globally. The pathogen secretes effector proteins into plant cells during infection, capable of modifying host processes to support the progression of disease. One such effector protein, PiAVR2, has been recently shown to interact with a family of Ser/Thr phosphatases in the plant, implicated in positive regulation of the brassinosteroid signal transduction pathway. This hormone signalling pathway is predominantly associated with aspects of plant growth and development, with links to both abiotic and biotic stress now coming to the fore. Recognition of the effector by the corresponding resistance protein StR2 requires the presence of BSL family members, indicating an indirect interaction between effector and resistance protein. On-going work aims to further characterise this indirect interaction by determining whether BSL function is required for recognition of PiAvr2, whether BSL function is essential for pathogen virulence, and the impact of the effector on the brassinosteroid pathway as a whole.

J Colhoun Poster

Insights into the recent emergence of powdery mildew on its 'new' host triticale: from origin to disease control

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New diseases of humans, animals and plants emerge regularly. Pathogenic fungi in particular have been responsible for highly destructive emerging diseases in plants that negatively influence agriculture worldwide. This study focuses on the recent emergence of powdery mildew (*Blumeria graminis*) on triticale, the artificial intergeneric hybrid between wheat and rye. This emergence is probably triggered by a host range expansion of the wheat powdery mildew. In a first part, we tried to gain more precise information on the evolutionary processes that led to this host range expansion. Results reveal a genetic structure in *B. graminis* with population differentiation according to geography and host specificity. In addition, evidence is brought forward demonstrating that the host range expansion of wheat isolates to the new host triticale occurred recently and multiple times at different locations in Europe. In a second part, we investigated the presence of powdery mildew resistance in current commercial triticale cultivars, including its cellular basis of resistance. Using molecular markers, the presence of race-specific resistance genes was identified in certain triticale cultivars. Additionally, cultivars highly resistant at the adult-plant growth stages were identified. We also provide evidence that the formation of non-penetrated papillae is predominant in triticale resistance to powdery mildew, while hypersensitive response acts as a second line of defence, to cut the fungus off from nutrients, when penetration resistance failed. Altogether, the results presented in this study offer valuable information in devising strategies for durable powdery mildew resistance breeding in triticale and other cereals.

Invited Speaker

How oomycete pathogens of Arabidopsis cause or fail to cause disease

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Plant disease resistance mechanisms are initiated by surface receptors and cytoplasmic receptors that respectively recognize conserved or variable pathogen components. To suppress defence, pathogens deliver effector molecules into host cells. Understanding these effectors is important to identify new probes to host defence mechanisms and develop durable resistance strategies. Although the effector complements of bacteria are becoming well defined, and the mechanisms of many bacterial effectors are quite well understood, the effectors of the fungal and oomycete pathogens that cause the most serious crop losses are still poorly characterized.

As a model system, we work with the downy mildew pathogen *Hyaloperonospora arabidopsidis (Hpa)* and two other oomycete pathogens, *Albugo laibachii and A candida*. We used Illumina paired read sequencing to assemble sequences of multiple races of *Albugo laibachii*, a pathogen that is particularly effective at shutting down host defence, and also of multiple *A candida* races. We are using association genomics to correlate genetic variation in the secretome of *Albugo laibachii* with virulence or avirulence on specific Arabidopsis accessions. In addition, we are using the MAGIC inbred lines of Kover and Mott, to reveal transgressive segregation for susceptibility to *Brassica*-infecting *A. candida* strains, in order to identify genes for non-host resistance. An update on recent progress will be presented. Finally, we are investigating genetic exchange between different pathotypes of Albugo candida, and the possible role of introgression in pathogen evolution.

Invited Speaker

Trade-offs: the need for compromise in breeding for disease resistance in wheat and barley

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The majority of current wheat varieties carry either the *Rht-B1b* (*Rht1*) or *Rht-D1b* (*Rht2*) alleles of the so-called 'Green Revolution' dwarfing genes. These gain-of-function (GoF) alleles encode mutant forms of DELLA proteins that are less responsive to the effects of gibberellic acid (GA) and result in reduced crop height. The semi-dwarf stature is highly desirable in modern agriculture as it permits the application of high levels of nitrogen fertiliser to increase yields without the risk of crops falling over, lodging. DELLA proteins have been implicated in the response to biotic stress in the model plant, *Arabidopsis thaliana*. Using defined wheat *Rht* near-isogenic lines and barley *Sln1* GoF and loss-of-function (LoF) lines, the role of DELLA in response to biotic stress was investigated in pathosystems representing contrasting trophic styles (biotrophic, hemibiotrophic, and necrotrophic). In general, GoF mutant alleles in wheat and barley were shown to confer a resistance trade-off with increased susceptibility to biotrophic and hemi-biotrophic pathogens and increased resistance to necrotrophic pathogens whilst the converse was conferred by a LoF mutant allele. However, for resistance to Fusarium head blight the situation was more complex and it appears that a susceptibility factor has also been introgressed into many varieties through linkage to *Rht-D1b* (*Rht2*). Similar to Arabidopsis, a resistance trade-off to pathogens with contrasting pathogenic lifestyles has been identified in monocotyledonous cereal species. Thus both pleiotropy and linkage effects associated with the GA-insensitive DELLA dwarfing genes impact on disease resistance. A better understanding of the nature and magnitude of these effects under different conditions is required to rationalise their deployment in wheat varieties. The use of alternative semi-dwarfing genes may be appropriate to provide the desired crop architecture without compromising disease resistance.

J Colhoun Poster

The molecular characterisation of two gain-of-function *R3a** variants

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The potato *R3a* gene, a member of the CC-NB-LRR type resistance gene family, recognises the essential *Phytophthora infestan*s effector, *Avr3a_KI*. However, the closely related virulent allele, *avr3a_EM*, which is homozygous in more than 70% of wild *P. infestans* isolates, evades this recognition. Gain-of-function variants of *R3a* (*R3a**) have been engineered by an iterative process of random mutagenesis and shuffling of the leucine rich repeat (LRR)-encoding region of *R3a* which is associated with *Avr3a* recognition. Functional *Agrobacterium tumefaciens* transient assays (ATTAs) were carried out with the two best-performing *R3a** variants in the model Solanaceae *Nicotiana benthamiana*. Results comparing the two shuffled variants to wild-type *R3a*, showed a gain-of-recognition of the effector *avr3a_EM* as well as enhanced disease resistance towards *P. infestans* isolates, including the *avr3a_EM* homozygote 88069 tdT.

Recognition of Avr3a_KI by the wild-type R3a protein occurs in the host cytoplasm and R3a is subsequently re-localised to fast moving vesicles of different sizes. Co-localisation studies have identified these vesicles as pre-vacuolar compartments (PVCs). This re-localisation does not occur in the presence of avr3a_EM. However, confocal microscopy has revealed that the two R3a* variants are re-localised to PVCs upon co-infiltration with both forms of Avr3a, indicating a shared mode-of-recognition between wt R3a and the two R3a* variants. It is hoped that when a shuffled *R3a** gene is deployed together with other *R* genes in potato, it will confer more durable resistance to late blight disease.

J Colhoun Poster

Effects of host resistance on maturation of *Leptosphaeria maculans* and *L. biglobosa* (cause of phoma stem canker) in *Brassica napus* (oilseed rape)

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Phoma stem canker is an important disease in most countries growing oilseed rape. The sexual spores of the pathogens (*Leptosphaeria maculans* and *L. biglobosa*) produced in pseudothecia on infected winter oilseed rape stubble in autumn are the most important inoculum for infection of newly emerged crops. We investigated effects of cultivar resistance and environmental conditions (precipitation and temperature) on maturation of pseudothecia on stem debris. Stems of nine winter oilseed rape cultivars with different combinations of resistance (*R*) genes and quantitative resistance (QR), including a susceptible cultivar Drakkar with no known resistance, were collected after harvest in 2011 and 2012 from Rothamsted. They were then incubated under natural conditions at the Bayfordbury field station, University of Hertfordshire. The results indicate that pseudothecial maturation of the susceptible cultivar Drakkar and cultivars Adriana (*Rlm 4* + QR), ES-Astrid (QR) and Excel (*Rlm 7*) differed between autumn 2011 and 2012. There were differences between summer 2011 and 2012 in severity of phoma stem canker in the field experiment at Rothamsted, which is probably a reflection of the very low rainfall in September 2011. Previous work has shown that the rate of pseudothecial development is dependent on rainfall. In 2011, there were few differences between cultivars but maturity was delayed. However in 2012, pseudothecia matured much earlier and faster on Drakkar than on the other cultivars ($P < 0.05$). This has implications for the subsequent severity of stem canker. The impact of cultivar resistance on the maturation of pseudothecia and also the possibility that *L. maculans* retards the development of pseudothecia from *L. biglobosa* need further investigation.

Invited Speaker

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Genome evolution in filamentous plant pathogens: the bigger the better?

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Many species of fungi and oomycetes are plant pathogens of great economic importance. To date the genomes of more than 30 of these filamentous plant pathogens have been sequenced, revealing remarkable diversity in genome size and architecture. Whereas the genomes of many parasites and bacterial symbionts have been reduced over time, the genomes of several lineages of filamentous plant pathogens have been shaped by repeat-driven expansions. In these lineages, the genes encoding proteins involved in host interactions are frequently polymorphic and reside within repeat-rich regions of the genome. This talk will review the properties of these adaptable genome regions and the mechanisms underlying their plasticity. I will also provide an update on our work on genome evolution in the lineage of the Irish potato famine organism *Phytophthora infestans*. Many plant pathogen species, including those in the *P. infestans* lineage, evolve by host jumps followed by adaptation and specialization on distinct hosts. However, the extent to which host jumps and host specialization impact genome evolution remains largely unknown. We resequenced several representative genomes of four sister species of *P. infestans*. This work revealed extremely uneven evolutionary rates across different parts of these pathogen genomes (a two-speed genome). These analyses enable us to understand host specialization and adaptation all the way from the genome perspective to the biochemical level.

J Colhoun Poster

Effect of *Lr34* and *Lr46* on fungal diseases of wheat

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Lr34 and Lr46 are adult plant resistance genes providing durable resistance against biotrophic pathogens like rusts and powdery mildews in wheat. In seedlings, however, these genes were found to increase susceptibility to Septoria tritici blotch (STB), caused by the fungus *Mycosphaerella graminicola*. A similar effect was observed in adult plants tested in polytunnels. If this trade-off operates in field conditions, there may be significant consequences for the use of *Lr34 and Lr46* to control rust and mildew in areas where STB is prevalent.

The hypothesis that leaf age has a role in *Lr34* and *Lr46* resistance to mildew and susceptibility to STB was tested. In particular, it was hypothesised that enhanced senescence in plant leaves can make them resistant to biotrophs while making them more susceptible to necrotrophic pathogens. Leaf age altered significantly the effect of *Lr34* and *Lr46* on STB. The plant material tested included the Indian spring wheat Lal Bahadur (LB) and near-isogenic and mutant lines developed from LB. In young leaves, LB was less susceptible to STB than near-isogenic lines carrying *Lr34* or *Lr46*. The opposite pattern was observed, however, in older leaves.

Lr34 and *Lr46* appear to favour the necrotrophic phase of *M. graminicola* in younger leaves while the biotrophic phase may not be supported in older leaves, resulting in reduced infection. *Lr34* and *Lr46* are increasingly effective against powdery mildew in older leaves, to the point where the plant may be completely resistant. These observations indicate that leaf senescence may be an important factor in the effects of *Lr34* and *Lr46* on diseases such as mildew and Septoria.

J Colhoun Poster

Ensifer adhaerens OV14: an alternative approach to genetic modification in plants

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When equipped with the unitary transformation vector pCambia5105, *Ensifer adhaerens* OV14 can genetically transform *Arabidopsis*, tobacco and potato. To aid the development of *Ensifer*-mediated transformation (EMT) as an alternative to *Agrobacterium*-mediated transformation the whole genome sequence of OV14 is being examined. Firstly, a draft was completed using the Illumina platform and a second round of sequencing is in progress using the PacBio platform. The two data sets will be combined with remaining gaps filled via Sanger sequencing. From the draft sequence, OV14 contains a total genome of 7.69 Mbps, with a GC content of 61.28%. Using Artemis Comparison Tool the draft sequence was aligned against the main chromosome of *Sinorhizobium meliloti* 1021. Six scaffolds from the OV14 draft aligned strongly to the *S. meliloti* 1021 data and they have been isolated from the remaining data. The residual pool of data was screened and cleaned of sequencing artefacts and is believed to represent up to 5 additional replicons. OV14 contains homologs of two *Agrobacterium tumefaciens* Ti plasmid based virulence genes, *virD2* and *virD4*, and homologs of all reported *A. tumefaciens* chromosomal virulence genes. Like many bacteria that interact with eukaryotes OV14 possesses genes for the synthesis of phosphatidylcholine, a phospholipid typically found in eukaryotic cell membranes and only present in 10% of bacterial species. OV14 is the first bacterial species outside the *Agrobacterium* group which has shown transformation efficiencies close to that of *A. tumefaciens* (Wendt *et al*., 2011). Using genomic data from the plant pathogen *A. tumefaciens*, the plant symbiont *S. meliloti*, and rhizosphere living OV14 we will compare genes involved in plant–microbe interactions to gain a better understand of the mechanisms behind T-DNA transfer in OV14.

J Colhoun Poster

Use of arabinoxylan polymers for plant defence

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The ability of a plant cell wall-derived arabinoxylan polymer to control foliar pathogens of cultivated crops is being studied in field and controlled environment experiments. The results obtained in three previous consecutive seasons show a significant effect on disease level and progress, green leaf area and yield of barley (*Hordeum vulgare*). The experimental data suggests a priming effect of the polymer on plant resistance to pathogens, which could be beneficial for overall plant fitness under conditions of pathogen challenge. This discovery offers the potential for development of a novel, cost-effective and environmentally benign measure for crop disease control, contributing to current anti-resistance strategies and helping to prolong life of existing agrochemicals.

J Colhoun Poster

Rhynchosporium leaf blotch response to biochar application in a barley system

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Biochar is the solid product obtained by the thermal decomposition of organic waste material under a limited supply of oxygen and at relatively low temperatures. Due to its unique make-up and carbon-rich composition it can serve as a tool to sequester CO_2-C in soils where it can also act as a soil conditioner.

Improved crop resistance to foliar and soil-borne fungal pathogens following biochar application to soil or growth media has previously been demonstrated. The underlying mechanisms of disease reduction are not well understood, but might be the result of a series of direct or indirect effects that influence signalling pathways. Biochar has been shown to induce systemic resistance in strawberry plants against *Botrytis cinerea* and *Podosphaera apahanis*.

The biological impact of biochar on the phytopathology of a major cereal grain has not yet been investigated. The aim of this project is to explore the interactions of biochar and *Rhynchosporium commune* in a spring barley system, and to screen for potential underlying biochar mechanisms that effect pathogen development. A comparative response study of spring barley to *R. commune* infection following biochar application to soil in a controlled environment was carried out and showed significant leaf blotch suppression. Biochar derived volatiles may attribute to disease suppression as biochar amended growth plates both directly and indirectly inhibited fungal mycelia growth *in vitro*. The results are discussed in this poster.

J Colhoun Poster

ABA-mediates a NAC transcription factor *HvNAC6* in response to abiotic and biotic stress in barley

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Transcription factors have been shown to be involved in the crosstalk between abiotic and biotic stress-signalling networks. In an attempt to investigate the *in vivo* functions of the barley NAC transcription factor, *HvNAC6*, we generated transgenic barley plants by an RNA interference (RNAi)-based method. Our results indicate that *HvNAC6* participates in an abscisic acid (ABA)-dependent stress-signalling pathway and is a central component of barley penetration resistance towards *Blumeria graminis* f. sp. *hordei* (*Bgh*) attack. We have shown that exogenous ABA stimulates resistance to attempted *Bgh* penetration, suggesting that ABA is a positive regulator of penetration resistance. This, in turn, implicates *HvNAC6* as a positive regulator of ABA signalling that is required for maintenance of effective penetration resistance towards *Bgh*. Furthermore, we are currently measuring ABA levels and expression of a positive regulator of ABA signalling, *HvPKABA1*, known to correlate with ABA levels, during *Bgh* infection. We have also demonstrated that alteration of *HvNAC6* expression modulates ABA responsiveness in barley, i.e. *HvNAC6* RNAi plants were less sensitive to ABA. Following drought treatment, *HvNAC6* RNAi plants showed a higher rate of water loss than WT. A significant reduction of ABA marker transcript levels for *HvPKABA1* was also observed in *HvNAC6* RNAi plants under drought stress. We therefore suggest that ABA-mediated responses to both abiotic and biotic stress are regulated by *HvNAC6* in barley.

J Colhoun Poster

Developing *Ensifer*-mediated transformation (EMT) as a robust platform for genetic manipulation of crop species

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A Gram-negative bacterium, *Ensifer adhaerens* OV14 (equipped with the unitary vector pCAMBIA5105) can genetically transform *Arabidopsis*, *Nicotiana tabacum* and *Solanum tuberosum* with transformation efficiencies of 0.12, 21 and 37%, respectively (Wendt *et al.,* 2011). To build upon this and expand the application of *Ensifer*-mediated transformation (EMT), this research is focussed on expanding the host range for EMT and optimising the culturing conditions of OV14. Screening OV14 against fourteen different antibiotics, at six different concentrations in solid and liquid media, illustrated that OV14 is only susceptible to gentamicin (10 μg ml^{-1}) and tetracycline (10 μg ml^{-1}). However, under high concentrations of kanamycin (>1500 μg ml^{-1}), OV14 can be transformed with *nptII* gene-based bacterial selection vectors. We have confirmed that OV14 is receptive to both chemical transformation and electroporation and also has the ability to accept circular plasmids from other Gram-negative bacteria such as *Agrobacterium*; for example, we have stably transferred the Ti-plasmid from *Agrobacterium* strain GV3101 into OV14 and we can now use this OV14_Ti strain as a host for binary plant transformation vectors. EMT offers an alternate to the heavily patented *Agrobacterium*-mediated transformation (AMT), and is available to interested parties to test on their crop species of choice.

J Colhoun Poster

Characterisation of mutations in the succinate dehydrogenase gene for potential fungicide resistance in *Ramularia collo-cygni*

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The fungus *Ramularia collo-cygni* (*Rcc*) has been present as a major barley pathogen in Scotland since 1998. Succinate dehydrogenase inhibitors (SDHIs) have been used and recommended as an effective treatment in controlling the disease. All of the currently available data suggests that *Rcc* is still sensitive to all SDHI fungicides. However, development of resistance to this chemical group is classified by FRAC (Fungicide Resistance Action Committee) as medium to high risk. *R. collo -cygni* has already been exposed to SDHI fungicides for a number of growing seasons. Therefore, the risk of resistance development is high, given that only a single point mutation was required in the target gene to develop high levels of fungicide resistance in other related plant pathogens (Miyamoto *et al*., 2010; Fraaije *et al.,* 2012; Scalliet *et al*., 2012).

In this project we look for possible mutations responsible for SDHI resistance development in *Rcc* and we aim to characterise mutants in terms of their fitness and pathogenicity. We test pathogen isolates in a fungicide sensitivity assay in order to obtain the range of baseline sensitivity to SDHI fungicides within *R. collo-cygni* population. We examine the diversity of the population using newly designed microsatellites markers and we try to define its evolutionary potential, in terms of fungicide resistance. Finally, we want to produce an effective assay for monitoring genetic changes that correlate with fungicide resistance that will enable the detection of *Ramularia* resistant isolates and the production of resistance control strategies.

J Colhoun Poster

Downy but not out: using genetic mixtures to improve yield stability under disease pressure

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Plant genotypic mixtures have the potential to increase yield stability in variable, often unpredictable environments, yet knowledge of the specific mechanisms underlying enhanced yield stability remains limited. Field studies are constrained by environmental conditions, which are not completely controllable and therefore not fully reproducible. A suitable model system would allow reproducible experiments on processes operating within crop genetic mixtures under disease pressure. Genotypic diversity of *Arabidopsis thaliana* was manipulated under growing conditions with high levels of competition. Four phenotypically dissimilar genotypes were grown in monocultures and mixtures under high levels of competition in the presence or absence of the pathogen *Hyaloperonospora arabidopsidis*. Seed production, flowering time and rosette size were recorded for multiple replications of glasshouse experiments. Disease reduced the competitive ability of susceptible genotypes, decreasing rosette size and seed production in mixtures. The effect of disease on plant fitness was greater when there was more intense competition between plants. Yield stability was achieved in mixtures under disease pressure because more resistant genotypes compensated for lost seed production by susceptible genotypes. This study indicates that the mixing ability of plant genotypes can be predicted from phenotypic traits such as rosette size, seed production, and host–pathogen compatibility, and implies that a phenotypic screen of cultivars could improve the selection of suitable components of genotypic mixtures in agriculture intended to be resilient to environmental stress.

J Colhoun Poster

Virus-mediated heterologous gene expression in wheat, barley and Sharon goatgrass

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The Two Blades group aims to clone novel resistance genes effective against Ug99 from *Aegilops sharonensis* and deploy them in wheat as a single transgenic cassette to provide durable disease resistance. Key to this goal is the development of molecular genomic and reverse genetic tools to facilitate the cloning and functional characterisation of novel *Sr* genes. One such tool is a high-throughput effector delivery system for use in effecteromics. Recent work in the Two Blades group has identified viruses that could potentially be used for heterologous expression of candidate effectors from Ug99 in *Aegilops sharonensis*. The system is currently being developed further by attempting to express a number of different positive controls that should exhibit a hypersensitive-like response (HR) when expressed *in planta*. Once established, this system will provide a rapid phenotyping platform for mapping populations segregating for resistance to Ug99. It will also allow us to untangle intricate *R*/*Avr* interactions between the plant and pathogen and to functionally characterise different *Sr* genes by screening with single effectors and observing the manifestation of a HR. This information will then guide decision-making with regards to the most suitable *Sr* genes to include in a transgenic cassette to obtain more durable disease resistance.

J Colhoun Poster

Analysing virulent and avirulent *Leptosphaeria maculans* isolates to understand *R* gene-mediated resistance in *Brassica napus*

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Phoma stem canker (*Leptosphaeria maculans*) is a major disease on oilseed rape (*Brassica napus*) in the UK. *B. napus R* gene-mediated resistance against *L. maculans* is associated with a gene-for-gene interaction but is often not durable since pathogen populations change from avirulent to virulent (Sprague *et al*., 2006). A single *L. maculans* gene *AvrLm4-7* interacts with two *B. napus R* genes, *Rlm4* and *Rlm7* (Parlange *et al*., 2009). It has been suggested that *Rlm7* is more durable than other *R* genes (Clarke, pers. comm.). The fitness cost of virulence against *Rlm1* and *Rlm4* has been used to investigate durability of these *R* genes (Huang *et al*., 2010). This work aims to investigate durability of *Rlm7*.

Twenty isolates from cultivars carrying the *Rlm7* gene (Roxet and Excel) obtained in 2011/2012 and were characterised at the *AvrLm4-7* locus using cotyledon inoculation tests on cultivars carrying *Rlm4* or *Rlm7* genes. All isolates obtained from Excel and most isolates from Roxet produced resistant phenotypes on cultivars carrying the *Rlm7* gene. To investigate changes in fitness and aggressiveness associated with changes from avirulent to virulent at the *AvrLm4-7* locus, four isolates from Excel and four from Roxet that had produced resistant or intermediate phenotypes were characterised by inoculation onto cotyledons of a susceptible cultivar (Drakkar) and several cultivars carrying the *Rlm7* gene (Excel, Roxet and Hearty).

Future work will include molecular characterisation of theses isolates. UK isolates for testing will be obtained in the cropping season 2012/2013 from cultivars carrying the *Rlm7* and *Rlm4* genes.

J Colhoun Poster

RNA-seq and metabolite studies of the barley/powdery mildew interaction during climate change

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The predicted changes in the world's climate are believed to affect the physiology of plants, and their interaction with pathogens. It is generally hypothesized that crop plants may become more prone to diseases in the future, but it is difficult to generalize, and not much information is available from experiments using multi-climatic factors. Furthermore the molecular and biochemical mechanisms behind the observed and predicted changes in plant disease susceptibility are not fully understood.

Previously, we have examined how climatic factors are affecting disease severity in spring barley (*Hordeum vulgare*) towards fungal pathogens with opposite lifestyles: the biotrophic *Blumeria graminis* f. sp. *hordei* (powdery mildew) and the hemibiotrophic *Bipolaris sorokiniana* (spot blotch), and observed that development of the diseases was affected differentially by the climatic factors. Disease severity of powdery mildew was decreased when plants were grown in a phytotron with increased levels of temperature, [CO_2] and [O_3] as single factors. However, combinations of the factors lead to increased disease severity. To learn about the molecular and biochemical mechanisms involved, we have chosen to dig deeper into the well-known barley–powdery mildew interaction and have made RNA-seq analysis (whole transcriptome) and metabolite studies, to elucidate how barley plants acclimates to the climatic factors introduced, and how this can explain the observed changes in disease severity. Preliminary results from these analyses will be presented on the poster.

J Colhoun Poster

Slowing the increase in fungicide resistance – does rate of application matter?

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Septoria tritici blotch (STB), caused by the fungal pathogen *Mycosphaerella graminicola* is the most destructive disease of winter wheat in Ireland. Triazole fungicides are the backbone of STB control. However, efficacy of these fungicides has declined in recent years. This has been due to selection of strains of *M. graminicola* with reduced fungicide sensitivity. The Fungicide Resistance Action Committee (FRAC) advises to always use the full recommended rates to minimise the rate at which fungicide sensitivity declines, but this advice has been hotly contested. The use of mixtures as a method of reducing selection has been better supported by experiment.

To assess the effect of using different application rates of triazoles on the selection of resistant *M. graminicola* strains and STB control, field trials were conducted at three locations over two years. At each location the efficacy of epoxiconazole and metconazole (applied in mixtures, alternations and as solo products) used at the either full or half the recommended rate was determined.

In 2011, disease control was best with the full rate mixture. Over all compositions the full rates provided better disease control. However, half rate treatments clearly reduced selection, except in the mixture. In this case, the dose relationship was reversed for epoxiconazole, indicating the effect of mixing fungicides appears to be specific to the exact mixture components and the sensitivity distributions of the populations treated.

J Colhoun Poster

Harnessing natural variation to identify avirulence genes of the Arabidopsis white rust

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Albugo sp, ("White rusts") are obligate biotrophic oomycete plant pathogens that infect plant species of the family *Brassicaceae*. *Albugo laibachii* (*Al*) specifically infects *Arabidopsis thaliana* (*At*). Since *Al* can colonise ~90% of *At* accessions without eliciting a strong defence response we postulate that *Al* secretes effector proteins to suppress host immunity. When the *Al* genome was sequenced, it was revealed that the pathogen secretome does not contain an over-abundance of the major known oomycete pathogen effector class, the RXLRs. In order to identify real *Al* effectors we decided to identify "avirulence genes": effectors that are recognised in some host accessions and can elicit a strong defence response. Since the *Al* system is not amenable to genetic mapping, we took an association genomics approach. We have Illumina sequenced seven field isolates of *Al*, and identified a wide range of differential susceptibilities on 50 *At* accessions. Putative recognised effectors were predicted according to (i) association of polymorphisms to specific differentials, and (ii) population genomic statistics such as dN/dS ratio and Fu's Fs test. So far, four of the top candidates have been tested for recognition using the GUS eclipse assay – a system for transient expression via particle bombardment. Two candidates show strong GUS eclipse in specific resistant accessions, indicating that they may be recognised effectors. We are currently testing if these candidates can significantly affect the *in planta* growth of *Pseudomonas* bacteria and cause a cell death phenotype when expressed in inducible resistant lines.

J Colhoun Poster

Mapping and characterisation of the *Cf-Ecp2* resistance genes in tomato and *Nicotiana paniculata* that recognise the core fungal effector Ecp2

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The effector protein Ecp2, originally characterised in the tomato leaf mould fungus *Cladosporium fulvum*, is a member of a superfamily of putative effectors found in multiple lineages within the fungal kingdom (Stergiopoulos *et al.,* 2010, 2012). Plant resistance (*R*) genes that recognise Ecp2 with a hypersensitive response – *Cf-Ecp2* – have been found in *Solanum pimpinellifolium* (Currant Tomato) and various species of *Nicotiana* (Lauge *et al.,* 1998; De Kock *et al.,* 2004). The tomato *Cf-Ecp2* genotype has also been shown to recognize Ecp2-1 from *Mycosphaerella fijiensis*, the causal agent of Black Sigatoka (Stergiopoulos *et al*., 2010). Therefore, the transfer of *Cf-Ecp2* genes to other plant species might provide resistance against fungal pathogens containing *Ecp2* homologues. We will report on our progress with mapping, cloning and characterisation of *Cf-Ecp2* in both tomato and *N. paniculata.*

J Colhoun Poster

Phyt or blight: a disease resistance role for phytate in potato

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Phytate (inositol hexakisphosphate or $InsP_6$) is an important signalling molecule in plants. It accumulates in seeds and tubers in complex with mineral cations, providing a store of phosphate and nutrients for germination. Recent interest in developing low-phytate crops has been sparked because of its negative effects on humans, in which micronutrient malnutrition can occur by consuming a high phytate diet, and on the environment, as undigested phytate in animal waste can pollute aquatic ecosystems. Previously, we found mutant low-phytate *Arabidopsis thaliana* plants were more susceptible to a variety of viral, bacterial and fungal pathogens. This suggests an additional role for phytate in basal resistance (Murphy *et al.*, 2008, The Plant Journal). To explore whether this is conserved in an economically relevant crop we used RNAi in potato to knock-down expression of inositol-pentakisphosphate 2-kinase (*IPK*) – which encodes the last enzyme in $InsP_6$ biosynthesis. Knock-down *IPK* potato plants exhibit around a two third reduction in leaf and tuber phytate compared to empty-vector controls, are delayed in their development and have altered leaf morphologies. Initial disease resistance experiments using the bacteria *Erwinia carotovora* ssp. *carotovora* indicate this pathogen can accumulate to higher levels in low-phytate potato leaves, implying basal resistance is compromised. This suggests a conserved role for phytate in disease resistance and future pathology experiments will determine whether basal resistance to other economically important potato pathogens, such as *Phytophthora infestans*, is also reduced. This research indicates there may be unforeseen negative fitness consequences for engineering crops with reduced phytate levels.

J Colhoun Poster

Environmental conditions determine the costs and benefits of virus infection and RNA silencing in *Arabidopsis*

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In natural environments RNA viruses are estimated to be present in about 70% of individuals of various plant species including *Arabidopsis thaliana*. *Cucumber mosaic virus* (CMV) is one of the most prevalent viruses in *Arabidopsis* and qualitative resistance to CMV seems to be rare. Given that CMV infection may incur high fitness costs this begs the question why qualitative resistance is not more widespread. In the field plants are often confronted with pathogen attacks and environmental stresses such as drought simultaneously. The signalling networks regulating a plant's response to both types of stresses may therefore overlap so the plant can tailor its response to minimize fitness losses as a consequence of adverse conditions. One node that is shared by both plant antiviral defense and abiotic stress response networks is the RNA silencing effector ARGONAUTE1 (AGO1) which controls antiviral silencing and a microRNA-mediated drought tolerance mechanism. We found that under normal conditions CMV infection incurred fitness costs and that these costs were even higher when the plant's antiviral silencing mechanism was disrupted. Strikingly, under drought conditions the situation was reversed and CMV infection enhanced plant survival. The CMV 2b protein, which suppresses antiviral silencing by binding small RNAs and AGO1, played a crucial role in promoting drought tolerance, but this was independent of its silencing suppressor activity and likely depended on its interference with abscisic acid signalling and root physiology instead. We conclude that virus-induced drought tolerance may serve both susceptible plants and viruses to survive periods of environmental stress.

J Colhoun Poster

Mutation of the kinase domain of the brassinosteroid receptor BRI1 enhances barley resistance to *Fusarium* diseases

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Brassinosteroids (BRs) are hormones that influence plant growth, development and defence responses. The BR receptor protein Brassinosteroid Insensitive 1 (BRI1) has been characterised in several plant species. Semi-dwarf barley 'uzu' vareties have a mutation in the kinase domain of *Bri1.* In studies conducted using barley genotypes Akashinriki and Bowman and their 'uzu' derivatives, we show 'uzu' is more resistant to Fusarium head blight (FHB) disease. Resistance was characterised as the uzu plants having >38% lower disease symptoms and >25% higher yield as compared to parent lines Akashinriki and Bowman. Seedling experiments showed that the 'uzu' derivative of Akashinriki was also 87% more resistant to Fusarium seedling blight as compared to the parent line. Virus-induced gene silencing of *Bri1* lead to enhanced susceptibility of detached leaves to *Fusarium culmorum* (>2 times more disease than plants treated with the empty VIGS vector). We are currently determining the effect of the uzu mutation on downstream BR signalling and the functionality of the kinase domain of the uzu *Bri1.*

J Colhoun Poster

The life history of *Ramularia collo-cygni*

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The filamentous fungus *Ramularia collo-cygni* causes the late season disease of spring and winter barley called Ramularia leaf spot (RLS). It has become an increasingly important problem for European farmers in the past decade and has recently been reclassified as a major disease of barley in the UK. The lack of apparent varietal resistance to the disease has led to significant amounts of fungicide being applied to crops in north-western and central Europe in order to maintain green leaf area and prevent significant yield loss. These factors have contributed to an increasing focus on achieving a better understanding of the fundamental biology of this elusive pathogen in order to develop more successful strategies of RLS management. Therefore, disease development throughout the life cycle of the host barley plant has been analysed by the employment of transgenic *R. collo-cygni* isolate, expressing the GFP reporter molecule, and confocal microscopy. We have been able to examine the previously uncharacterised seedborne stage and illustrate the mode of fungal transmission into barley seedlings. We have also analysed the potential sexual reproduction in the fungus by utilising a range of correlative techniques, such as cryo-scanning electron microscopy, confocal microscopy and light microscopy. Here we describe for the first time the nature of speculated spermogonial stage called *Asteromella* and in addition, present preliminary evidence suggesting the existence of a perfect stage that, if functional, could resemble closely related *Mycosphaerella* species.

J Colhoun Poster

The role of silicon and potassium carbonate in controlling epidemics of *Podospheara aphanis* on strawberry in the field

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Strawberry powdery mildew is a major disease of strawberries, which is caused by *Podosphaera aphanis*. The fungus mycelium is on the plant leaves, stems, shoots, buds; flowers and fruit surfaces, which causes yield loss. Whilst it can be controlled with fungicides, they cannot be used close to harvest because of the 'harvest interval', therefore growers need to used other products which limit disease but are not registered pesticides. Strawberry growers frequently use potassium carbonate in a silicon-based wetter in the interval immediately prior to harvest. The work reported here aimed to investigate the disease control achieved by the potassium carbonate and the silicon-based wetter, used singly and in combination. The trial was set up in an open field with the susceptible variety Elegance. The trial used a randomised block design with the following treatments: untreated, K50 (potassium carbonate), 0.25% concentration silicon wetter with K50, 0.5% concentration silicon wetter and 0.5% concentration silicon wetter with K50.

The results using the AUDPC show that high rate silicon wetter and K50 together gave the best control of the disease, with low rate silicon wetter and K50 also giving control. The silicon wetter alone at both concentrations also gave some control of the disease but K50 alone gave little control and was very similar to the untreated control.

J Colhoun Poster

Patterns of infection within the *Zymoseptoria* species complex

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Phytopathogenic fungi co-evolve with their hosts and in response to their environment. The *Zymoseptoria* species complex provides a unique opportunity to study the influence of adaptive evolution in three very closely related grass pathogens. These pathogenic fungi have a common origin in the Middle East but are adapted to different hosts and ecosystems. *Zymoseptoria pseudotritici* and *Z. ardabiliae* can infect the leaves of wild grasses whereas the worldwide distributed *Z. tritici* (syn. *Mycosphaerella graminicola*) causes leaf blotch disease of cultivated wheat species *Triticum aestivum* and *T. durum*.

Our goal is to assess how adaptive evolution during speciation and specialization to different hosts and environments has shaped the infection progress and the infection patterns of the three *Zymoseptoria* species. We aim to investigate how these fungi develop in compatible and non-compatible hosts and we will characterize possible morphological differences between biotrophic and necrotrophic growth. For this purpose we have modified and applied a recently developed technique for microscopic structure analysis of root colonizing fungi for *Zymoseptoria*–host interactions in leaf tissue. This technique combines selective staining, microtomy and confocal laser scanning microscopy to visualize and characterize the *in planta* interactions of host and pathogen.

Our preliminary data from the *Z. tritici*–*T. aestivum* interaction suggests that specialization to a narrow range of agricultural hosts is reflected in a fast, efficient and extensive host infection. We hypothesize that adaptive evolution led to different infection progress of pathogens of wild and domesticated grass species resulting in spatially and temporally variable patterns of infection.

J Colhoun Poster

Exploiting novel plant genes for the development of future crops

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Fusarium head blight (FHB) disease poses a substantial threat to wheat quality and consumer safety due to associated yield losses and mycotoxin contamination of grain. Reducing the level of mycotoxin contamination in wheat at the start of the production chain by means of improved FHB resistance would be of both toxicological and economic importance. Previous gene expression studies identified a number of transcripts upregulated in response to the *Fusarium* mycotoxin deoxynivalenol (DON); their DON-induced transcript levels that were significantly higher, and occurred earlier, in the DON resistant cultivar CM82036 as compared to susceptible cultivar Remus. Using virus-induced gene silencing (VIGS), we found that heads with reduced transcript levels developed more DON-induced bleaching as compared to control treatment. Successful transformation of the gene into the model plant *Arabidopsis thaliana* had no apparent negative effects on plant development. We will also overexpress this gene in wheat and, using these monocot and dicot overexpression plants, we will investigate the potential of this gene to enhance disease resistance and tolerance to abiotic stressors such as cold.

J Colhoun Poster

Pathogenic and transcriptomic studies of the *Phytophthora ramorum*–*Rhododendron* interaction

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Phytophthora ramorum, the causal agent of sudden oak death, has caused the death of large numbers of oaks species and tanoak in west coast of the United States. In the Republic of Ireland, *P. ramorum* is more commonly found on shrubs such as *Rhododendron* and *Viburnum*, where it may cause browning of leaves, lesions or cankers, wilting and dieback. Parallel massive sequencing of cDNA (RNA-seq) based on next-generation sequencing (NGS) techniques has been available to measure levels of transcripts and their isoforms that are expressed in any tissues. This approach has been more and more used to measure the expression levels of genome-wide genes from the fungus and host interaction. A new project underway will assess the pathogenicity of *P. ramorum* to the host *Rhododendron*. Using closely related, but pathogenically variable isolates of *P. ramorum*, and both resistant and susceptible species of *Rhododendron*, we will use transcriptomics in order to decipher pathogen and host factors that respectively contribute to virulence and resistance.