2013 HGCA PhD Symposium

Abstracts
# AGENDA

HGCA PhD Symposium 15th May 2013
Gateway Building, Sutton Bonington Campus, The University of Nottingham

## 10h30 ARRIVAL AND COFFEE

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<td>11h10</td>
<td>3656: Insights into the defence of honey bees against insecticides</td>
<td>Selcan Alptekin</td>
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<td>3777: Exploring the genetic and mechanistic basis of resistance to Take-all disease in wheat</td>
<td>Sarah-Jane Osborne</td>
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<td>11h55</td>
<td>Communication and Knowledge Transfer</td>
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<td><strong>Poster Presentation Slides (5 mins each)</strong></td>
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### LUNCH 12h50 TO 14h00

**POSTERS FOR DISCUSSION OVER LUNCH**

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<td>3757: Competitive crop cultivars: optimizing yield and sustainable weed suppression</td>
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<td>3690: Improved fermentation in wheat straw</td>
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<td>14h15</td>
<td>3741: Bioenergy from wheat straw</td>
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<td>14h45</td>
<td>“The Appliance of Science on the Farm”</td>
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## 15h30 SYMPOSIUM CLOSE AND DEPART

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The Problem
Insecticide synergists can often be used to increase efficacy of insecticides against resistant insects. Perhaps the best known synergist is piperonyl butoxide (PBO) which inhibits both major metabolic enzyme systems (P450s and esterases) responsible for conferring resistance. It would be beneficial to develop synergists which control pests but not affect beneficial insects.

Project Aims
To elucidate fundamental PBO-P450 interactions; to increase the control of pests without affecting beneficial insects (e.g. honeybees).

Benefits to the Industry
This project may deliver greater control of pests using less insecticide. This could reduce the cost of pest control and the risk of environmental damage.
Insights into the Induced Defence of Honey Bees Against Neonicotinoids

Selcan Alptekin\textsuperscript{1, 2}, Chris Bass\textsuperscript{1}, Lin Field\textsuperscript{1}, Mark J. Paine\textsuperscript{2}, Miriam Daniels\textsuperscript{3}, Caroline Nicholls\textsuperscript{4} And Graham D. Moores\textsuperscript{5}

1. Rothamsted Research, 2. Liverpool School of Tropical Medicine, 3. Syngenta, Jealott’s Hill, 4. HGCA, 5. Apreslabs Ltd

The current concern regarding the adverse effects of neonicotinoids on honey bee health is resulting in many studies that investigate the effects of this class of compounds on economically important pollinators. Due to their positive impact on crop protection - low toxicity to mammals, birds and fish, systemic control on plant-sucking insect pests (aphids, whiteflies, thrips, some coleopteran and lepidopteran), selective toxicity- neonicotinoids became the preferred new generation of synthetic insecticide [1]. It is vital to understand the effects of neonicotinoids on honey bees to gain advantages from these innovative chemicals with regards controlling pest species safely and effectively.

This study focuses on which mechanism(s) contribute to the defence of bees against neonicotinoids. It is known that neonicotinoids can be metabolised by certain cytochrome P450 monooxygenases, heme proteins that contribute to insecticide metabolism in many organisms. Indeed, neonicotinoid resistance is reported to be most commonly mediated by P450 detoxification [2]. Although honey bees have a reduced P450 gene number (46 P450s) compared to other insect genomes, it is not known whether this results in a lower pesticide detoxification activity [3].

To better understand the detoxification function and response against xenobiotics of specific P450s in honey bee, induction experiments (feeding bees low (non-lethal) concentrations of insecticide), bioassays and microarray analyses were used to identify inducible P450s following specific insecticide exposure.

RD-2012-3777 Exploring the genetic and mechanistic basis of resistance to Take-all disease in wheat

The Problem
Take-all, caused by the fungus *Gaemmannomyces graminis* var tritici, is one of the most damaging diseases of wheat and barley in the UK and elsewhere. This soil-borne fungus attacks cereal roots causing stunted plants, premature senescence, white heads and in severely infected fields, severe loss of yield. Typically, losses of between 1 to 3 tonnes / hectare are experienced by farmers. The disease is most prevalent in short rotations, when consecutive wheat crops are grown in the 2nd and 3rd rotation positions or in 1st wheat crops when there has been poor control of grass weeds and/or cereal volunteers in the previous non-cereal crop. The disease is most prevalent in wet soils. However in dry seasons, even slight to moderate Take-all infection weakens the plant’s root ability to penetrate the soil and, as a consequence, significant grain yield losses can occur. Global research over the past thirty years has failed to identify any good sources of resistance in hexaploid wheat germplasm (*Triticum aestivum*) and despite the use of chemical, biological and cultural control methods the Take-all fungus is still one of the most difficult pathogens of wheat to control.

Project Aim
To characterize further wheat germplasm which can be used to improve the resistance of hexaploid wheat crops to Take-all through conventional breeding and to evaluate the use of *in situ* soil moisture probes to monitor for varietal differences in maintaining root function in a high Take-all risk situation

Benefits to the Industry
The risk of wheat crops becoming moderately or severely infected with Take-all disease is always on the mind of farmers, estates managers, crop agronomists and crop consultants as they devise high economic return short arable cropping sequences involving wheat. If the industry could be confident that a seed-based genetic solution to control Take-all disease is likely to become available, then this will provide novel cropping options and also increase the overall profitability of the UK wheat crop. The economic advantages from this research project are likely to occur when wheat crops are routinely grown in the 2nd rotational position or for 1st wheat crops where grass weeds are difficult to control effectively for various reasons. Maintenance of a healthy, Take-all free plant root system, will maximize the use of the fertilizers applied to wheat crops.
Exploring the genetic and mechanistic basis of resistance to Take-all disease in wheat

Sarah-Jane Osborne, Vanessa McMillan, Richard Whalley, John Foulkes and Kim Hammond-Kosack

Plant Biology and Crop Science, Rothamsted Research, Harpenden, Hertfordshire, AL5 2JQ, UK.

Take-all, caused by the fungus *Gaeumannomyces graminis* var. *tritici* (*Ggt*), is a root pathogen that devastates cereal crops worldwide. There is no form of genetic control for take-all disease available to farmers; therefore current methods rely on crop rotation and the use of partially effective chemical seed dressings. Field trials at Rothamsted Research have recently indicated promising differences between both hexaploid and diploid genotypes in their susceptibility to *Ggt* infection. Characterisation of wheat germplasm which possess a level of resistance to take-all in field trials will enable exploration of the genetic basis of resistance. Previous trials have revealed that *Triticum monococcum* (*Tm*) accession MDR031 has a level of resistance to *Ggt* infection, whilst *Tm* accession MDR043 has been found to be comparable to the highly susceptible hexaploid wheat cultivar Hereward. A preliminary pot test also shows a trend for lower take-all infection for MDR031. However, this difference was quite small at the seedling stage in the pot test compared to adult plant resistance displayed in the field. Further work is required to explore the seedling pot test as a screen for resistance and to deploy PCR based methods to quantify the changes in *Ggt* fungal biomass over the infection time course. *Magnaporthe oryzae*, a rice pathogen related to *Ggt*, could be utilised as a surrogate species in order to expand our knowledge on the cellular aspects of the resistance phenotypes observed previously. During this PhD project, field trials with mapping populations generated by crossing resistant and susceptible *Tm* genotypes will be evaluated. In addition, field experiments will be done to explore the susceptibility of the roots of different wheat genotypes to another root dwelling fungus, namely *Phialophora* species, that is potentially a *Ggt* antagonist.
RD-2010-3730 Value of resistance genes for controlling Septoria tritici in high-yielding wheat varieties

The Problem
Despite recent success in eliminating highly susceptible varieties, Septoria tritici continues to be the major foliar disease of wheat in the UK. It is important for UK farmers to be able to grow wheat varieties which produce high yields even if the options for chemical disease control are greatly restricted. The data imply that some Septoria resistance genes are associated with reduced yield, thus selection for increased yield from 1980 to 2000 inhibited selection for Septoria resistance.

Project aims
Genes which improve resistance to Septoria with no adverse impact on yield are of great value to wheat breeders and thus to farmers. This project will help identify genes that provide durable Septoria resistance without a yield penalty, ultimately providing farmers in the UK with wheat varieties which combine good resistance to Septoria with high yield and lower requirements for fungicide applications.

Benefits to the industry
New EU regulations will significantly restrict the availability of fungicides from 2014, intensifying from 2019. The economic viability of UK farming and food security both in the UK and in our export markets depends on being able to maintain efficient production of wheat, so it is important for UK farmers to be able to grow wheat varieties which produce high yields even if the options for chemical disease control are greatly restricted. This project will contribute to the long-term improvement in the level of resistance to Septoria in wheat varieties while minimising undesired side-effects of disease resistance.
Escaping the trade-off between yield and Septoria tritici blotch

Christopher Judge and James K.M. Brown

Crop Genetics, John Innes Centre, Norwich, NR4 7UH

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 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. The different rate of senescence has been shown in both adult plants and seedlings. 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.
**RD-2011-3757 Competitive crop cultivars: optimising yield and sustainable weed suppression**

**The Problem**
The loss of active ingredients arising from new EU regulation (EC 1107/2009), the increasing threat of herbicide resistance and the lack of new herbicide modes of action has created a perfect storm for weed control in the UK. Particularly for black-grass, the most economically important weed in UK wheat, there is an unsustainable reliance on a small number of active ingredients. Without the development of more sustainable weed control strategies, the future profitability of cereal production in the UK is under serious threat.

**Project Aims**
To exploit the natural variability in the suppressive ability of cereal cultivars to support integrated weed management strategies in a way that doesn't compromise weed free yield.

**Benefits to the Industry**
The combination of the database on eco-physiological traits of the varieties on the recommended list and the simulation model will result in two major deliverables to the industry:

1. Development of management guidelines on the optimal use of cultivars in sustainable weed management in combination with other cultural control options, including a cost benefit analysis of different combinations of cultural and chemical control options.

2. A practical, robust system for indexing new cereal cultivars, even before they are commercially released, in terms of their relative ability to suppress weeds on the basis of morphological traits that can be measured simply and non-destructively.
Identifying the traits in cereals that confer greater suppressive ability against *Alopecurus myosuroides* (Huds.)

I. K. S. Andrew¹, J. Storkey¹, D. Sparkes².

¹Rothamsted Research, Department of Agroecology, Harpenden, Hertfordshire, United Kingdom AL5 2JQ, ²University of Nottingham, Sutton Bonington Campus, Sutton Bonington, Leicestershire LE12 5RD.

Herbicide resistance is increasing, no new modes of action are available and there is public pressure to reduce agriculture inputs. Many cultural control methods may be utilised to manage weeds. Cereal cultivars have been demonstrated to differ in their ability to compete with weeds, but this has seen limited application in commercial agriculture. The aim of this project is to establish which cereal traits contribute to the suppression of *Alopecurus myosuroides*, and if there is a yield penalty imposed by these traits. Fifteen cultivars of wheat, two barley cultivars and one oat cultivar were assessed for their ability to suppress *A. myosuroides*. These cultivars were grown in containers alongside *A. myosuroides* at Rothamsted Research, UK, and *A. myosuroides* seed return and biomass were measured. Ecophysiological traits of the crop during the first six weeks of growth were quantified through destructive sampling. Height, tiller number and height/width ratio were measured throughout the growing season, and flag leaf measurements taken during flowering. Grain weight per 1000 was measured. Two-sided correlations were used to search for relationships between cultivar traits and *A. myosuroides* seed return and biomass. The study has revealed traits that may be used to develop a protocol to quickly and easily rank cultivars on their suppressive ability, such as early height and flag leaf length. Further work is required to establish if the relationships observed in this experiment exist in the field, and are consistent across seasons.
The nutritional value for poultry of biofuel co-products

The Problem
Distillers dried grain and solubles (DDGS) are a by-product from distilleries, breweries and biofuel production with value as animal feed. However, the high fibre content in the residual grain means its feed value is currently restricted to ruminants. There is considerable data on the nutritional value of maize DDGS, but very little on wheat DDGS, particularly from modern biofuel plants. From research with maize DDGS, it is clear that the availability of amino acids, especially lysine, is influenced by processing.

This project will involve investigating the nutritional content and value of co-products for poultry and processing methods (which will include the use of enzymes for improving the material).

Project Aims
To determine and improve the nutritional value of wheat DDGS from bio-fuel production in the UK and develop recommendations for its use in poultry diets.

Benefits to the Industry
Detailed information on the various co-products from the biofuel industry as well as industrial treatments of them should enhance the value of the co-products to the producer, and allow the poultry industry to judiciously design diets with the relevant co-products. This will allow a cost effective use of co-products in the diets of poultry.
Utilisable energy content, apparent and standardised amino acids digestibility and true phosphorus utilisation of wheat-DDGS for broilers and turkeys

Adebiyi, A. and O. Olukosi
Avian Science Research Centre, SRUC, Auchincruive, Ayr, KA6 5HW

The metabolisable energy content (AME and AMEn), the true ileal or total tract utilisation of P and the apparent- or standardised ileal amino acids digestibility (AIAAD and SIAAD, respectively) of wheat-DDGS with or without exogenous enzymes were determined for broilers and turkeys using 6 experiments. Three levels of wheat-DDGS (0, 300 or 600 g/kg of diet) and 2 levels of a combination of xylanase, amylase and protease (XAP) (0 or 0.25 g/kg) were used to determine energy utilization, 3 levels of wheat-DDGS (200, 400 or 600 g/kg of diet) and 2 levels of phytase (0 or 0.25 g/kg) were used to determine P utilisation, whereas SIAAD was determined using a nitrogen-free diet without or with supplemental protease and a diet containing wheat-DDGS as the source of AA without or with 0.25 g/kg of protease. Dietary treatments were arranged in a randomised complete block design, replicated 7 times and fed for 7 d (ME), 5 d (P) or 3 d (AIAAD and SIAAD). For broilers, AME values (MJ/kg) of wheat-DDGS without or with XAP were 15 or 15.5, respectively whereas AMEn was 14 and 14.5, respectively. Corresponding AME values for turkeys were 14 or 14.9 whereas AMEn was 13 or 13.8, respectively. For broilers, AIAAD ranged from 35 to 75% whereas SIAAD ranged from 51 to 84%. Supplemental protease improved ($P < 0.05$) the SIAAD of Arg, Leu, Phe, Met, Val and Pro. For turkeys, AIAAD was lower than 50% for all AA except for Glu (70%) and Pro (81%) whereas SIAAD ranged from 41 to 89%. Except for Cys and Pro, protease improved ($P < 0.05$) the AIAAD and SIAAD of all other AA. For broilers, true P utilization of wheat-DDGS was 93.6% at the terminal ileum or 92% at the total tract. Respective values for turkeys were 76 or 71%. It was concluded that wheat-DDGS is a valuable source of dietary energy and P for broilers and turkeys and exogenous enzymes can further improve the dietary value.
RD-2009-3690 - Improved fermentation of wheat straw

The Problem
Wheat straw represents a potential source of biomass for the production of liquid transportation fuels to replace petrol. However, wheat needs to be optimised for several key parameters to make this process more effective.

Project Aims
The aim of the project is to identify traits in winter wheat germplasm that determine enhanced straw fermentation.

Benefits to the Industry
If wheat straw can be optimised for fermentation and the production of bioethanol, without compromising grain yield or quality, then ‘dual purpose’ wheat crops can be grown, with the grain used for food or feed and the straw for biofuel production. This would provide a new income stream for growers and alleviate the competition for arable land between crops grown for fuel or food.
Improved Wheat Straw for Biofuel Production

Johar Roy, Gregory Tucker and Debbie Sparkes

University of Nottingham, School of Biosciences, Sutton Bonington Campus, BBSRC Sustainable Bioenergy Centre (LACE Program), Loughborough, Leicestershire, LE12 5RD, UK

Production of first generation liquid biofuels from feedstocks such as wheat and maize grains has been criticised due to competition for agricultural land between crops grown for food or fuel. An alternative is to produce liquid biofuels from non-food crops like miscanthus and agricultural by-products such as cereal straw. These second generation biofuel crops are rich in cellulose but, the main problem with these products is that cellulose is very well protected by hemicellulose and lignin and is not easily available for enzymatic digestion (Saha et al., 2005).

Wheat straw represents a potential source of biomass for the production of liquid transportation fuels to replace petrol as 6.3 million tonnes of wheat straw were generated in the UK as agricultural by-products in 2007 (Copeland and Turley, 2008). Current commercial cultivars of wheat have been selected according to grain yield and quality, not straw yield or suitability for bioethanol production. There is a lack of data on the relative straw yield of different cultivars and whether there is variation in digestibility of straw for bioethanol production. Wheat cultivars vary in their straw strength and hence lodging susceptibility, which may be expected to increase or decrease with straw digestibility (Jensen and Magid, 2011). It will be important to ascertain whether there is a relationship between straw strength (lodging resistance) and straw digestibility for bioethanol production. This work investigates the variation in key parameters that would be important to identify a wheat ideotype for dual purpose use: grain for food and straw for fuel.

A field experiment was established in October 2009, at the University of Nottingham to evaluate 40 cultivars of bread wheat in terms of biomass production, partitioning, straw yield and digestibility of straw for bioethanol production. Fourteen contrasting cultivars were selected for detailed assessments of biomass accumulation, lodging susceptibility and digestibility. In October 2010, the same fourteen winter wheat cultivars, plus Glasgow, a new, high biomass cultivar, were established in a second field experiment and grown with and without the use of plant growth regulators (PGRs) to control crop height and lodging susceptibility.

There were no significant differences between cultivars in total biomass production at harvest in 2009 and 2010. However, there were differences in grain yield, straw yield, harvest index and straw digestibility in both years. PGR application had no significant effect on total biomass or grain and straw yield; neither did PGRs affect straw digestibility but as expected, PGR application significantly reduced straw length. There was a negative relationship between cultivar height and straw digestibility which is hypothesised to be due to the greater stem:leaf ratio of taller cultivars. No consistent relationship was found between straw digestibility, stem failure wind speed and stem material strength which indicates that cultivars with the highest digestibility are not necessarily more prone to lodging. Moreover, potential bioethanol yield did not vary between cultivars.
RD-2010-3729 - Development of novel methods for detecting and quantifying viable inoculum of \textit{Oculimacula yallundae} and \textit{O. acuformis}

\textbf{The Problem}
Eyespot caused by \textit{Oculimacula yallundae} and \textit{O. acuformis} is considered the most damaging stem-base disease of cereals in temperate countries. Losses due to the disease are associated with direct losses in grain yield of up to 30\% and indirect losses due to eyespot induced lodging. In the UK, yield losses have been notoriously difficult to predict due to the sporadic nature of the disease and discrepancies with visual assessment of the disease during the early growth stages of the crop.

\textbf{Project Aims}
To determine the role and contribution of inoculum quantity and viability from different sources (crop debris, infected leaf sheaths, stems) in disease development throughout the growing season. To determine any predictive relationship between viable inoculum early in the season and eyespot disease and yield loss at harvest.

\textbf{Benefits to the Industry}
A method based on RNA, which detects only viable inoculum, by accounting for the number of viable propagules necessary to initiate eyespot epidemic and yield loss will facilitate more accurate disease forecasting and improve the predictive risk model which already incorporates other risk factors and environmental conditions.
Novel methods for detecting and quantifying *Oculimacula yallundae* and *O. acuformis* to improve our understanding of the relationship between pathogen inoculum levels, eyespot disease and yield loss in winter wheat.

**Abigail Mason¹, James Woodhall², Jeff Peters², Matt Dickinson¹ and Rumiana Ray¹**

¹ University of Nottingham, Sutton Bonington Campus, Leicestershire, LE12 5RD  
² The Food and Environment Research Agency, Sand Hutton, York, YO41 1LZ

The aim of this project was to investigate the role of initial inoculum of *Oculimacula* species in the development of eyespot disease and yield loss in winter wheat, using novel methods for pathogen detection. DNA of individual *Oculimacula* species was sequenced from various regions for the design of a novel species-specific assay for pathogen detection and quantification, which will be validated using inoculated plants from a current field experiment. To study the effects of initial inoculum on wheat physiology, winter wheat grown under controlled conditions or in field was inoculated with $1 \times 10^7$ (high) or $1 \times 10^4$ (medium) fungal spore concentrations. Fluorescence and gas exchange measurements were made using portable fluorometer and LI-COR photosynthesis system. Single tillers were used to investigate the relationship between eyespot infection, pathogen biomass and stem water movement. Water potential in stems was studied using a pressure chamber. Water movement was impaired in plants with high DNA of *O. acuformis*. Photosynthetic efficiency was reduced in plants infected with *O. yallundae*. Under controlled environment conditions, plants suffered lodging, greater disease severity and lower thousand grain weight in response to infection by *O. yallundae*. Whiteheads incidence and reductions in grain number were observed when plants were infected with *O. acuformis*. To determine the predominant species in English first or second wheat fields, a survey was carried out in 2012 and 2013. Soil and plants were sampled throughout the season and processed for DNA extraction and pathogen quantification. *Oculimacula* spp. were successfully quantified in agricultural soil and *O. yallundae* was found as the predominant species present prior to sowing in 2011. The observed differences in predominance, disease progression and yield loss caused *Oculimacula* species indicate the need to better understand the epidemiology of these pathogens in order to effectively control eyespot disease and predict yield loss.
RD-2012-3773 Identification and characterization of Rhynchosporium genes activating barley resistance

The Problem
Rhynchosporium is one of the major diseases of barley in the UK and worldwide causing yield losses of up to 40% and reducing grain quality. The development of sustainable strategies for the management of Rhynchosporium depends on an improved understanding of the biology of the pathogen causing this disease and its interactions with barley.

Project Aims
Match *R. commune* genes with known barley *R* genes and select candidate fungal genes useful for identification of novel sources of resistance to Rhynchosporium.

- Identify candidate triggers of resistance comparing genome sequences of 9 *R. commune* strains.
- Characterise abundance of candidate triggers of resistance in *R. commune* spores and during barley colonisation.

Express candidate triggers of resistance in diverse barley varieties including cultivars with corresponding resistance genes for cultivar-specific recognition.

Benefits to the Industry
The proposed project will greatly increase our knowledge about *R. commune* genes, their role in infection development and potential for recognition of their products by the host plant barley that can lead to development of durable resistance. It will also reduce grower reliance on fungicides and place greater emphasis on durable host resistance.
Identification and characterisation of *Rhynchosporium commune* genes activating barley resistance

Louise Gamble\(^1\), James Lynott\(^1\), Adrian Newton\(^1\), Paul Birch\(^1,2\), Anna Avrova\(^1\)

\(^1\) Cell and Molecular Sciences, James Hutton Institute, Invergowrie, Dundee, UK
\(^2\) Division of Plant Sciences, University of Dundee, Dundee, UK

*Rhynchosporium commune* is one of the most destructive fungal pathogens of barley worldwide. The pathogen causes scald and is responsible for yield losses of up to 40% and reduced grain quality. During infection pathogens secrete a wide variety of protein molecules called effectors which facilitate disease by interfering with plant defence mechanisms. Through co-evolution, plants have developed resistance proteins to detect these molecules resulting in an immune response. Pathogen avirulence (Avr) genes encode effectors that are recognised by a corresponding resistance gene in the host plant. For *R. commune*, one avirulence gene - AvrRrs1 (*Nip1*) has been identified to date. *Nip1* is recognised in barley cultivars carrying the cognate resistance gene *Rrs1* resulting in an incompatible interaction. Barley *Rrs1* resistance deployed to prevent *R. commune* infection has proved ineffective. *R. commune* has managed to overcome this resistance by alteration or deletion of the *Nip1* gene as it is not essential for pathogenicity. Several barley major R genes have been identified but avirulence genes other than *Nip1* remain unknown. Resistance genes recognising essential Avr genes are likely to be more durable. The research aims to identify less variable *R. commune* Avr genes to aid the discovery of novel, more durable forms of resistance to this pathogen. Sequenced *R. commune* strains are being tested for virulence/avirulence on barley cultivars carrying major R genes. Results are being correlated with alterations found in the protein sequences of each strain to identify potential Avr candidates for further analysis. Expression analysis of selected *R. commune* specific candidate genes has revealed some potential effectors which are highly abundant during the early stages of infection. These candidates will be selected for targeted gene disruption to reveal effectors that are essential for pathogenesis. Further characterisation of selected genes will include *in-planta* expression for cultivar specific recognition – using co-bombardment or BSMV mediated expression.
The Problem
The growing world population and increased demand for bioenergy will necessitate a sustainable biofuel policy which uses second generation technology to efficiently utilise the co-products of straw from cereal production. Estimates from recent Farm Business Survey data suggests that circa 70% of cereal straw is currently chopped and incorporated into soil in Eastern England. This suggests that there is a potentially a large volume of straw available for use in second generation biofuel production. However, sustainable biofuel production is predicated on efficient energy input-output balances at the crop and farm level, combined with efficient digestibility of the straw in the fermentation process.

Project Aims
Generate data that could usefully inform the recommended varieties list for a given set of relative output prices for grain and straw. An integrated aim of the study would thus be to use the methodologies and results developed within this research programme to inform grower decision making.

Benefits to the Industry
The proposed study will estimate the Life Cycle Analysis (LCA) of individual wheat varieties and, alongside grain and straw yield measurements, will capture the energy input-output balance to measure Net Energy (NE) potential per hectare from each variety. Drawing upon data generated within the Nottingham Bioenergy Centre, this will facilitate a Digestible Straw Yield (DSY) potential to be produced for each variety investigated.
Sustainable bioethanol from wheat straw – an economic - ecological analysis

Toby Townsend, Debbie Sparkes and Paul Wilson

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The development of a lignocellulosic biofuel industry will increase demand for crop residues such as wheat straw. An understanding of the economic and environmental consequences of this new demand will facilitate the design and implementation of an effective market and policy framework. The aim of this project is to assess how increased demand might affect the value of different wheat cultivars and determine how this will influence farmer decision making.

To do this, three models combining economic and Life Cycle Assessment (LCA) components have been created to assess wheat cultivars with varying straw and grain yields. The economic component uses yield and price data, as well as grain quality and straw digestibility data to generate cultivar value distributions based on various straw price scenarios. The LCA component quantifies the environmental impacts, such as CO₂ emissions, of each cultivar. The models use Monte Carlo simulations to take account of the variability in the inputs and generate output distributions allowing risk modelling.

The models use publicly available cultivar data and data from field trials and laboratory analysis. As well as determining yields and digestibility of multiple wheat cultivars, the field trials have investigated the effects of nitrogen fertiliser and plant growth regulator application on these traits.

The model outputs will be used in an analysis of farmer decision making and will be complemented with a farmer survey that will assess farmer responses to the development of a new straw market. This project will lead to recommendations for the provision of information to assist farmer decision making should this market develop.