

**Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024****Supervisor:** Prof Gerard Bishop ([gerard.bishop@niab.com](mailto:gerard.bishop@niab.com))**Website:** <https://www.niab.com/about/people/professor-gerard-bishop>**Department / UPI:** NIAB**Research area:**

The NIAB potato group's research can be encapsulated in the statement "understanding how potatoes grow determines how to grow potatoes". The group works closely with industry to maximize the relevance and adoption of new knowledge. Current research has a strong agronomic focus, so is mostly field based, supported by a range of post-harvest analysis. This includes understanding the genetic variation underlying the different optimal nitrogen rates for varieties and modelling of seed tuber planting rates to obtain required yields. Group interests also include new varieties via gene editing, production of novel chimeras, novel irrigation strategies and developing methods to reduce the impact of potato pests and pathogens. These interests fit within the farming-systems approaches of the wider NIAB Agronomy Group, targeting more sustainable and regenerative potato production. Those interested in projects that have the potential for more immediate application should come and discuss potential options.

**Supervisor:** Dr Lesley Boyd ([lesley.boyd@niab.com](mailto:lesley.boyd@niab.com))**Website:** <https://www.niab.com/about/people/dr-lesley-boyd>**Department / UPI:** NIAB**Research area:**

The impact of yellow rust infection on yield: Background: It is well known that disease reduces yield. However, recent insights indicate that the loss in yield is not simply due to a loss of green tissue, but a direct effect on photosynthesis initiated by the pathogen. An effector of the yellow rust pathogen *Puccinia striiformis* f. sp. *tritici* (Pst) has been identified that interacts with a component of the cytochrome b6-f complex, a critical component of photosynthesis. The effector Pst\_12806 binds to the C-terminal Rieske domain of TaISP reducing electron transport rates, photosynthesis and the production of chloroplast derived ROS.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life**Supervisor:** Dr Phil Howell ([phil.howell@niab.com](mailto:phil.howell@niab.com))**Website:** <https://www.niab.com/about/people/dr-phil-howell>**Department / UPI:** NIAB**Research area:**

Interested in applying genetics to help solve real world problems through plant breeding. Active across different crop types including cereals (especially wheat and barley), oilseeds, pulses fibre crops. Overarching interest is in tapping into genetic diversity and using this to improve yield and quality under reduced inputs, to sustainably drive food and nutritional stability. Most of my research includes data, lab, glasshouse and field work, and often includes collaboration with industry partners from along the supply chain (predominantly plant breeding, farming and food manufacturing).

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**Supervisor:** Dr Kostya Kanyuka ([kostya.kanyuka@niab.com](mailto:kostya.kanyuka@niab.com))

**Website:** <https://www.niab.com/about/people/dr-kostya-kanyuka>

**Department / UPI:** NIAB

**Research area:**

Molecular Plant-Pathogen Interactions

My group is interested to understand how pathogens cause disease on plants, and how plants resist pathogens at the mechanistic and molecular level with the aim of developing sustainable solutions for disease control in major crops such as wheat and other cereals. Not so long ago we isolated a gene from wheat that confers isolate-specific resistance to Septoria leaf blotch disease of wheat (Nature Genetics 2018, 50:368-74). This gene turned out to encode a protein belonging to the wall-associated kinase protein (WAK) sub-family of plasma-membrane spanning receptor-like kinases specific for plants. There are 26 WAKs in a model dicot *Arabidopsis thaliana*, where some of these proteins have been characterized and shown to play roles in growth, development, pathogen defence, or tolerance to abiotic stresses (J Exp Bot 2022, 73:22-37). This protein family has dramatically expanded in wheat where we identified over 600 members (Science 218, 361:eaar7191). The function of most individual members of this fascinating protein family in wheat remains unknown. And we are now interested to address this knowledge gap by identifying and functionally characterising WAKs and particularly those contributing to defence against pathogens.

We have data from our recent phylogenetic, gene expression (RNAseq), and haplotype variation analyses (exon and promotor capture) of the entire wheat WAK family which should help pick some interesting leads, as well as powerful genomics technologies such as virus-induced gene silencing and TILLING in place to enable gene function analysis in wheat.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Supervisor:** Dr Matthew Milner ([matthew.milner@niab.com](mailto:matthew.milner@niab.com))

**Website:** <https://www.niab.com/about/people/dr-matthew-milner>

**Department / UPI:** NIAB

**Research area:**

I am interested in all things related to plant nutrition. This includes how elements are taken up from the soil, how they are sensed and finally transported through the plant to help create the wide variety of phenotypes important to agriculture today.

We have access to plant transformation of a number of species being here at NIAB and are looking to transform the food we eat and produce.

**BBSRC DTP secondary strategic theme:** Biosciences for an integrated understanding of health

## Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024

**Supervisor:** Dr Brian Ferguson ([bf234@cam.ac.uk](mailto:bf234@cam.ac.uk))

**Website:** [www.fergusonlab.path.cam.ac.uk](http://www.fergusonlab.path.cam.ac.uk)

**Department / UPI:** Pathology

**Research area:**

In order to fight off a virus infection, host cells sense and respond to infection by producing interferons and inflammatory cytokines. We are offering rotations and full PhD projects in the area of innate immune sensing of viruses with a specific focus on how viral nucleic acids trigger host defence mechanisms. In this context we will use molecular techniques to define the signalling pathways that operate in antiviral immunity and a complementary comparative immunology approach to understand how different host species sense the same pathogens. We are also studying the viral mechanisms of inhibition of these pathways and will make use of the same systems to understand, at the molecular level, how specific viruses, particularly poxviruses inhibit innate sensing pathways.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Supervisor:** Dr Jeongmin Choi ([jc913@cam.ac.uk](mailto:jc913@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/directory/jeongmin-choi>

**Department / UPI:** Plant Sciences

**Research area:**

Improving crop resilience through symbiosis with beneficial microbes.

Nutrient intake is a fundamental aspect of life. Around 80% of land plants obtain soil minerals through a mutually beneficial association with arbuscular mycorrhizal (AM) fungi. The symbiosis provides various benefits, including nutrition uptake and improved plant performance under environmentally stressful conditions.

My research group aims to understand the molecular mechanisms underpinning how environmental factors interact with plant-microbial symbiosis.

There are two main research questions in my lab.

- How do environmental factors regulate AM symbiosis?
- How does AM symbiosis help plants become more resilient to harsh environments?

Understanding factors and mechanisms regulating these processes will help us utilise symbiosis in a dynamic and broader range of environmental settings, which will become increasingly important for food security as global climate becomes more unpredictable.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024**

**Supervisor:** Prof Nik Cunniffe ([njc1001@cam.ac.uk](mailto:njc1001@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/directory/cunniffe-nik>

**Department / UPI:** Plant Sciences

**Research area:**

I focus on modelling the spread, detection, evolution and control of plant pests and pathogens. My theoretical work uses deterministic, stochastic, and spatial models to improve strategic understanding. My applied work concentrates on using models to understand how detection and control can be optimised.

Projects in the group tend to require mathematical modelling and/or computer programming. Professor Cunniffe is therefore particularly interested in hearing from students with training in mathematics, physics, computer science or engineering. However, students from other backgrounds are very welcome, so long as they are interested in learning more about these topics. Such students with training in agronomy, biology and ecology are also encouraged: in the past similar students have been very successful here.

**BBSRC DTP secondary strategic theme:** Transformative technologies

**Supervisor:** Prof Julia Davies ([jmd32@cam.ac.uk](mailto:jmd32@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/research/groups/transport>

**Department / UPI:** Plant Sciences

**Research area:**

Extracellular ATP (eATP) is an important neurotransmitter in humans and has now been found to be a plant cell regulator. ATP is released to the extracellular space to act as a growth regulator and stress signal (particularly for wounding and pathogen attack). We were the first to show that eATP causes an increase in cytosolic free calcium as a potential second messenger and have since shown that in roots it generates a propagative calcium wave from the tip.

We have identified some of the calcium channels involved and now need to find out how the wave is generated downstream of the eATP receptors and what the consequences are for leaves in terms of an adaptive response. Whilst this section of the project would use Arabidopsis, we also need to determine if eATP signalling employs calcium as a second messenger in crops. To this end we have generated a wheat line expressing a cytosolic calcium reporter and have also identified putative eATP receptor genes in wheat. The encoding proteins now need to be tested for receptor activity.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024**

**Supervisor:** Dr Lida Derevnina ([ld645@cam.ac.uk](mailto:ld645@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/research/groups/crop-pathogen-immunity>

**Department / UPI:** Plant Sciences

**Research area:**

Understanding immune receptor networks: from mechanism to application.

Plants are continuously exposed to a diversity of pathogens and pests, some of which cause devastating diseases. To fend off these invading organisms, plants have evolved complex immune systems. Intracellular nucleotide-binding leucine rich repeat (NLR) proteins are major components of the plant immune system. NLRs recognise pathogen molecules and activate immune signalling to restrict pathogen growth and hinder disease progression. Genome analyses have revealed that plants encode anywhere between 50 and 1,000 NLRs. Some of these NLRs are functional singletons operating as single biochemical units, while others function in pairs or in networks. Paired and networked NLRs consist of functionally specialised “sensor” NLRs that detect pathogen effectors and “helper” NLRs that translate pathogen recognition into resistance. The Derevnina lab aims to elucidate the molecular mechanisms underpinning plant immune function, with emphasis on understanding how pathogens have evolved to disable immunity mechanisms to enable disease infection. We study the interactions between plant parasitic nematodes and tuberous crops (potato and sweet potato) and will utilise our knowledge of these interactions to drive and develop sustainable solutions of management of these devastating pathogens. We will use a combination of genomics, biochemical, molecular, and cellular approaches combined with functional characterisation in the model plant species *Nicotiana benthamiana* to address the following questions:

- How important is the NLR network across plant species?
- How do sensor and helper NLRs function together?
- How do pathogens interfere with NLR network mediated immunity?

**Supervisor:** Dr Sebastian Eves-van den Akker ([se389@cam.ac.uk](mailto:se389@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/research/groups/plant-parasitepathogen-interactions>

**Department / UPI:** Plant Sciences

**Research area:**

Plant-parasitic nematodes are a major, and in some cases dominant, threat to food security all over the world. This so called "orphan disease" of plants is objectively important but often overlooked in farming systems because the parasites are below-ground, root pathogenic, organisms.

Our goal is to understand the fundamental and fascinating biology of plant-nematode interactions in sufficient detail in order to identify sustainable routes to control these organisms in agriculture. Projects in the lab will be tailored to suit our common interest. They can include a variety of approaches (e.g. wet or dry lab, genetics, genomics, and molecular biology), and typically focus on either the plant-side of the interaction or the nematode side of the interaction (e.g. effector biology, resistance and susceptibility, sex determination, biotechnology).

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

## Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024

**Supervisor:** Prof Beverley Glover ([bjg26@cam.ac.uk](mailto:bjg26@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/research/groups/evolution-and-development>

**Department / UPI:** Plant Sciences

**Research area:**

PhD projects are available to study the evolution and development of floral traits that are important in attracting animal pollinators. By understanding how plants build traits that attract particular animals we aim to understand the diversification of the flowering plants. These projects allow us to engage with plant breeders to optimize pollinator attraction and ensure healthy insect populations and improved food security.

We use molecular genetic, developmental and evolutionary techniques to address these problems, and our lab incorporates a bee behavioural facility to explore pollinator responses to mutant and transgenic flowers.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Supervisor:** Prof Julian Hibberd ([jmh65@cam.ac.uk](mailto:jmh65@cam.ac.uk))

**Website:** <http://hibberdlab.com/>

**Department / UPI:** Plant Sciences

**Research area:**

Our research focusses on understanding and improving photosynthesis. C4 photosynthesis operates because spatial partitioning of photosynthesis increases concentration of CO<sub>2</sub> around RuBisCO (Hibberd and Covshoff, 2010). This allows C4 plants to be amongst the most efficient on the planet (Sage et al., 2011), and so bioengineering the C4 pathway into C3 crops would allow significant increases in yield (Hibberd et al. 2008; von Caemmerer et al. 2012). Projects are available in areas relating the transcriptional regulation of gene expression in plants.

We recently discovered a bipartite transcription factor module that generates bundle sheath expression in the C3 model *Arabidopsis thaliana* (Dickinson, Kneřova et al., 2020), and a members of a family of a transcription factor family that was not previously known to be involved in photosynthesis. Projects are available in which the role of these newly identified transcription factors is investigated in C4 species, and the extent to which they can be used for bioengineering.

**BBSRC DTP secondary strategic theme:** Transformative technologies

## Research Areas within Bioscience for Sustainable Agriculture and Food / AY 2023 -2024

**Supervisor:** Dr Leonie Luginbuehl ([lhl28@cam.ac.uk](mailto:lhl28@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/directory/leonie-luginbuehl>

**Department / UPI:** Plant Sciences

### Research area:

The arbuscular mycorrhizal (AM) symbiosis, which is formed by most land plants and AM fungi in the soil, is one of the oldest and most widespread symbioses on Earth. This symbiosis provides significant benefits to both partners - plants receive essential mineral nutrients acquired by the fungal network in the soil, and in return deliver photosynthetically fixed carbon to the fungus.

Plants that associate with AM fungi typically display enhanced mineral nutrition, improved growth, and increased yield. However, with up to 20% of the photosynthesis products being allocated to the fungus, the symbiosis is associated with a substantial carbon cost for the plant. A fundamental but unsolved question is how plants regulate nutrient trade during AM symbiosis and ensure that the symbiosis remains mutually beneficial.

The aim of our research is to identify the molecular mechanisms that allow plants to control carbon allocation to the fungus, and to understand how symbiotic, endogenous, and environmental factors affect the amount of carbon that is delivered to the fungus. A better understanding of the molecular mechanisms that control nutrient trade will inform engineering and breeding efforts to optimise the cost-benefit balance of AM symbiosis and maximise yield in crop plants. To address these questions, we combine carbon tracing and (single-cell) transcriptomics approaches with targeted mutagenesis, microscopy imaging, and molecular biology techniques in the model species rice and *Medicago truncatula*.

**BBSRC DTP secondary strategic theme:** Understanding the rules of life

**Supervisor:** Prof Uta Paszkowski ([up220@cam.ac.uk](mailto:up220@cam.ac.uk))

**Website:** <https://www.cropsciencecentre.org/staff/professor-uta-paszkowski>

**Department / UPI:** Plant Sciences

### Research area:

The arbuscular mycorrhizal (AM) symbiosis is a fascinating mutualistic interaction between roots of most land plants and fungi of the phylum of the Glomeromycota. The development of this life-long alliance starts with reciprocal recognition in the rhizosphere, reprogramming both symbionts for the anticipated association. The interaction proceeds towards extensive root colonization which culminates in the formation of fungal feeding structures, the arbuscules, inside root cortex cells.

As the arbuscule develops, the plant cell dramatically increases membrane biogenesis to envelope the growing hyphal structure. Thereby a hugely enlarged intracellular surface area is created between the two organisms, appearing ideally adapted for the exchange of signals and nutrients.

The nature and complexity of the establishment of AM symbioses must be the result of a well-orchestrated exchange of molecular signals between the plant and the fungus. The nature of some of the signals has been discovered in recent years, providing a first insight into the type of chemical language spoken between the two symbiotic partners.

My group has taken molecular genetics and lately advanced imaging approaches to elucidate the molecular mechanisms underpinning this apparently harmonious symbiosis. These have led us to



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propose fundamentally new communication mechanisms operating during this intimate plant-fungal partnership. PhD projects are available that built on our recent observations, integrating well with then overall research interest of the group.

**BBSRC DTP secondary strategic theme:** Bioscience for sustainable agriculture and food

**Supervisor:** Prof Alex Webb ([aarw2@cam.ac.uk](mailto:aarw2@cam.ac.uk))

**Website:** <https://www.plantsci.cam.ac.uk/research/groups/circadian-signal-transduction>

**Department / UPI:** Plant Sciences

**Research area:**

We investigate circadian rhythms driven the mysterious internal time keepers that acts as 24 hour cellular clocks. We have recently proposed that circadian biology can be used to improve crop production and sustainability in the practice of “chronoculture” (Steed et al. 2021 Science 372, 10.1126/science.abc9141). We offer projects that build on our major discoveries of a Ca<sup>2+</sup>-based signalling pathway forms part of the Arabidopsis circadian oscillator (Dodd et al., 2007 Science 318, 1789 -1792; Marti et al., 2018 Nature Plants 4, 690-698), entrainment of the circadian clock to sugar signals (Haydon et al., 2013 Nature 502, 689–692; Frank et al., 2018 Current Biology 28, 2597-2609), circadian clocks optimise plant and crop performance (Dodd et al., 2005 Science 309, 630 – 633; Wittern et al., 2021 <https://doi.org/10.1101/2021.09.03.458922>), dynamic adjustment of circadian period contributes to circadian entrainment (Mombaerts et al. 2019 PLOS Computational Biology 15: e1006674; Webb et al., 2019 Nature Communications, 10, 550) and oscillations of cytosolic-free calcium encode information (Martí et al., 2013 Plant Physiology 163, 625 – 634; ; Lopez-Hernandez et al., (2020) Plant Cell. 32, 3346—3369).

The following projects, which build on these discoveries are open for application. We can provide more detail to interested applicants.

1. Engineering the internal and external environment of leafy crops to enhance indoor growth and provide food for space exploration
2. The circadian clock as a regulator of yield traits in wheat
3. The mechanisms of circadian gating of signalling
4. Mechanism controlling the propagation of Ca<sup>2+</sup> signals in plants

**BBSRC DTP secondary strategic theme:** Bioscience for sustainable agriculture and food

**Supervisor:** Dr Gareth Pearce ([Gpp28@cam.ac.uk](mailto:Gpp28@cam.ac.uk))

**Website:** <https://www.vet.cam.ac.uk/directory/gpp28%40cam.ac.uk>

**Department / UPI:** Veterinary Medicine

**Research area:**

Animal Welfare

Animal Health

Marine megavertebrate conservation