CEPAMS

CAS-JIC Centre of Excellence
for Plant and Microbial Science

Xiaofeng Cao
CEPAMS Director

> *"CEPAMS is truly a synergy of the very best science and the very best scientists in China and the UK. I believe that this synergy has tremendous potential for excellent scientific output and global public good"*

Ray Dixon
CEPAMS Director

> *"CEPAMS strives for both excellence and impact. I believe that it is only through combining scientific excellence with strategic relevance that we can address the major societal and environmental challenges that lie ahead"*

The CAS-JIC Centre of Excellence for Plant and Microbial Science

The CAS-JIC Centre of Excellence for Plant and Microbial Science (CEPAMS) brings together three world-leading laboratories in the UK and China to support the global aspirations of food security and sustainable health care. The Centre nurtures excellent science and focuses on the improvement of food crops and the production of high value, beneficial products from plants and microbes.

Mission – To maximise the synergy of CAS and JIC research, working together for excellent science and global public good

Vision – Excellent strategic plant and microbial science transforms global nutrition and health

Culture and spirit – CEPAMS is built on trust and friendship. Members of the CEPAMS Community expect of each other both scientific rigour and cross-cultural respect.

Background

The partnership between the John Innes Centre (JIC) and the Chinese Academy of Sciences (CAS) is built on a strong history of scientific links which stretch back to the earliest days of UK-China research collaboration. For example, former Vice-President of CAS, Professor Zhihong Xu was a visiting researcher at JIC in 1979. JIC now counts over 100 scientifically active alumni in China, many of whom have reached senior positions in the Chinese science system (one of them was Theresa May's host during her visit to a Chinese agricultural research centre in 2018). A group of these alumni initiated a discussion of the "JIC in China" concept which directly led to CEPAMS being developed by JIC and CAS.

Leading

Over twenty world-leading CEPAMS collaborative research projects between the UK and China

Vision

Excellent strategic plant and microbial science transforms global nutrition and health

Mission

To maximise the synergy of CAS and JIC research, working together for excellent science and global public good

Growing

Ten new CEPAMS laboratories, led by international scientists and conducting world-class research

Sharing

Mobility of researchers between the UK, regular international CEPAMS Symposia

Yang Bai

Yang Bai joined CEPAMS from the world-renowned Max Planck Institute for Plant Breeding Research in Cologne in 2016, the first of six CEPAMS Group Leaders appointed in 2016/2017. He has already been awarded prestigious “1000 Talents” status in China and expanded his group to twelve scientists.

Yang studies the microbes that are associated with healthy plant growth. New techniques in molecular biology enable him to explore an incredibly diverse microbiome. A better understanding of this microbiome will be essential to the development of sustainable agriculture and future food security globally.

Microbes and Nutrition

Roles of microbiota in crop nutrition and disease resistance.

Microbiota and Gene Expression

How microbiota reshapes plant transcriptome and epigenome.

Metagenomics Analysis

Combining sequencing and analysis methods of metagenome and metatranscriptome

Xiufang Xin

Xiufang Xin joined CEPAMS in 2017 from the DoE Plant Research Laboratory at Michigan State University. She has already established her research group in CEPAMS’ brand new laboratories in Shanghai and has been awarded the prestigious “1000 Talents” status in China.

Xiufang studies the interactions between plants and microbes, including pathogens and commensal microbes (i.e. microbiota). On the former, her interest lies in the interplay between the plant's immunity and the pathogen's virulence mechanisms, in the context of influences by environmental factors. On the latter, her interest lies in how plants control a "healthy" microbiome and how microbiome affects plant health. Both of these interests are crucial to sustainable agriculture globally.

Plant Immunity Dynamics

The interplay between bacterial pathogenesis and plant immunity

Environment and Disease

The mechanisms of environmental influence on plant diseases

Plant-microbiome interactions.

How plants maintain the leaf microbiome and how leaf microbiome influences plant health.

Evangelos Tatsis

Evangelos Tatsis was the first internal candidate to join CEPAMS when he made the move to CEPAMS in Shanghai from the John Innes Centre in 2017. Evangelos is originally from Greece and has also worked at a Max Planck Institute in Germany.

Evangelos studies beneficial natural products in plants. Chinese medicinal plants make a vast range of these products, for example the anti-malarial drug artemisinin. Evangelos aims to understand and then engineer the metabolic pathways which are responsible for making these natural products in Chinese medicinal plants thus enabling future health benefits globally.

Vast potential of natural products

Plants produce an enormous diversity of beneficial compounds

Metabolic pathways

Understanding exactly how plants produce these products

Genome enabled approach

Using bioinformatics, molecular biology, and enzymology techniques, coupled with a plant-based synthetic biology platform

Fei Lu

Fei Lu joined CEPAMS in 2017 from the Institute for Biotechnology and Life Science Technologies at Cornell University. He has returned to IGDB in Beijing where he studied for his PhD (winning the President's award for the Outstanding Graduate of the Chinese Academy of Sciences).

Fei is using novel approaches to identify regions of DNA in maize and wheat that are responsible for important aspects of the plant's growth, development and health. His work is at the cutting edge of computing, machine learning, evolution and their application to plant biology. His work has great potential to improve major crop species and contribute to global food security.

Functional Genome Prediction

Approaches to pinpoint large-effect and causative variants controlling phenotypes

"Cross-free" Breeding

Developing genomic editing technologies, to speed up crop improvement.

Developing Models for Wider Use

Utilising research from miaze and wheat to benefit genic improvement of many other crops.

Cao Xu

Cao Xu joined CEPAMS in 2017 from the Cold Spring Harbor Laboratory. His influential work there on development in tomatoes was featured on the cover of Nature Genetics in 2015. Cao is another returning success story, having completed his PhD at IGDB in Beijing.

Cao studies the way that plant cells communicate with each other to ensure that plants develop appropriately and function optimally. He is interested in how these communication mechanisms evolved and how they can be altered to improve tomato plants and their resistance to stress. As some crops face greater environmental and biological stresses in future, his work is important in terms of food security.

Small Peptide Signaling

Developing novel strategies to fully reveal the plant peptide cell-to-cell communications.

***Cis*-regulatory Evolution**

Using genetics, genomics, and gene editing to explore *cis*-regulatory elements evolution.

Accelerate Crop Domestication

Editing cis-regulatory elements to accelerate and engineer crop domestication.

Jeremy Murray

Jeremy Murray was the second internal candidate to join CEPAMS when he made the move to CEPAMS in Shanghai from the John Innes Centre in 2017. Jeremy is originally from Canada and has also worked in the US at the Noble Foundation

Jeremy is intrigued by the way that plants called legumes (e.g. beans or peas) and bacteria in the soil have a mutually beneficial relationship – a “symbiosis”. He studies the interaction and communication between plants and their associated bacteria. He recognises that optimising symbiosis can have dramatic impacts on the growth and health of legume plants with implications for future yields, especially in areas where artificial fertilizer is unavailable or environmentally unwanted.

Legume Symbiosis with Rhizobia

Investigating the symbiotic interaction between rhizobia and legumes which is called nodulation

Selecting the Appropriate Symbiont

How the plant host can select the appropriate symbiont from such a vast ocean of bacteria

Models for Symbiotic Development

Using transcription factor mutants and single-cell transcriptomics we have drawn the first clear infection thread gene regulatory networks

Research Projects

- **Development of production systems for bioactive natural products from Chinese medicinal plants** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Sequencing the diploid oat (*Avena strigosa*) genome** (John Innes Centre & Shanghai Institute of Plant Physiology & Ecology)
- **Wheat association genetics** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Discriminating between symbiosis and PAMP signalling in rice** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Iron signalling in Arabidopsis** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Development of production systems for bioactive natural products from Chinese medicinal Plants** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Mechanism and Significant of Chromatin reconfigurations in Plant germline** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Nitrate transport targets of the wheat NAC2 transcription factors** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Functional and population analysis of genomic islands of diversity in the Antirrhinum species group** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Growth control and organ size** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Geminiviral cell-to-cell trafficking: interaction of the geminiviral C4 protein and the plant BAM1 receptor kinase** John Innes Centre, Shanghai Centre Plant Stress Biology)
- **Editing long distance transport and storage to optimize the site of nitrogen assimilation in drought and salt-stress** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Linking the dots of plant immune signalling through the identification of RLCK substrates** (The Sainsbury Laboratory, Institute of Genetics and Developmental Biology)
- **Coordinated regulation of plant height and branching** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Understanding agronomic resilience - Why is oat different?** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **A Platform for Alkaloid Pathway Discovery** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Coupling of RNA processing and transcription** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Identifying the role of *Streptomyces coelicolor* natural products in interspecies interactions** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Functional characterisation of aphid cathepsin B effectors** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)
- **Functional analysis of bi-directional nitrate transporters in rice and wheat** (John Innes Centre, Institute of Genetics and Developmental Biology)
- **Structural analysis of *Mycobacterium tuberculosis* drug-resistance-related proteins** (John Innes Centre, Institute of Microbiology)
- **Revealing the RNA structural basis of sugar-dependent degradation of miRNA precursors during the juvenile to adult developmental phase transition in plants** (John Innes Centre, Shanghai Institute of Plant Physiology & Ecology)

Development of production systems for bioactive natural products from Chinese medicinal plants

Xiao-Ya Chen | Cathie Martin

At least five thousand plant species are used medicinally in China. Xiao-Ya Chen and Cathie Martin are exploring how some of these plants produce bioactive compounds which may help to treat disease.

In one example, they have unlocked the biosynthetic pathway through which the Chinese skullcap plant produces compounds which have beneficial anti-viral, anti-oxidant (and potential anti-cancer) effects. In another example, they are exploring the biosynthetic pathway through which Shan Dou Gen produces compounds which are traditionally used to treat jaundice, hepatitis, bladder tumours and melanoma.

An understanding these pathways provides the tools with which Chen and Martin will increase the production of bioactive natural products in plants. This, in turn, will enable further research on the biological efficacy of these natural products and ultimately therapeutic use.

Zhao Q., Zhang Y., Wang G., Hill L., Weng J. K., Chen X. Y., Xue H., Martin C. (2016) A specialized flavone biosynthetic pathway has evolved in the medicinal plant Scutellaria baicalensis. Science Advances 2, 4.

Understanding and exploiting mechanisms controlling seed size and seed yield

Yunhai Li | Mike Bevan

Yield in cereal crops is a key determinant of global food security. Maize, wheat and rice together provide more than 50% of the human population's total calorie intake.

Yunhai Li and Mike Bevan are exploring the mechanisms which coordinate the transition in plants from cell proliferation (number of cells) to cell expansion (size of cells) during organ growth. Variation in this mechanism can result in an increased duration of cell proliferation, leading to increased organ and seed size (and therefore potentially crop yield). They have characterised a protein which contributes to this transition and may therefore limit organ size. This protein can now be used as a target for the development of new varieties of plants to determine the impact on yield.

Dong H., Dumenil J., Lu F. H., Na L., Vanhaeren H., Naumann C., Klecker M., Prior R., Smith C., McKenzie N., Saalbach G., Chen L., Xia T., Gonzalez N., Seguela M., Inze D., Dissmeyer N., Li Y., Bevan M. W. (2017). Ubiquitylation activates a peptidase that promotes cleavage and destabilization of its activating E3 ligases and diverse growth regulatory proteins to limit cell proliferation in Arabidopsis. Genes & Development 31, 197-208.

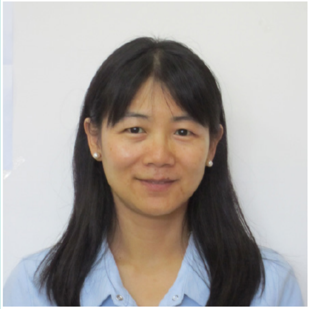
Identifying anti-viral defence mechanisms in plants

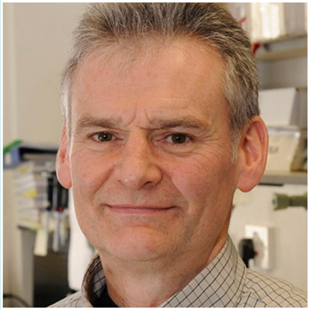
Rosa Lozano-Duran | Christine Faulkner

Crop losses due to plant pathogens vary between 10 and 20% globally. At a time when demand for food staples is rising and disease risks are changing due to climate, a better understanding of plants own defence mechanisms could be significant.

Rosa Lozano-Duran and Christine Faulkner are exploring the molecular mechanisms through which plants defend themselves against invading pathogens. For example, they have identified proteins in the plant which regulate RNA silencing as a key anti-viral defence mechanism and also a suppressor protein which the virus employs to disarm the plant's defence mechanism. It is hoped that these breakthroughs could lead to increased disease resistance in plants

Rosas-Diaz T., Zhang D., Fan P., Wang L., Ding X., Jiang Y., Jimenez-Gongora T., Medina-Puche L., Zhao X., Feng Z., Zhang G., Liu X., Bejarano E. R., Tan L., Zhang H., Zhu J. K., Xing W., Faulkner C., Nagawa S., Lozano-Duran R. (2018), A virus-targeted plant receptor-like kinase promotes cell-to-cell spread of RNAi. Proceedings of the National Academy of Sciences 115 (6), 1388-1393.





Structural analysis of *Mycobacterium tuberculosis* drug-resistance-related proteins

Kaixia Mi | Tony Maxwell

Tuberculosis (TB) is the world's deadliest bacterial infectious disease, with around 2 billion people infected worldwide and more than 1.5 million deaths every year. Although drug treatments for TB are available, resistance is a serious problem and new TB drugs are urgently needed.

Tony Maxwell and Kaixia Mi are exploring resistance to fluoroquinolone antibiotics in *Mycobacterium tuberculosis*. They are studying a bacterial enzyme (topoisomerase DNA gyrase) which is a well-validated target for antibiotics (including fluoroquinolone) and the Mycobacterium fluoroquinolone-resistance protein MfpA which confers resistance. The mode of operation of MfPA and its partner protein MfpB is currently unknown.

The knowledge obtained in this project will be of value in terms of our understanding of antibiotic resistance and the development of new TB therapies. The results may provide explanations for unresolved clinical fluoroquinolone resistance and will potentially reveal new ideas for antibiotic targeting.

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