Coming soon...

BSPP Presidential Meeting 2015

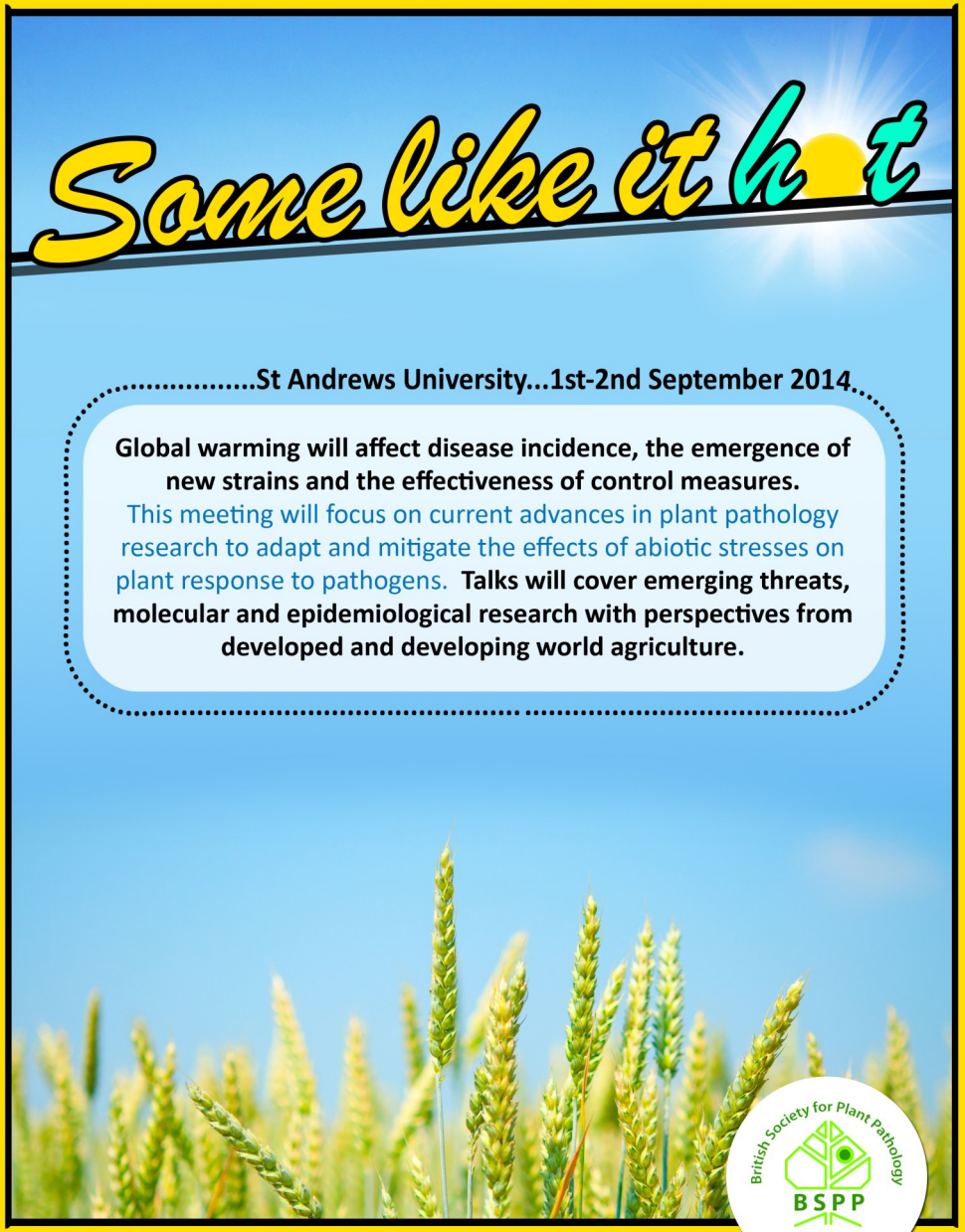
Theme: The impact of plant pathology on everyday lives

in late 2015
@ the University of Bristol

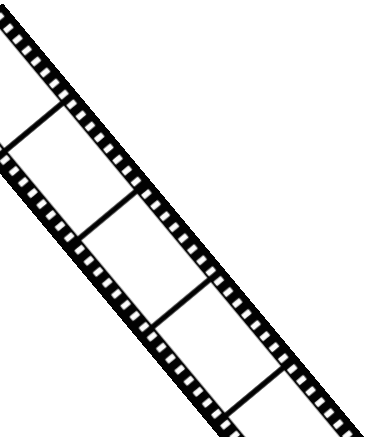
Gary Foster
President-elect

British Society for Plant Pathology
BSPP

British Society for Plant Pathology Presidential Meeting



Notes and Quotes



President's Welcome

The main theme of this year's meeting is to consider the effects of global warming on pest and pathogen incidence and disease processes. The cast of distinguished speakers will present and appraise ongoing research, highlight threats, gaps in knowledge and new approaches that can be deployed to combat the risks from current and emerging pests and pathogens. There will be perspectives from developed and developing agriculture systems. We hope the social occasions (including the ceilidh) will encourage much discussion and provide new ideas for research and stimulate new collaborations. In addition to the invited talks there will be competitions for the P H Gregory and J Colhoun Prizes for best oral and poster presentations (respectively) from postgraduate students or early stage researchers. Unfortunately, we don't have a prize for best ukulele player.

We hope you enjoy the meeting and that no-one gets the fuzzy end of the lollipop.

The Organizing Committee
Lesley Torrance and Elizabeth Orton

I play the ukelele, and I sing, too

Image from Wikimedia Commons
Cropped screenshot from trailer of the film *Some Like it Hot* (1959) in the public domain

We wish to thank Will Kay for designing the eye-catching poster, Carol Jenner for preparing the abstract booklet, and Steve Whisson for his continuing assistance and support. We also wish to thank Tesco (Cupar) for their kind donation.

BSPP Presidential Meeting 2014: Some like it hot
The Gateway Building, Gateway Galleries, North Haugh, University of St Andrews, St Andrews, KY16 9RJ, UK

Monday 1 September

9.00–9.45 **Sarah Gurr**
Fungi challenge global food security and plant ecosystem health

9.45–10.30 **Karen Garrett**
Adapting disease management to global change: understanding the linked networks that determine risk and sustainability

Tea/coffee

11.00–11.45 **Nicola Spence**
Prioritising actions to enhance plant biosecurity: the UK Plant Health Risk Register

11.45–12.15 **Mike Jeger**
Climate change and pest risk assessment for plant health

Lunch

1.30–2.15 **Jim Beynon**
Using systems biology modelling to reveal regulatory networks controlling plant stress responses

2.15–2.45 **Lesley Torrance**
The effect of abiotic stress on virus infection

2.45–3.15 **Jorunn Bos**
Molecular events during plant–aphid interactions

Tea/coffee

P H Gregory talks 3.45–4.45
Posters (and AGM)

J Colhoun poster

The bean virus police: investigating plant–aphid interactions

Francis O. Wamonje[1], Alex M. Murphy[1], Valentine Aritua[2] and John. P. Carr[1]

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The potyviruses bean common mosaic virus (BCMV) and bean common mosaic necrosis virus BCMNV), and to a lesser extent cucumber mosaic virus (CMV, a cucumovirus), are major constraints on common bean (Phaseolus vulgaris) production in Africa. Virus control options are limited because plants carrying the *I* gene for BCMV resistance are susceptible to BCMNV-induced necrosis and recessive resistance genes provide limited resistance. Aphids transmit cucumoviruses and potyviruses. There is increase in the geographical range of aphids and the viruses they spread due to climate change. As part of a multipronged approach, we have developed and used molecular tools based on the *cytochrome oxidase subunit-1* gene to accurately determine aphid species caught in bean farms from different agro-ecological regions of Uganda. We have also developed a reverse transcription-PCR technique to identify what viruses individual aphids sampled from leaves or water trapped in the field are carrying. Previous work by several groups using *Arabidopsis*, tobacco, cucumber and potato has shown that viruses alter the attractiveness of plants to aphids and influence aphid feeding behaviour. These studies suggest that virus-induced changes in aphid–plant interactions may initially recruit aphids to acquire virus before promoting their dispersal to infect new hosts. To better understand bean viral epidemiology and to develop strategies to inhibit virus transmission, we are conducting initial studies with *M. persicae* and the bean specialist aphid, *Aphis fabae.* We present preliminary data on free-choice experiments on the effect of a BCMNV and CMV infection on aphids on a farmer-preferred variety of bean.

J Colhoun poster

Integrated crop protection of tomato against *Botrytis cinerea* through enhancing its endogenous defence mechanisms

Daniel de Vega Perez and Adrian C. Newton

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Horticultural crops, such as tomato, are challenged, before and after harvest, by many microbes such as fungi, bacteria, viruses and nematodes. Some of these are pathogens and can cause disease in susceptible hosts. Plants have defence mechanisms that can prevent disease if triggered at the right time in the right amount, reducing or removing the need for application of other toxic crop protection chemicals. Conventional crop protectants lose their efficacy due to pathogen resistance from their widespread use, for example benzimidazoles and dicarboximides where resistance in *Botrytis cinerea* strains is now a problem. Therefore there is a challenge to find new, more sustainable and benign crop protectants. Resistance elicitors (RE) could fill this role as they can trigger defence mechanisms that can result in broad-spectrum "induced resistance". Plant hormones salicylic acid (SA) and jasmonic acid (JA) are required for systemic resistance against biotrophic and necotrophic fungal pathogens, becoming key factors in tomato resistance against the necotrophic fungus *Botrytis cinerea*. SA and JA signalling pathways can be induced in tomato throughout the use of RE in order to fight against this pathogen. Furthermore, cell-wall defence can be a potent instrument to combat pathogen attack in the early stages of the infection. Callose, the high molecular weight β-(1,3)-glucan polymer, is considered as an important factor for plant penetration resistance, acting as a physical barrier against invading pathogens such as *Botrytis cinerea.* We demonstrate their potential, singly and in combination, through characterisation using these means as well as defence gene expression.

7.00 Dinner and Ceilidh

Tuesday 2 September

9.00–9.30 **Eleanor Gilroy**
Phytophthora infestans effector PiAVR2 targets StbBSL1 to activate the brassinosteroid pathway

9.30–10.00 **Michael Taliansky**
Sub-nuclear structures provide new genetic sources of plant resistance to biotic and abiotic stresses

Tea/coffee

10.30–11.15 **Ian Barker**
Managing risk for smallholder farmers in an uncertain future

11.15–11.45 **Greg Forbes**
Changes in plant–pest dynamics of potato systems in a warming Andes

11.45–12.15 **Michael Rutherford**
A perspective on coffee diseases: coffee wilt disease – a case study

Lunch

1.30–2.15 **Helge Sierotzki**
Challenges for disease control now and in future: a research perspective for plant pathogen control under changing environmental conditions

2.15–2.45 **Mojgan Rabiey**
Is *Piriformospora indica* a magic fungus?

2.45–3.15 **Rick Bennett**
A systems approach to plant pathology

Closing remarks

Tea/coffee/departure

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) 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) Ann. Rev. Phytopathol. 35: 1—14).

J Colhoun poster

Cucumber mosaic virus modifies plant–aphid interactions

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Cucumber mosaic virus (CMV) encodes five proteins, including the CMV 2b protein, which disrupts plant defences. *Nicotiana tabacum* (tobacco) plants infected with a 2b deletion mutant of the subgroup IA strain of CMV, strain Fny (FNY-CMVΔ2b) were more resistant to aphids (*Myzus persicae*) with lower survival and colony growth compared with aphids on plants infected by wild-type Fny-CMV. This suggests that on tobacco, Fny-CMV infection or certain CMV viral gene products might elicit aphid resistance and the 2b protein is able to counteract this during a wild-type Fny-CMV infection.

The CMV genome comprises of three positive-sense RNAs: RNA 1 encodes protein 1a, RNA 2 encodes proteins 2a and 2b, RNA 3 encodes the movement and coat proteins. Tobacco infection with the strain Fny-CMV induces higher aphid survival and colony growth in comparison to mock infection, whilst infection with a subgroup II CMV strain, LS-CMV, induces even higher aphid survival and colony growth in comparison to infection with Fny-CMV. Interestingly, whilst infection with Fny-CMVΔ2b induces aphid resistance, infection with LS-CMVΔ2b does not. Reassortant CMV genomes containing genomic RNA mixtures derived from these two different strains of CMV, the Fny- and LS-, is currently used for experiments to map the elicitor of aphid resistance in tobacco during Fny-CMVΔ2b infection. Strikingly, whilst wild-type CMV infection fosters aphid survival in tobacco, in Arabidopsis it induces aphid resistance. This indicates that CMV has plant species-specific effects on host–aphid interactions.

J Colhoun poster

Investigating the sporulation pattern of *Zymoseptoria tritici,* a pathogen of wheat

Anna M. M. Tiley, Gary D. Foster and Andy M. Bailey

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Zymoseptoria tritici is an ascomycete fungus which causes Septoria Tritici Blotch, a major disease of wheat. A potential way to control this pathogen is to prevent asexual sporulation by inhibiting development of the asexual fruiting body and spores. The recent sequencing of the *Z. tritici* genome has provided useful insights into the pathogen, and can be used identify candidate genes for investigation.

Comparative genomic analyses have been used to identify potential genes involved in asexual sporulation in *Z. tritici.* Key genes already known to be important for this process in other model ascomycete fungi were BLAST searched against the *Z. tritici* database to find potential homologues. Of the 84 genes analysed, 21 potential homologues were found in *Z. tritici.* Molecular genetic analyses were conducted on the candidate genes to elucidate their temporal and spatial expression patterns across the time course of infection. Of these, 5 have been selected for further study to assess their role in asexual sporulation in *Z. tritici.* Reliable sporulation of *Z. tritici* has also been successfully established *in vitro.* This will help future research into the fungus, particularly in the identification of knock-out mutants. The most recent results from these ongoing investigations will be presented.

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*, *Phytophthora*, *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: 377–381).

Fungi challenge global food security and plant ecosystem health

Sarah J. Gurr[1,2] and Dan Bebber[1]

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Fungal diseases have been increasing in severity and scale since the mid-20th Century and now pose a serious challenge to global food security and ecosystem health (Gurr *et al*., 2011, *Fungal Biology Reviews* **25**, 181–188). Indeed, we have demonstrated recently that the threat to plants of fungal infection has now reached a level that outstrips that posed by bacterial and viral diseases combined (Fisher *et al*., 2012, *Nature* **484**, 185–194).

This presentation will highlight some of the more notable persistent fungal and oomycete plant diseases of our times. It will draw attention to the emergence of new pathotypes affecting crop yields and to fungi and oomycetes decimating our natural and managed landscapes. I shall review some of our recent work looking at the movement of fungi polewards in a warming world (Bebber, Ramatowski and Gurr, 2013, *Nature Climate Change* **11**, 985–989), at the global distributions of crop pests and pathogens (Bebber *et al.,* 2014, *New Phytologist*, DOI: 10.1111/nph.1272) and at the saturation rate of crops by such organism (Bebber, Holmes & Gurr, 2014, *Global Ecology & Biogeography*, in press).

I shall conclude with some thoughts on the emergence of fungi in natural and crop ecosystems, of future threats and challenges and disease mitigation.

Poster

Effects of different fungicides on the severity of phoma stem canker

Thomas Sewell[1], Yongju Huang[1,] Henrik Stotz[1], Mike Ashworth[2], Philip Walker[3], Faye Ritchie[3] and Bruce D. L. Fitt[1]

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Phoma stem canker, a disease of oilseed rape (*Brassica napus*) caused by sibling pathogens *Leptosphaeria maculans* and *L. biglobosa*. Both pathogens follow a monocylic disease cycle that causes leaf spotting in autumn/winter and stem cankers in spring/summer. Most severe cankers decrease transportation of water and nutrients. Fungicides are important for phoma stem canker control. Triazole fungicides currently dominate the market, although reduced sensitivity in some plant pathogen species is a concern. Moreover, *L. maculans* and *L. biglobosa* have shown differing level of sensitivity to triazole fungicides. Therefore, increased knowledge on controlling phoma stem canker using non-triazole based fungicides is essential. Field trials were established for 2013/2014 cropping season. Four fungicides were applied: penthiopyrad, picoxystrobin, prothioconazole and a novel fungicide. Spray timings were divided into three sprays T1 (phoma leaf spotting incidence ≥10%), T2 (3/4 weeks post T1) and T3 (Sclerotinia). Phoma leaf spotting incidence and stem canker severity were recorded. In vitro sensitivity testing was done on one *L. maculans* (ME24) and one *L. biglobosa* (68) isolate. Prothioconazole showed no noteworthy advantage over the novel fungicide in canker severity scoring. No significant difference in growth inhibition was observed between *L. biglobosa* and *L. maculans* ($P \leq 0.05$) when treated with novel fungicide. Canker severity indicates that the novel fungicide has a similar efficacy to triazole fungicides. Fungicide sensitivity testing shows that *L. biglobosa* does not have an increased sensitivity to non-triazole fungicides. This interaction suggests that the novel fungicide could be used to control both *L. maculans* and *L. biglobosa*.

J Colhoun poster

Effects of light and temperature on potyvirus infection

Douglas Pyott

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Plant viruses are ubiquitous in natural growing environments and represent a constant and significant limitation to plant growth. This viral burden is of great economic importance due to the losses imposed by viral infections in crop plants. It has long been recognised that variations in environmental conditions can dramatically alter plant–virus interactions and may even dictate the outcome of infection. The light and temperature conditions plants are grown under have repeatedly emerged as important factors dictating both viral load and symptom development for a number of different phyto–viral systems. Potyviruses represent one of the two most specious groups of plant viruses and collectively present a large threat to agriculture. It has been well documented that potyvirus infections become more severe with increasing temperature, though characterisation of this phenomenon remains scarce. Similarly, details of how plant–potyvirus interactions are affected by light conditions are ill defined. This poster will present initial results reflecting the influence these environmental factors have on the dynamics of *Turnip mosaic virus* (TuMV, genus *Potyvirus*) in susceptible host plants.

Adapting disease management to global change: understanding the linked networks that determine risk and sustainability

Karen A. Garrett

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Understanding the impact of new information and other IPM components supports the development of optimization strategies, linking disciplinary perspectives. Methods are needed for better defining and quantifying system traits such as sustainability, resilience, and transformability, and for identifying key system control points where small investments can have large payoffs from research, extension, and policies. We developed 'impact network analysis' as a new system-level analysis of the impact of research products on biological systems, integrating how impact occurs through linked networks of communication, decision-making, and biophysical processes. Such a system-level perspective is needed to address problems such as integration of agricultural disease and pest management in climate change scenario analyses.

Prioritising actions to enhance plant biosecurity: the UK Plant Health Risk Register

Nicola Spence

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There are thousands of pests which can affect the health of plants and trees and the assessment of risk drives the EU plant health regime which targets those pests identified as highest risk. Defra has developed a plant health risk register which ensures we are directing risk management activity most effectively, as it is unrealistic to expect that we can provide effective protection from all pests. The risk register is an open dynamic tool, which is updated in response to new developments by the UK-wide Plant Health Risk Group which undertakes a monthly review of threats.

Potentially serious pests are subject to a detailed Pest Risk Analysis (PRA) following internationally agreed methodologies. Import inspections are based on risk-based EU targets and in addition inspections are carried out of other material focusing on those trades posing the greatest risk. Inland inspections and surveillance are also risk-based; using EU decisions, outcomes of PRA or targeting premises assessed as providing the greatest potential for distributing pests. Risk assessment feeds into the development of contingency plans and approaches to outbreak management to ensure that actions taken are correctly targeted, proportionate and effective.

J Colhoun poster

Exploring virulence factors in the rubber tree pathogen *Corynespora cassiicola*

Murnita M. Mahyudin, Gary Foster and Andy Bailey

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Corynespora cassiicola is a cosmopolitan fungus with a broad host spectrum. One of the hosts is the rubber tree, *Hevea brasiliensis* where it causes devastating leaf defoliation. To date, control of the disease is mainly focused on the application of fungicides, but this only provides short term control. This study aims to understand the disease mechanisms of this fungus, exploiting whole-genome sequence data and using transformation as a tool to analyse gene function. Detailed investigations by molecular means hopefully will contribute to designing a more efficient control method to reduce the detrimental effects of the disease. A transformation system for *C. cassiicola* mediated by *Agrobacterium tumefaciens* was successfully established with resistance to hygromycin B as the selectable marker. The protocol was optimised with regards to *Agrobacterium* strains, *C. cassiicola* isolates, and other parameters. Combination of isolate CLN16 and *A. tumefaciens* strain LBA4404 carrying pCAMDsRed gave the highest number of transformants and expression of DsRed allowed observation of the fungus *in planta* using basil as tester plants. *De novo* whole genome sequence has been obtained for an isolate, with an assembled genome of 42.5 Mb. The genome does not appear to encode a cassiicolin protein toxin; however, other candidate virulence factors are currently being identified by similarity to those from other species and we will report progress towards their characterisation by targeted gene disruption. Once the candidate genes have been disrupted, their roles in pathogenesis will be determined using plant pathogenicity assays.

Poster

Combined approach to foot rot of peas

K. L. Maguire[1] and A. Charlton[2]

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Foot rot is becoming an increasing problem for peas grown in the UK. Although peas are grown in rotation one year in five there are increasing incidences of foot rot in both vining and combining peas. Vining peas are concentrated in areas close to the factories as the crop needs to be frozen within 150 minutes of harvest, and therefore land close to the factories is favoured for growing peas with an associated risk of increased incidence of foot rot in these areas. Combining peas do not have these restrictions but there is still an increasing disease problem. Foot rot is caused by *Fusarium spp.* and *Phoma medicaginis.* In recent years *Aphanomyces euteiches* has also become a contributing factor to this disease complex. In a combined approach the incidence of these pathogens is being identified and monitored as well as testing varieties for resistance.

Climate change and pest risk assessment for plant health

Mike Jeger[1], Marco Pautasso[2] and Giuseppe Stancanelli[2]

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Climate change is very likely to affect each of the steps in the invasion process of new plant health threats, although to varying degrees depending on the host–pathogen system involved. In this overview, we argue that to improve the reliability of pest risk assessment under rapidly changing climates, there is a need to make use of a diversity of methodological approaches, from the analysis of large-scale and long-term datasets to controlled experiments of interacting global change drivers. There is evidence that first reports of plant diseases have shifted towards the poles over the last few decades, as a consequence of climate warming but perhaps also of increasing sampling effort in extra-tropical countries. At the same time, methodological advances are now making it possible to simulate in glasshouses the effects on plant diseases of the combination of temperature, humidity and CO_2 concentration shifts. More effort in the involvement of plant health stakeholders in research and management of the effects of climate change on plant diseases is essential. A similar need exists as far as interdisciplinary collaboration with veterinary and public health sciences are concerned, for example in exchanging experiences about how better to communicate risk to the public. Given the increasing magnitude of the literature on plant health and climate change, we need to ensure long-term funding of early-career researchers for systematic review and modelling of climate change effects on plant pathogens and invertebrate pests.

Using systems biology modelling to reveal regulatory networks controlling plant stress responses

Jim Beynon and the PRESTA Consortium

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Global food security is the major challenge for biological sciences in the coming years. As plants cannot avoid environmental stress they have developed response networks to alleviate their impact. These networks are likely to be complex as they involve detection and signalling components as well as many feedback mechanisms to fine-tune their output to avoid extreme consequences to the plant. To complicate the issue, at any one time a plant may be exposed to multiple stresses, both biotic and abiotic, that will alter the output from the stress response networks induced. However, there is likely to be a significant overlap in the gene regulatory networks mediating response to environmental stress. We are taking a Systems Biology modelling approach to begin to elucidate the transcriptional response networks that underlie plant responses to stress. We have carried out high-resolution time course microarray analyses on plant responses to biotic (*Pseudomonas syringae, Botrytis cinerea*) and abiotic (high light and drought) stress and developmental senescence and used Variational Baysian State Space Modelling to infer transcriptional response networks. This has allowed us to define a high level network regulating responses to multiple stresses and we are validating and extending this network.

J Colhoun poster

Factors contributing to sustainable strawberry production

B. Liu, A. M. Hall, X. Jin and K. G. Davies

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In the UK strawberry production is very intensive, over the last 20 years yields have doubled and the harvest period greatly extended whilst the area used by the crop has been reduced. This rise in yield per hectare has been achieved by precision use of varieties, fertilizers, irrigation, polythene tunnels and pesticides. The challenge now is to improve long-term sustainability of production whilst maintaining yield. The most important yield threatening disease of strawberry is powdery mildew caused by *Podospheara aphanis*. The work reported here assessed the use of a silicon nutrient to reduce disease levels. The use of wild pollinators of the strawberry crop is also evaluated as a major contribution to sustainability when compared to the more normal practice of buying in pollinators.

J Colhoun poster

Functional characterization of aphid candidate effectors and their potential host targets

Camille Lenoir[1,2,3], Patricia A. Rodriguez[1,3], Maelle Jaouannet[1,3], Paul Birch[1,2,3] and Jorunn Bos[1,2,3]
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Aphids are phloem-feeding insects that, like other plant parasites, form close associations with their host plants. In recent years, aphid effector discovery strategies have led to significant conceptual advances in plant–aphid interactions research. Aphid stylets form an interface with the host plant where signals are exchanged. While feeding and probing, aphids secrete saliva, containing effector proteins, directly into the host–stylet interface. We predict that these effectors interact with host targets to manipulate plant cell processes and promote infestation. This project aims to functionally characterize aphid candidate effectors and to identify and characterize their potential host targets. We selected 5 candidate effectors from the aphid species *Myzus persicae* based on homology to predicted effectors from the pea aphid. Overexpression of GFP-fusion proteins in *Nicotiana benthamiana* showed that two effectors localised to the endoplasmic reticulum (ER), one effector localised to the nucleus, and the remaining two effectors, were detected in the cytoplasm. To identify host targets, we screened these candidate effectors against a *N. benthamiana* yeast-2-hybrid (Y2H) library. We identified several putative targets of interest, including a plant chitinase and E3 SUMO-ligase. Validation of interactions is currently in progress using co-immunoprecipitation and co-localization studies. In addition, we are currently performing functional assays with both candidate effectors and putative host targets to investigate their role in plant-aphid interactions. Understanding how aphid effectors manipulate host cell processes will provide novel insights into how we may develop durable and sustainable aphid control in economically important crops.

The effect of abiotic stress on virus infection

Lesley Torrance

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Climate change (including the occurrence of extreme weather events such as heat waves and droughts) will affect crop productivity and the incidence of pests and pathogens. Combating the negative effects of environmental change will require the development of crops with improved stress tolerance. Although there are many studies of the effects of individual stresses on plants, there is evidence that plants respond differently on simultaneous exposure to different stresses. Abiotic stresses are known to alter plant physiology and biochemistry, affecting growth and development and the predisposition of plants to infection. The response of plants to heat stress often appears to compromise disease resistance, increasing susceptibility to infection by pathogens. There is a need for a better understanding of the interactions that occur in perception and signalling pathways when plants are subject to both abiotic stress and pathogen. Identifying common regulators or heat tolerant resistance factors will assist in breeding strategies to select plant genotypes that are resilient to combined stresses. This paper will briefly review the effect of abiotic stress on virus infections and present some recent work on the effect of increased temperature on virus resistance in the potato–*Potato virus Y* (PVY) pathosystem.

Molecular events during plant–aphid interactions

Jorunn Bos

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Aphids are phloem-feeding insects that cause significant damage to economically important crops through feeding and transmission of viruses. Aphid species vary in their ability to infest different host species. Whilst most aphids are specialized to feed on one of several host species, some aphid species have a remarkably broad host range. One interesting observation is that probing of leaf tissues takes place during host and nonhost interactions, suggesting that molecular interactions and dialogue takes place. To be able to develop novel aphid control strategies it is essential we investigate the molecular basis of aphid–host and –nonhost interactions. The availability of aphid genomes and transcriptomes has already contributed to novel insights and helped reveal that aphids, like other plant parasites, secrete effectors inside their host that are involved in manipulation of host cell responses. The next step is to investigate the functions of these effectors and their host targets and understand their contribution to plant–aphid interactions. Our work shows that aphid effectors may target different cellular processes, including vesicle trafficking and protein methylation in order to promote virulence. In addition, we have used plant transcriptomics to investigate host and nonhost responses to different aphid species. Surprisingly, we found that the overall plant response during host and nonhost interactions with aphids is very similar. However, we also identified a small set of plant genes showing opposite gene expression patterns in host and nonhost interactions. Functional characterization of these genes to understand their role in plant–aphid interactions is in progress.

J Colhoun poster

Molecular and microscopic studies on the *Potato mop-top virus* – *Spongospora subterranea* interaction

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Potato mop-top virus (PMTV) is transmitted by *Spongospora subterranea* and both pathogens cause economically important diseases of potato tubers; however, the mechanism of transmission is not fully understood. The coat protein (CP) of PMTV has two gene products: CP (90% of the expressed protein) and CPRT (in which the CP stop codon is suppressed to produce a larger read-through (RT) product; approx. 10%). A natural deletion mutation in the RT domain of the CPRT protein abolishes transmission of PMTV by *S. subterranea*. Here, we investigated the subcellular localization and co-localisation of PMTV CP, $CPRT^{wt}$ and two CPRT mutants, $CPRT^{stopmut}$ (produces 100% full-length CPRT) and $CPRT^{stopRTmut}$ (produces 100% CPRT which lacks the transmissible region in the RT domain). PMTV encodes three triple gene block (TGB) proteins that are essential for cell-to-cell movement of the virus. They are part of the viral ribonucleoprotein complexes (vRNPs) that traffic through plasmodesmata, but TGB1 is also known to associate with microtubules. The interactions of the PMTV TGB1 protein with $CPRT^{stopmut}$ and $CPRT^{stopRTmut}$ proteins were investigated using bimolecular fluorescence complementation. Two distinct cytoplasmic phenotypes were observed when the proteins were expressed. PMTV TGB1 and $CPRT^{stopmut}$ were found to interact and the complex was associated with microtubules, but the TGB1 and $CPRT^{stopRTmut}$ interaction did not localize to microtubules. These results suggest that an interaction between the PMTV CPRT and TGB1 proteins which occurs on plant microtubules may play a role in the transmission of PMTV by *S. subterranea*.

J Colhoun poster

Determination of the pathogen population structure of *Pyrenopeziza brassicae*, causal agent of light leaf spot on brassicas

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Light leaf spot, caused by the fungal pathogen *Pyrenopeziza brassicae*, is currently the major disease problem in oilseed rape production in the UK. Furthermore, *P. brassicae* can also be found on vegetable brassicas such as cabbage, cauliflower and Brussels sprouts. It is still unknown if the same strains of the pathogen are able to infect both oilseed rape and vegetable brassicas. Effective control of light leaf spot is difficult to achieve. Chemical control of the disease is challenging as fungicides must be applied when the pathogen grows symptomless in plant tissue (Figueroa *et al*., 1994). Exploiting plant resistance against the pathogen could help control the disease but current commercial cultivars show poor light leaf spot resistance. The aim of the project is to identify the pathogen population structure, to determine if the same strains are able to infect oilseed rape and other brassicas, and to gain a better understanding of the plant–pathogen interactions. Therefore, isolates of *P. brassicae* are being collected from infected leaf (oilseed rape, vegetables) and bud tissue (Brussels sprouts) from nine cultivars, which have been drilled at four sites in England (Cambridgeshire, Herefordshire, Lincolnshire, Yorkshire) and one site in Scotland (Aberdeenshire). The isolates will be studied morphologically and molecularly using neutral markers to determine differences between the isolates. Certain isolates will be used for *in planta* screenings to investigate differential interactions between isolates and potential host cultivars.

P H Gregory prize speaker

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 *Zymoseptoria tritici*. 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. 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 *Z. tritici* 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.

P H Gregory prize speaker

The role of barley *mlo* genotypes and light in the infection biology of the fungus *Bipolaris sorokiniana*

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Bipolaris sorokiniana causes Spot blotch disease and has increased severely in areas that have become warmer and more humid within the last years. The fungus is a hemi-biotroph that invades the host in a symptomless manner and quickly shifts to a necrotrophic lifestyle. Phytotoxin release by the fungus leads to cell death. As a consequence, macroscopic symptoms occur on the leaf in form of necrotic spots, and necrosis development is seen as an indicator of disease severity. Mlo is a *G-protein coupled receptor* that acts as a suppressor of cell death. Barley *mlo* mutants are more susceptible to fungal pathogens with a necrotrophic lifestyle, including *B. sorokiniana*. However, the role of phytotoxins and the *mlo* mutation is not fully understood in this interaction. We investigated symptom occurrence, fungal biomass and toxin sensitivity to *B. sorokiniana* and the possible effects of light conditions in 5 different barley genotypes and their *mlo* daughter lines. Variation in symptoms and fungal biomass was mainly due to the genetic disposition and environmental effects. The *mlo* mutations contributed only in some cases to increased susceptibility, although, these lines were more toxin sensitive. When light conditions during *B. sorokiniana* infection were manipulated, no symptoms occurred on infected leaves after incubation in darkness. Surprisingly, these symptomless plants had substantially higher amount of fungal biomass. This raises the question when and how toxins and cell death are valuable and needed for fungal infection and colonization, and highlights the need for a better understanding of the biology of *B. sorokiniana*.

Poster

Potato cyst nematodes will like it warm!

Agata Kaczmarek[1], Helen Kettle[2], Katrin McKenzie[2] and Vivian Blok[1]

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Potato cyst nematodes (PCN) are persistent and economically important pests of potato with widespread distribution in the UK. Withdrawal of chemical control options is exacerbating the management of PCN multiplication and spread. An important factor in PCN multiplication is soil temperature but this relationship has not be well characterised. We have been undertaking experiments in controlled environments and in the field to examine the impact of temperature on the life cycle and population dynamics of PCN.

Average soil temperatures in potato drills differ with geographic location and the growing season. Our results indicate that both species of PCN, *Globodera rostochiensis* and *G. pallida*, are likely to increase more rapidly and in greater numbers with susceptible cultivars at sites with warmer soils. Current average soil temperatures in potato drills are below the optima for multiplication of both species. If soil temperatures increase in the future due to climate change, PCN multiplication is expected to increase further in UK conditions.

The data from the controlled environment experiments have been used to develop a model which can simulate the PCN life cycle based on local soil temperature data. This can be used to predict multiplication rates and assess the risk of multiple generations within one growing season.

J Colhoun poster

A systems approach to the control of strawberry powdery mildew

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A systems approach to the control of strawberry powdery mildew (*Podospheara aphanis*) is important, as the disease is never absent from the crop. Work reported here shows that the disease is present in the crop whether new plants are bought in from a propagator, or the plants have been in the growing medium for one or more seasons. The work also shows that control measures used in one growing season reduce the disease carry over thus reducing the initial inoculum in the following season. The work also demonstrates that the use of a late autumn fungicide spray, and a fungicide spray pre- and post-fleece and mulch use in the spring also reduces the number and maturity of overwintering chasmothecia, thus also contributing to a reduction in initial inoculum.

P H Gregory prize speaker

Effects of phytic acid content in *Arabidopsis thaliana* on resistance against *Pseudomonas syringae* pv. *tomato*

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Inositol hexa*kis*phosphate (InsP_6) was proposed as a signal in basal defence responses against pathogens (Murphy *et al.*, 2008). Decreased expression of specific genes controlling InsP_6 biosynthesis in *Arabidopsis* mutants for *AtIPK1* (*Inositol Pentakisphosphate Kinase)* and *AtIPS2* (*Inositol Phosphate Synthase 2*) but not *AtIPS1* affects the plants' susceptibility to a range of pathogens. We are manipulating InsP_6 biosynthetic pathways to investigate the role(s) of inositol polyphosphates in plant defence. As T-DNA insertion mutants for a third member of the *AtIPS* gene family, *AtIPS3*, have not been tested, we challenged *atips3* mutant plants with *Pseudomonas syringae* pv. *tomato*. Plants of both *atips3* and *atips2* mutant lines were more susceptible to bacterial infection than wild-type plants. This was true for infection with virulent and avirulent bacteria. *Atips2*, *atips3*, and *atipk1* mutant plants were not compromised in their ability to exhibit systemic acquired resistance induced by primary infection with avirulent bacteria. In wild-type plants, the PAMP flg22 induces callose deposition. In *atipk1* plants, this was compromised. However, flg22 induced the inhibition of seedling growth in both wild-type and *atipk1* plants. This suggests that FLS2-mediated recognition of flg22 in PAMP-triggered immunity is still intact in *atipk1* plants. Instead, IPK1 may be involved in regulating downstream signalling pathways in PAMP-triggered immunity, and expression of marker genes is currently being tested.

P H Gregory prize speaker

Shuffling resistance genes to protect solanaceous plants

Laura J. Stevens[1,2], Sean Chapman[2], Petra C. Boevink[2], Stefan Engelhardt[1], Xinwei Chen[2], Paul R. J. Birch[1,2] and Ingo Hein[2]

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The potato resistance protein R3a recognises the essential effector Avr3a_KI from the oomycete pathogen *Phytophthora infestans*, causing a hypersensitive response (HR) in the host which prevents further spread of infection. However, the product of the closely related virulent allele *avr3a_EM*, which is homozygous in 72% of *P. infestans* isolates in the Toluca Valley, Mexico, evades recognition and is able to cause disease on plants expressing R3a.

Gain-of-function variants of R3a (R3a*) were engineered by an iterative process of random mutagenesis and PCR shuffling. Studies with the best-performing R3a* variants in the solanaceous model host *Nicotiana benthamiana* reveal a gain-of-recognition of avr3a_EM.

Recognition of Avr3a_KI by wild-type R3a occurs in the host cytoplasm and both proteins subsequently relocalise to prevacuolar compartments (PVCs). avr3a_EM does not cause this relocalisation. Confocal microscopy has revealed that R3a* variants relocalise to PVCs upon co-infiltration with either form of Avr3a, indicating a shared mode-of-recognition between wt R3a and R3a* variants. It is hoped that a shuffled *R3a** gene, deployed with other *R* genes in potato, would confer durable resistance to late blight disease.

Poster

Temperature affects the effectiveness of *R* gene mediated resistance against *Leptosphaeria maculans* (phoma stem canker) in *Brassica napus* (oilseed rape)

Yongju Huang[1], Lucia Robado de Lope[1], Georgia Mitrousia[1], Henrik U. Stotz[1], Nicholas J. Larkan[2], Roger S. Rimmer[2] and Bruce D. L. Fitt[1]
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Phoma stem canker (*Leptosphaeria maculans*) is an economically important disease on oilseed rape (*Brassica napus*) in Europe, Australia and North America. Effective control of this disease relies on the use of two types of resistance: major resistance (*R*) gene-mediated qualitative resistance and quantitative resistance (QR). Plant–pathogen interactions are known to be affected by environmental factors, including temperature. To investigate effects of temperature on durability of *R* gene-mediated resistance to *L. maculans*, oilseed rape cultivars or breeding lines with different *R* genes in backgrounds with/without QR were inoculated at 20°C and 25°C. Cotyledons of 12-day old plants were wounded and a drop of 10µl of 10^7 spores/ml conidial suspension placed over the wound. There were differences in temperature sensitivity between the ten different *R* genes (*Rlm1, Rlm2, Rlm3, Rlm4, Rlm5, Rlm6, Rlm7, LepR1, LepR2* and *LepR3*) tested and there were differences in response to temperature for the same *R* gene in different cultivars. Background QR affected the temperature sensitivity of *R* gene-mediated resistance. To avoid the effects of background QR and investigate plant defence responses, near isogenic lines of Topas with *R* genes *Rlm4* or *LepR3* were used. Cotyledons of 12-day old plants were infiltrated with 10 µl of 10^6 spore/ml conidial suspension at 20°C and 25°C. There were differences in defence responses between *Rlm4* and *LepR3*, with *Rlm4* responding more quickly and more strongly than *LepR3* at the higher temperature. Understanding effects of temperature on interactions between hosts and pathogens will help to breed cultivars with durable, temperature-resilient resistance.

Poster

Identification and characterisation of *Rhynchosporium commune* pathogenicity factors

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Rhynchosporium commune is the causal agent of scald, one of the most destructive diseases of barley. Grain quality can also be affected leading to significant yield losses. *R. commune* populations are highly diverse and can change rapidly overcoming barley resistance and fungicides control and thus leading to infection. Little is known about *R. commune* pathogenicity factors. At the moment is recognized the action of secreted effector proteins released to suppress host immune system. A small family of necrosis inducing peptides (NIPs) have been identified; their infiltration into barley and some dicotyledonous leaves (*Rohe et al*., *1995*) caused necrosis resembling the disease symptoms (Wevelsiep *et al*., 1991). The principal objective of the project is the understanding of molecules released by pathogen during the interaction. Analysis of transcripts produced by *R. commune* during infection of barley plants is a valuable resource for identification of pathogenicity factors. At the same time gene knockout can be used to elucidate gene function.

INTERMISSION

Posters

6.00 p.m. BSPP Annual General Meeting

7.00 p.m. Dinner

Ceilidh
Dance the night away!

Phytophthora infestans effector PiaAVR2 targets StBSL1 to activate the brassinosteroid pathway

Dionne Turnbull[1,2,4], Susan Breen[1,2,3], Shaista Naqvi[1,4], Miles R. Armstrong[2], Stefan Engelhardt[2], Frédéric Brunner[5], Paul R. J. Birch[1,2] and Eleanor M. Gilroy[1]

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Recent work by several groups has highlighted that signalling following perception of the plant growth promoting hormone Brassinosteroid (BR), or mutants with activated BR signalling, antagonises PAMP-triggered Immunity (PTI) in *Arabidopsis*. We have uncovered a mechanism by which the potato late blight pathogen *Phytophthora infestans* antagonises PTI through activation of the BR pathway. Previous work has shown that PiAVR2 is an RXLR-EER effector from *P. infestans* that is recognised in some potato cultivars by particular members of the R2-like NB-LRR family. We have shown that PiAVR2 interacts with the potato ortholog of the *Arabidopsis* BRI1 SUPPRESSOR 1 (BSU1)-LIKE 1 (BSL1). BSL1 belongs to a family of kelch repeat containing serine/threonine phosphatases that function in the BR pathway, although the link between BSLs and BR signalling has been mostly built on experiments in *Arabidopsis* using BSU1 which is not present in potato. Our data shows that both the presence and activity of BSL1 are important for recognition of PiAVR2 by R2-like NB-LRRs. We will go on to describe our on-going research to characterise both the role of PiAVR2 and BSL1 in the crosstalk between the BR pathway and PTI in potato and *Nicotiana benthamiana*. We provide evidence that PiAVR2 manipulates plant defence by activating the BR pathway through modification of BSL1 and that both BSL1 and the BR pathway are important virulence targets for *P. infestans* to promote disease progression.

Poster

Identifying components of PAMP-triggered immunity in brassicas

Bethan M. Edmunds[1,2], Simon R. Lloyd[1], Henk-Jan Schoonbeek[1], Cyril Zipfel[2] and Christopher J. Ridout[1]

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PTI (PAMP-triggered immunity) contributes to quantitative disease resistance in crops; natural phenotypic variation in PAMP (pathogen-associated molecular pattern) responsiveness can be exploited to extend durable background resistance to varieties with or without major *R* genes through breeding. The identification of novel components of PTI is therefore essential. A significant and reproducible quantitative trait locus (QTL) controlling the flagellin-triggered oxidative burst in *Brassica oleracea* A12 × Green Duke (GD) mapping population was found on chromosome 9. Transcriptomic analysis of the parental lines identified non-synonymous SNPs, and the addition of KASPar markers enabled fine-mapping of the region. The interval contains 393 genes of which one is annotated as *CYCLIC NUCLEOTIDE-GATED ION CHANNEL 2* (*CNGC2*). A12 × GD progeny demonstrating low flg22-triggered ROS (reactive oxygen species) have the GD allele at the locus in which *CNGC2* resides, including AG1012. A reciprocal association between Ca^{2+} influx and ROS production upon PAMP recognition is being forged in the literature. *Arabidopsis thaliana* plants which are homozygous for the recessive *cngc2* mutation retain gene-for-gene resistance through elevated salicylic acid (SA) and ROS but fail to produce the hypersensitive response (HR) to an avirulent pathogen. We will characterise *CNGC2* and *CNGC4* in PAMP responsiveness using knock-out mutants in *Arabidopsis* and by overexpressing *CNGC2* in AG1012; all lines are co-transformed with R-GECO and YC3.6 reporters to establish the effect on Ca^{2+} influx. The mapping population will be supplemented with further recombinants in the QTL to provide better resolution to the interval and to narrow the candidate gene list.

Poster

Emerging diseases and symptoms detected in UK gardens

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The Royal Horticultural Society (RHS) provides a free advice and diagnostic service to its UK members. During 2013 alone, the advisory service dealt with over 57,000 gardening related questions, with more than 5% of enquiries requiring the expertise of a Plant Pathologist. Where diagnosis was possible, many common plant pathogenic genera were identified including *Armillaria, Erysiphe, Phytophthora* and *Puccinia*.

It has been estimated that there are over 22.5 million gardens in the UK, accounting for 4% of the UK's land surface area, and these represent an important pathway from cultivated habitats to natural ecosystems. The RHS is in a unique position, receiving diseased plants from these habitats throughout the UK. Detection of new pathogens to the UK, such as *Erysiphe deutziae*, new records of uncommon pathogens already in the UK, such as *Gymnosporangium sabinae*, and host shifts have all been recorded. The importance of studying plant pathogens in gardens will be presented using examples received through the advisory service.

Sub-nuclear structures provide new genetic sources of plant resistance to biotic and abiotic stresses

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The nucleolus and Cajal bodies (CBs) are prominent sub-nuclear domains involved in crucial aspects of cell function such as RNA metabolism, the cell cycle and aging. These compartments are a common destination for proteins encoded by different plant viruses, although the mechanisms behind this are poorly elucidated. However, a few studies have uncovered diverse processes by which viruses can hijack host nuclear proteins to permit pathogenesis. Indeed, we have shown that the ability of the umbraviral movement protein to mediate systemic infection strictly depends on its interaction with CBs, the nucleolus and the major nucleolar protein, fibrillarin. We have also found that a key "signature" component of CBs, coilin, affects a variety of interactions between host plants and viruses. Moreover, the effects of coilin on these interactions are manifested differently: coilin contributes to plant defence against tobacco rattle virus, tomato black ring virus, barley stripe mosaic virus and tomato golden mosaic virus. In contrast, with potato virus Y and turnip vein clearing virus, coilin serves to increase virus pathogenicity. Thus fibrillarin and coilin have novel, unexpected natural functions that may be recruited or subverted by plant viruses for their own needs or, in contrast, are involved in plant defence mechanisms that suppress host susceptibility to the viruses. Our preliminary results also suggest a role of both fibrillarin and coilin in the signal transduction mechanisms in response to other pathogens and environmental cues. Altogether, these findings place sub-nuclear structures to the frontline of plant defence against biotic and abiotic stresses.

Managing risk for smallholder farmers in an uncertain future

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The Syngenta Foundation is a non-profit organization established by Syngenta under Swiss law. The Foundation can access company expertise, but is legally independent and has its own board. We focus on "pre-commercial farmers"; Syngenta works primarily with commercial growers. The Foundation works with partners in developing countries and emerging markets. Our aim is to help small farmers become more professional growers. We do this by extending science-based know-how, facilitating access to quality inputs, and linking smallholders to markets in profitable ways. This adds value for rural communities, and sustainably improves food security.

The Syngenta Foundation believes that managing risk is the key to allow smallholder farmers to invest in their own businesses in the face of uncertainty, which now must include climate uncertainty. Award winning micro-insurance products allow seeds and other inputs to be insured against drought or even excess rain. Breeding for heat tolerance and resistance to emerging diseases, like maize lethal necrosis, provide new tools and products to protect farmers' livelihoods. Linking conservation agriculture techniques to bio-carbon credit schemes might provide new sources of income for sustainable land management.

Poster

Artificial evolution of the potato resistance gene *R3a* to detect the virulent form of AVR3a

Sean Chapman[1], Laura Stevens[1], Petra Boevink[1], Stefan Engelhardt[1], Colin Alexander[2], Nicolas Champouret[3], Paul Birch[1] and Ingo Hein[1]

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Engineering resistance genes to gain effector recognition is emerging as an important step in attaining broad, durable resistance. We have engineered the potato resistance gene *R3a* to recognize the virulent AVR3a^{EM} effector form of *Phytophthora infestans*. Random mutagenesis, gene shuffling and site directed mutagenesis were performed on the leucine-rich repeat (LRR) domain of R3a in an iterative process to identify R3a* variants that recognized AVR3a^{EM}. In transient assays the programmed cell death following recognition was enhanced, approximating that induced by recognition of the avirulent AVR3a^{KI} effector by wild-type R3a. Potato plants containing R3a* transgenes gained resistance to AVR3a^{KI} homozygous strains, but disappointingly not AVR3a^{EM} homozygous strains. The same resistant and susceptible phenotypes following challenges with late blight strains were found in transient assays when the R3a* genes were expressed from the R3a promoter. However, transient assays employing the strong 35S promoter demonstrated relocalization of both R3a* proteins and AVR3a^{EM} from the cytoplasm to prevacuolar compartments, mimicking the events in recognition of AVR3a^{KI} by wild-type R3a. Similarly, in transient assays where R3a* expression was driven by the 35S promoter there was partial resistance to AVR3a^{EM} homozygous strains. A modified R3a* form carrying an additional sensitizing amino acid change outside the LRR domain showed complete resistance to AVR3a^{EM} homozygous strains when transiently expressed from the 35S promoter. The utility of this modified R3a* form to confer broad spectrum resistance when expressed from its own promoter is currently being tested in transient assays prior to the generation of transgenic potato plants.

J Colhoun poster

Investigating secondary metabolism in *Zymoseptoria tritici*

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One of the most serious fungal diseases of wheat is septoria tritici blotch caused by *Zymoseptoria tritici*. This disease is typified by an asymptomatic latent phase, followed by a rapid onset of host cell necrosis. This sudden cell death has been speculated to be a result of toxins made by the fungus. Fungally derived toxins are often secondary metabolites, with the main classes being polyketides (PKs), non-ribosomal peptides (NRPs) and terpenes. Genome analysis of identified 9 PKS and 2 PKS-NRPS pathways in addition to the NRPS responsible for siderophore biosynthesis. Promoter::GFP fusions were made for all of these candidate genes and their expression followed though the disease cycle. However, only pPKS3 gave any apparent GFP expression. Disruption of PKS3 did not generate any mutant phenotype. In fungi, PPTase is needed not only for the PKS and NRPS activation, but also both lysine and siderophore synthesis. The *Z. tritici* aminoadipate reductase (Lys2) gene was disrupted and the *ZtΔlys2* mutant was auxotrophic to lysine. Pathogenicity testing of ZtΔlys2 showed only mild chlorosis, severely reduced pycnidial and spore numbers compared with a wildtype. Ornithine N-hydroxylase (SidA) was disrupted to prevent hydroxamate siderophore synthesis. The resulting *ZtΔSidA* mutant was auxotrophic for iron, more sensitive to the oxidative stress and showed slower (but not abolished) plant infectivity. Therefore, whilst pantetheine-based secondary metabolism is essential to *Z. tritici*, we cannot determine whether this is solely due to the lysine and iron effects, or whether there may also be secondary metabolism effects.

Changes in plant–pest dynamics of potato systems in a warming Andes

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Increasing temperatures appear to be one of the more certain consequences of climate change in the Andean highlands. Upward migration of pests and pathogens, as well as crop adaptation to higher altitudes could lead to agricultural encroachment on fragile *páramo* and *puna* ecosystems, which are crucial to local water supplies. Furthermore, global warming will probably mean that wild genetic resources in the Andean highlands will be exposed to new pest and disease threats. Inter-disciplinary and systems research is needed for sustainable adaptation. Farmers once used pest- and pathogen-free highlands to grow susceptible varieties or reduce seed lots of pathogen loads (e.g. cleaning potato seed), but these pathogen-scarce refugia may soon disappear. Alternative strategies include adoption of robust varieties with multiple resistances to upward-migrating pests and diseases, better IPM practices and increased farmer capacity to implement these practices. Using potato as an example, durable resistance to *Phytophthora infestans* and the major potato viruses (PVY and PLRV) and effective IPM for the Andean weevil (*Premnotrypes* spp.) and potato tuber moths (multiple species) appear to be a minimum requirement for future Andean potato production, whereas the upward spread of other biotic threats (e.g. of white flies and leafminers) is predicted through phenology modelling and GIS risk mapping. As IPM will require innovative control methods including biological control and effective rotation, new cropping systems involving marketable and/or nutritious alternative crops must be devised with full stakeholder involvement, as well as a basic scientific understanding of the anticipated effects of climate change on crop physiology.

A perspective on coffee diseases: coffee wilt disease – a case study

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Climate change has the potential to have an adverse or positive effect on plant health by aiding or restricting the activity and spread of pathogens as ecosystems adapt to change in temperature and precipitation. A recent multidisciplinary study investigated the spread of the coffee wilt disease (CWD) pathogen, *Fusarium xylarioides*, a taxon which has been shown to contain several lineages and which caused widespread destruction of the coffee industry in the Central African Republic in the 1940s. Despite eradication programmes instigated for subsequent outbreaks in other parts of West and Central Africa during the 20th century, the disease continues to cause problems in the region. Analysis, by a range of techniques, of *F. xylarioides* strains obtained from coffee trees affected by CWD in Africa, revealed correlations between genetic profile, host plant specificity and pathogen distribution. The results of this work are presented, together with some preliminary views as to potential phylogenetic events that may be linked to Biological Species Groups (BSG) as supported by rDNA intergenic spacer sequence analysis. The implications of the findings for the future cultivation of coffee and the distribution and impact of coffee diseases such as CWD will be discussed.

J Colhoun poster

Epidemiology and management of strawberry rot complex

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Postharvest strawberry losses are largely caused by *Botrytis cinerea*, *Mucor* spp. and *Rhizopus* spp. The former infection causes grey mould disease in strawberry fruits while *Mucor* and *Rhizopus* infection leads to soft rot disease. Recently in the UK, the incidence of strawberry soft rot caused by *Mucor* spp. and *Rhizopus* spp. is on the increase probably due to the reduction of fungicide usage. Information on the epidemiology and management of *Botrytis* is well known and documented but there is very little information on strawberry soft rot caused by *Mucor* spp. and *Rhizopus* spp. The real identity of the species in both genera responsible for causing soft rot in strawberry is also not known. The aim and objective of project is to understand the epidemiology of strawberry rot complex caused by *Mucor* spp. and *Rhizopus* spp., and to develop measures to reduce the amount of losses due to these fungi. Specific research areas include:

- develop methods for pathogen detection and quantification
- identify infection time
- assess the effects of biotic and abiotic factors on disease development
- understand the interaction among pathogens in causing fruit rot
- develop pre-harvest and postharvest strategies to manage the rot complex and reduce disease incidence

Poster

Combining disease resistance with biological control to reduce severity of spot blotch disease of barley

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Spot blotch is one of the most important diseases of barley (*Hordeum vulgare*) worldwide. The overall aim of this study was to investigate the potential of biological control in combination with disease resistance to control spot blotch. Spot blotch resistance was tested under greenhouse conditions with seedlings of four Libyan cultivars (ACSAD, Nibola, Rehan, and Wadi Utbah) and two UK cultivars (Gaelic and Pastoral). None of these was highly resistant, but Nibola was the most resistant. The ability of the organisms in three commercial biological control products, *Trichoderma harzianum* T-22 (Trianum), *Streptomyces lydicus* WYEC 108 (Actinovate) and *Bacillus subtilis* QST 713 (Serenade), to control spot blotch individually and in combination was investigated under greenhouse conditions with all six cultivars. *T. harzianum* T-22 was the most effective agent, and there was little benefit from using combinations of agents. With *T. harzianum* T-22, foliar application (before or at the same time as inoculation with the pathogen), soil treatment, and seed treatment reduced mean disease severity significantly, and effects for individual cultivars were mostly significant. Disease severity was lowest when *T. harzianum* T-22 was applied to the most resistant cultivar, Nibola. We are currently investigating the interaction between the pathogen, the biological control agent, and the host plant.

Challenges for disease control now and in future: a research perspective for plant pathogen control under changing environmental conditions

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Plant pathogens are highly dynamic and adaptable. Diversity is very high and requires a range of control measures. To discover and develop new chemicals, biologicals or traits, screen cascades must be well-established and reliable with low variability over many years. The definition of the pathogen spectra is made long before a product is launched to the market and needs to be stable. The potential changes during the 10 years of development phase are difficult to forecast, but could significantly affect product concepts. To allow comparability of data and reduce variability the strains of each pathogen used are not changed. Changes in range of species or within populations occur in nature, due to long distance migration, climate, fungicide resistance, host selection, host switch, geographical expansion of host, changes in cropping practices and introduction by trade or other human activity. Recent examples of changes of pathogen spectrum include soya rust in Brazil, Panama disease in banana and head blight of wheat. The forecast for disease spectrum depends on the time scale applied; however, in the mid-term, it is assumed that many current species will remain important (*Zymoseptoria*, *Phakopsora*, *Alternaria*, cereals rusts, downy mildews, etc). The ecological niche of a given pathogen is often not clear. In conclusion, screening cascades need to be flexible enough to be able to incorporate new pathogens and biotypes over the longer term. The fungal spectrum potentially infecting agronomically important crops needs to be monitored and the environmental and pathogenicity characteristics should fundamentally be better understood.

Is *Piriformospora indica* a magic fungus?

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Piriformospora indica is a mycorrhizal-like fungus with a broad-host-range, belonging to the order Sebacinales. Like mycorrhiza, *P. indica* has plant growth promoting effects; in contrast, it can be cultured axenically. *P. indica* assists in nutrient acquisition, increases resistance/tolerance to biotic/abiotic stresses. This makes it a promising candidate for biological control of plant diseases.

Fusarium crown rot (FCR) is a devastating disease of wheat in most part of the world. There is no fully effective control strategy available. Wheat seedlings were inoculated with UK isolates of *F. culmorum, F. graminearum* and/or *P. indica* under simulated UK autumn conditions in CE chamber. The amount of *Fusarium* DNA in roots grew rapidly in *Fusarium*-inoculated alone with visible brown symptoms. In pots co-inoculated with *P. indica, Fusarium* DNA was reduced with no visible symptoms. These results suggest that *P. indica* can protect wheat seedlings from FCR damage. This and effect on Fusarium Head Blight are being tested outdoors in the 2013–14 growing season. The effect of *P. indica* on other soil microorganisms was tested by PCR-denaturing gradient gel electrophoresis. Wheat seedlings growing in two soil types were inoculated with *P. indica*. Root and soil were collected at 2, 4, 6 and 8 weeks after inoculation. Results will be discussed. *P. indica* viability under UK winter condition was tested. Four different soil types were inoculated with *P. indica*. Soil samples were collected after winter for PCR/RT-PCR. *P. indica* was still alive in the soil in the absence of any plants after 4 months.

A systems approach to plant pathology

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Plant pathology is at the crossroads of a new frontier in science aimed at increasing agricultural productivity and reducing post-harvest losses through interdisciplinary collaborations to meet the future needs of a growing world population in a sustainable manner. This presentation will draw on the inherent interdisciplinarity of plant pathology through a systems approach. The American Phytopathological Society (APS) recently launched the Phytobiome Initiative as a comprehensive endeavor to connect our discipline to the worldwide community of plant scientists. This integrated systems approach to science will expand our knowledge of how microbial communities affect plant health by assessing community composition, function, and activities of all organisms in the plant biome. A successful Phytobiome effort requires fundamental and applied research accomplished through inter- and multidisciplinary collaborations with global partners in both the public and private sectors. A key to unlocking the mysteries of community composition is access to a robust system of microbial germplasm collections. Microbial collections are needed to solve a myriad of practical challenges in agricultural systems. They play diverse and critical roles in understanding plant resistance to diseases and the effects of climate change. Validated microbe reference strains, securely maintained in microbial genebanks, are essential for understanding global diversity and enable the metagenomic analyses needed to translate plant–microbe–environmental interactions. A overview of the framework to build and link a US system of microbial germplasm repositories to the worldwide community of scientists will be presented within the context of an integrated systems approach to the Phytobiome.