OpenPlant Forum

Smart Design for the Future Bioeconomy

29-31 July

Murray Edwards College, Cambridge

2019

BBSRC EPSRC

OPENPLANT FORUM PROGRAMME

Monday 29 July 2019

OPENPLANT BIOMAKER PROGRESS REPORTS & SHOWCASE

OpenPlant Biomaker is a five-month programme challenging interdisciplinary teams to (i) build low-cost instruments for biology or (ii) develop a biological resource or outreach project. Tools and resources developed will be openly documented and made freely available via *www.biomaker.org*. As we are midway through the challenge, interdisciplinary teams led by early career researchers from Cambridge and Norwich will present progress reports and pitch for follow-on funding.

13:00 LUNCH

14:00 TEAMS 1-15

14:00 Introduction
14:10 Open DLS: an open-source dynamic light scattering device for nanoparticles sizing
14:15 LunaFlow: bioluminescent plankton for 3D flow visualisations of pressure fields
14:20 Pressure controlled micro-manipulation of bioluminescent microorganisms
14:25 Stress priming for improved production of biotech-relevant compound in green alga
14:30 Mechanisms for direct electron transfer (DIET) between Geobacter and Methanothrix
14:35 Diabetes diagnosis and management using Arduino and mobile user interface
14:40 Developing an open and affordable 3D bioprinter
14:45 Droplet-based microfluidics to mimic the compartmentation of metabolism in multicellular systems
14:50 e-CO-SENSE: biophotovoltaic powered soil sensors
14:55 An open toolkit for engineering microbial interactions
15:00 Establishing a joint UK-Kenya Phytoplasma research initiative
15:05 Build your own DNA Dave
15:10 Low-cost SLM interface board for advanced microscopy
15:15 SAFE: safe air for everyone
15:20 Variable-time cameras with image recognition for inexpensive, large-scale monitoring of plant pollination events

15:30 COFFEE

16:00 TEAMS 16-25

16:00 Low-cost oxygen sensor for bioreactors
16:05 MACRO IMAGER: a low-cost multi-purpose large area macro digital photography phenotyping station
16:10 A behavioural chamber to evaluate rodent forelimb grasping performance
16:15 Low-cost incubator to grow mycelium biotextile
16:20 Aeroponics for all
16:25 AccuPatch: conductive microelectrode array for cancer tissue screening
16:30 In-situ 3D visualization using X-ray CT during mechanical testing of natural cellular materials
16:35 BrewerMicro: DIY microscope for counting yeast
16:40 IoHeat: a contained oasis in the coldroom
16:45 Engineering low-cost turbidostat systems for running microbial evolution experiments
16:50 Closing statements
17:00 End

17:00 DRINKS RECEPTION

18:00 SHOWCASE & BUFFET DINNER

Tuesday 30 July 2019

08:30 **REGISTRATION & COFFEE**

09:00 SESSION 1: PLANT & MAMMALIAN ENGINEERING

Open systems for engineering plants
Jim Haseloff, University of Cambridge

Mammalian synthetic biology: the current state of play
Susan Rosser, University of Edinburgh

10:30 **COFFEE**

11:00 SESSION 2: SYNTHETIC GENE SYSTEMS

Towards monitoring, prediction and control in mammalian cells
Leopold Parts, Wellcome Sanger Institute

Decode and reprogram a genome
Jun Biao Dai, Shenzhen Institute of Advanced Technology, China

Reprogramming the genetic code
Jason Chin, University of Cambridge

12:30 **LUNCH**

Poster session (odd numbers)

14:00 SESSION 3: MODELLING & MACHINE LEARNING FOR BIOLOGICAL SYSTEMS

Automated reasoning for biological networks
Sara-Jane Dunn, Microsoft Research

Understanding time-dependent gene-environment interactions: tools to design and analyse experiments
Daphne Ezer, Allan Turing Institute

Re-engineering geometric size control in fission yeast
Martin Howard, John Innes Centre

15:30 COFFEE

16:00 SESSION 4: ENTERPRISE FOR THE BIOECONOMY (PANEL)

Contextualisation of Colorifix
Jim Ajioka, Colorifix

Tropic's Inspiration, Work and Impact
Eyal Maori, Tropic Biosciences

Sugars on the surface – diagnostics and vaccines
Rob Field, Iceni Diagnostics

Phytocosmetics from metabolically engineered tomato extracts
Eugenio Butelli, Persephone Bio

A radically different approach to DNA synthesis using silicon chips
Tim Brears, Evonetix

17:00 FINISH

18:00 DRINKS RECEPTION & CONFERENCE DINNER
Murray Edwards College Fellows' Suite (registration required)

If you are registered but can no longer attend, please inform the registration desk as soon as possible so we can inform the next person on the waiting list.

Wednesday 31 July 2019

08:30 **COFFEE**

09:00 SESSION 6: NOVEL APPROACHES & TECHNOLOGIES I

UC2: an open-source optical toolbox for multi-modal imaging in the incubator
Benedict Diederich and René Lachmann, Leibniz Institute of Photonic Technology, Germany

Genome editing in patient-relevant model systems
Stephanie Mack, Cancer Research UK

Advances in genome editing of wheat and barley
Wendy Harwood, John Innes Centre

Understanding and engineering biological networks
Somenath Bakshi, University of Cambridge

On the way to a plant-made polio vaccine - successes and challenges
Daniel Ponndorf, John Innes Centre

Sexy Plant 2.0: for a sustainable bioproduction of insect pheromones
Kalyani Kallam, Earlham Institute

10:50 **COFFEE**

11:20 SESSION 5: REPROGRAMMING MULTICELLULAR SYSTEMS

DICER-mediated reprogramming of cell fate specification in *Marchantia polymorpha*
Mario Arteaga-Vazquez, University of Veracruz, Mexico

Systematic tools for reprogramming a simple plant *Marchantia polymorpha*
Susana Sauret-Gueto, University of Cambridge

Marchantia and the chloroplast
Eftychis Frangedakis, University of Cambridge

12:30 LUNCH AND POSTER SESSION

Poster session (even numbers)

14:00 SESSION 7: NOVEL APPROACHES & TECHNOLOGIES II

Systematic review of natural triterpene oxidation diversity provides focus to the search for new synthetic biology tools
Michael Stephenson, John Innes Centre

Improving *Nicotiana benthamiana* as a bioproduction system for proteins and small molecules
Quentin Dudley, Earlham Institute

Expanding the toolkit for plant cell wall polysaccharide engineering
Louis Wilson, University of Cambridge

Responses to oomycete infection in *Marchantia polymorpha*
David Hoey, University of Cambridge

Electronic control of gene expression in cyanobacteria
Stephen Rowden, University of Cambridge

Viruses in motion: a close look at virus maturation through cryo-electron microscopy
Roger Castells Graells, John Innes Centre

15:30 CLOSING REMARKS

15:35 COFFEE

16:00 MEETING OF THE SCIENCE ADVISORY BOARD
SAB and OpenPlant management group only

18:00 BBQ AT OTHERSYDE BAR
The Engineer's House, Cambridge CB5 8HN (By invitation only)

CONFERENCE INFORMATION

VENUE

Buckingham House Conference Centre
Murray Edwards College
Huntingdon Rd, Cambridge CB3 0DF
United Kingdom
Tel. +44 01223 762 267

SPEAKER PRESENTATIONS

Please be sure that you upload your presentation to the computer at the latest in the break before your session. Presentation files should be in powerpoint or pdf format. If you would prefer to use a Mac, please bring your own laptop and make sure you have a VGA or HDMI adaptor.

POSTERS AND LEAFLETS/LITERATURE

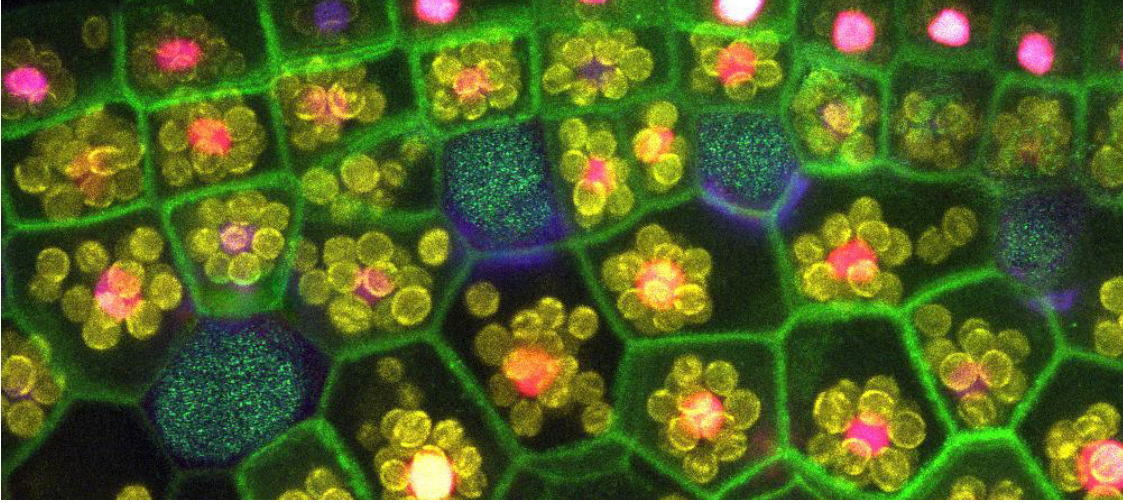
Poster boards and velcro will be available in the seminar room for those who have registered to bring a poster. You are welcome to attend your poster at any time during the breaks, but please make sure you stand next to your poster during lunch on Tuesday 30 July if you are allocated an even number and during lunch on Wednesday 31 July if you are allocated an odd number.

WIFI

Eduroam is available onsite or conference centre Wi-Fi is available at registration.

SOCIAL MEDIA

The OpenPlant Twitter account is @_OpenPlant and we will be tweeting on #OpenPlantForum. Please join the conversation!



PARKING

Parking is on a first come first serve basis. There are 70 spaces available and more parking is available in Storey's Way. The college can reserve spaces for anyone with a disability. Please enquire at the registration desk. More information about the car park can be found via *www.murrayedwards.cam.ac.uk/contact/find-us*

PHOTOS/VIDEOS

We will be taking photos during the forum that may be used on the website and to advertise future events. If you do not wish to appear in event photos, please make yourself known to the registration desk.

CONTACT US

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Photograph by Fernan Federici

POSTER ABSTRACTS

1. THE ROLE OF PECTIN METHYLESTERASES IN EARLY LAND PLANT DEVELOPMENT

Giulia Arsuffi[1], Thomas Torode[1], Keisuke Inoue[2], Ryuichi Nishihama[2], Takayuki Kohchi[2], Siobhan Braybrook[3], Sebastian Schornack[1]
[1]The Sainsbury Laboratory, University of Cambridge, [2]Kyoto University, Kyoto,[3]University of California Los Angelos, USA

Mechanisms to modulate cell wall properties enabling growth and development have been studied extensively in vascular plants. Yet, how these systems have evolved across the plant tree of life remains to be studied. De-esterification of pectin, a major cell wall component, is known to modulate cell growth and expansion in vascular plants. We detected de-esterified pectin in Marchantia in varying amounts across the thallus. To address a conserved role for pectin methylation changes we studied the role of *pectin methylesterase* (PME) genes in growth and development of the liverwort *Marchantia polymorpha*. The PME family is smaller in Marchantia compared to Arabidopsis and we found that *PME* genes, in particular *MpPME11*, are differentially expressed in growing vs non-growing areas of the thallus. The *MpPME11* promoter is active in the notch area. Similar to wild type plants treated with PME chemical inhibitors, *pme11* mutants display impaired thallus growth, slower regeneration and dorsal rhizoid overproliferation. Together, our data suggest that pectin de-esterification enzymes likely fulfil conserved roles in liverworts and vascular plants and that pectin remodelling may be a core strategy for developmental modulation.

2. THE ENGINEERING OF THE DIATOM PHAEODACTYLUM TRICORNUTUM FOR PLANT SPECIALIZED METABOLITE PRODUCTION

Andrew Diamond[1], Samuel S. Slattery[2], Jasmine A. Therrien[2], Aracely M. Diaz-Garza[3], Simon Barbabe[1], Bogumil Karas[2, 4], Isabel Desgagné-Penix[1]
[1]University of Quebec at Trois-Rivieres, Canada [2] Western University, Canada [3] Tecnológico de Monterrey Campus Guadalajara, Mexico, [4]Designer Microbes Inc.

The development of recent genetic tools has expanded the possibility for engineering the diatom *Phaeodactylum tricornutum*. Our goal is to use this microorganism as a platform for various synthetic biology applications including the production of plant specialized metabolites, like vanillin. Recently, the eight genes from the orchid *Vanilla planifolia* that are involved in the vanillin biosynthesis from amino acids were elucidated. However, some researchers showed that there was controversy in the proposed metabolic pathway of vanillin. The activity of the last enzymes involved in the pathway, vanillin synthase that converts ferulic acid into vanillin, is the main cause of this controversy.

We developed an episomal vector containing the eight genes encoding the biosynthetic enzymes involved in vanillin biosynthesis. Those genes have been linked in pairs using a 2A peptide linker that self-cleaved during translation. Those four constructions use different combinations of promoters and terminator to enhance the expression of transgenes.
We demonstrated that an episome of more than 33 kb can be propagated in P. tricornutum for long-term culture without rearrangements. RT-PCR analysis has demonstrated the expression of transgenes mRNA from the constructions present in a single episomal vector. Primary results from metabolomics analysis demonstrate that vanillin derivatives could be produced by the engineered P. tricornutum strains. Results indicate that P. tricornutum is a

promising candidate as a synthetic biology platform to produce plant specialized metabolites such as vanillin.

3. INVESTIGATING GENETIC MARKERS INVOLVED IN AIR CHAMBER DEVELOPMENT IN MARCHANTIA POLYMORPHA

Marta Tomaselli, Marius Rebmann, Eftychis Frangedakis, Susana Sauret-Gueto, Jim Haseloff
University of Cambridge

Marchantia polymorpha is considered to be one of the closest living relatives of early divergent land plants. It is an emerging plant model system with a small genome, low gene redundancy and a set of highly efficient molecular tools for genome manipulation. It has a simple sheet-like body structure with recognisable differentiated structures: rhizoids emerging from the ventral side and air chambers, small photosynthetic units, covering the dorsal layer. Air chambers are formed of a ring of cells called airpore which connects the plant with the environment, and they are filled with filamentous photosynthetic cells rich in chloroplast. They are continuously generated in the meristematic region, close to the apical cell, but very little is known about air chamber development or the transcription factors involved in the process.

In my PhD, I am aiming to build a developmental map of air chamber formation and investigate cellular markers (cell type specific promoters fused to fluorescent proteins) which are involved in this process. To expand the collection of available markers, a transcription factor promoter library has been generated and I am currently testing Marchantia orthologues to TFs involved in epidermal patterning or asymmetric cell divisions. An RNA-seq library comparing the transcriptome of WT and *NOPPERABO1* mutant plants, which completely lacks air chambers, at different time points has been prepared to further investigate genes involved in air chamber development. All the above will provide insights into air chamber patterning in Marchantia.

4. IMPROVING NICOTIANA BENTHAMIANA AS BIOPRODUCTION SYSTEM FOR PROTEINS AND SMALL MOLECULES

Quentin Dudley[1,2], Sarah O'Connor[3], Nicola Patron[1]
[1]Earlham Institute, [2]John Innes Centre, [3]Max Planck Institute for Chemical Ecology, Germany

The wild tobacco relative *Nicotiana benthamiana* is a commonly used plant for manufacturing proteins and reconstituting metabolic pathways which produce complex metabolites such as fragrances or medicines. In particular, the plant can transiently express heterologous multi-enzyme pathways in just a few days. However, small molecule compounds and their intermediate pathway metabolites produced in *N. benthamiana* are often over-glycosylated, oxidized/reduced, acylated or modified with glutathione by enzymes native to *N. benthamiana*. This unwanted activity has challenged efforts to reconstitute the 11-step pathway to strictosidine (an alkaloid precursor to the anti-cancer drug vinblastine). Therefore, to improve *N. benthamiana* as a bioproduction platform, we are using the RNA-guided Cas9 nuclease to deactivate the native enzymes that likely make unwanted modifications to the target metabolite. As a proof-of-concept, we have demonstrated activity of SpCas9 nuclease to make targeted double-strand breaks (producing insertion/deletions) that inactivate the

peroxidase NbPOX1. Next, we have used transcriptomic and phylogenetic analysis to select candidate genes for inactivation from among hundreds of possible enzymes. Finally, we have adapted cell-free protein synthesis (CFPS) to manufacture candidate glycosyltransferases to screen their activity towards pathway intermediates geraniol and cis-trans-nepetalactol.

5. GENSPACE: A COMMUNITY BIOLOGY LAB DESIGNING LOW-COST EXPRESSION OF INSULIN IN MARCHANTIA

Tina Shing Li Lai, William Shindel, Rachel Haberstroh, Jesseon Chang, Daniel Chan, Kris Sandine, Waldemar Matuska, Regina Goetz, Tricia Wang, Gordon Fleetwood, Grant Langseth, Eugene Fong, Vanessa Munoz, Irene Rostovsky, Lori Solondz, Aaron Kigler, Upom Malik, Rabaa Baitalmal, Edward Gordon, Lior Cole
Genspace, New York, USA

Insulin is a protein hormone with an essential role in keeping glucose homeostasis in check. Over 420 million people worldwide have diabetes, many of which depend on insulin therapy. As the disease continues to rise around the world, there is a need for making insulin production more sustainable and adaptable to the demands of local communities, especially socio-economically disadvantaged ones.

The OpenPlant Community Project at Genspace, the world's first community biology laboratory, is developing a low-cost table-top incubator for growth of the liverwort *Marchantia polymorpha*, genetically engineered to express insulin. The project draws from the uniquely diverse expertise of Genspace community members and from resources of the UK OpenPlant Initiative. Our liverwort incubator is equipped with a white LED strip as light source and a cooling fan for temperature control. These functions are computer controlled, and code written for this is available on the open-source platform, GitHub. A second version of the incubator, currently in development, collects images and analyzes them through computer vision to monitor growth and health.

To efficiently express insulin in the liverwort, we are employing Agrobacterium-mediated transformation. The liverwort is first transformed with the gene encoding red fluorescent protein (RFP) and gene insertion into the liverwort genome is analyzed by screening liverworts showing high levels of red fluorescence while retaining growth and health. Using CRISPR technology, the *RFP* gene is then replaced with the human insulin gene in those genomes. Through this community project, Genspace members seek to contribute to the mission of the UK Open Plant Initiative, developing and sharing tools for better and more sustainable bioproduction.

6. A LOW-COST, HIGH-THROUGHPUT PIPELINE FOR ASSESSING TRANSCRIPTION FACTOR BINDING AFFINITIES

Yaomin Cai[1], Will Nash[1], Susana Sauret-Gueto[2], Eftychios Frangedakis[2], Wilfried Haerty[1], Nicola Patron[1]
[1]Earlham Institute, [2]University of Cambridge

The affinity of a transcription factor (TF) to its binding site (TFBS) can have a large effect on the strength of promoter activation, and thus is very important to the regulation of a target gene. Techniques to assess the affinity of a TF to its TFBS, such as the protein binding

microarray (PBM), are useful tools for identifying novel TFBS and comparing the binding affinity of different TFs. However, such techniques are still not widely affordable. Microplate-based protein-DNA binding assays have been developed as a cheaper alternative, with the only limiting factor being the cost of the necessary DNA modifications.

In this project, we aim to establish an affordable platform for comparing relative TF-TFBS binding affinities. We utilise a non-modified DNA immobilising method. Our platform also includes a bioinformatic pipeline to suggest novel TFBSs based on existing, population level, natural genetic variation. So far, we have established and validated the protocol for the TRAMP assay. We have also resolved the bioinformatic pipeline to the point of generating preliminary predictions of TFBS variants effecting predicted binding affinity. We are now using TRAMP to test the affinities of a range of our predicted TFBSs to their corresponding TFs (from Arabidopsis and Marchantia), as well as further developing the bioinformatic tool to consider motif breaking SNPs. The effect of new TFBS variants on the promoter strength will be assessed in the next stage of our investigation.

7. ANALYSIS OF ANTICANCER METABOLITES IN TRADITIONAL CHINESE MEDICINE SKULLCAP

Man Zhao[1,2], Melanie-Jayne Howes[3], Alan Paton[3], Evangelis Talsis[4], Cathie Martin[2]
[1]Zhejiang university of technology, China, [2]John Innes Centre, [3]Royal Botanical Garden, London, [4]Institute of Plant Physiology and Ecology CAS-CEPUMS, China

Scutellaria barbata (Ban-Zhi-Lian) is a traditional Chinese medicine, which is used extensively in treatment of cancers, particularly metastatic cancers. The efficacy of *S. barbata* extracts at reducing cancer progression as well as an absence of harmful side effects of extracts has resulted in renewed research interest in this traditional Chinese Medicinal plant. We are working to find out which compounds are responsible for these anti-cancer properties as well as identifying which other closely related species have similar properties.

8. GENOMICS-DRIVEN DISCOVERY OF NOVEL TRITERPENE BIOSYNTHETIC PATHWAYS IN THE GRASSES

Guy Polturak, Martin Dippe, Michael Stephenson, Charlotte Owen, Anne Osbourn
John Innes Centre

Plants produce a wide array of triterpenes, which play important roles, including providing protection against phytopathogens. Various triterpenes have also proven to be highly beneficial for use by mankind in medicine, food, and cosmetics. To date, studies on triterpenoid-related metabolic pathways and biosynthetic gene clusters have largely focused on compounds produced in the eudicots. Conversely, very little is known about triterpene biosynthesis in monocots. Here, we employ a genomics-driven approach to identify and characterize novel triterpene-related metabolic pathways and gene clusters in the *Poaceae* (grasses) family, focusing on compounds with potential involvement in plant defence. Genome mining of members of the *Poaceae* family was performed, resulting in the identification of 43 putative triterpene clusters from 12 species. Investigation of a gene cluster in *Brachypodium distachyon* revealed a novel biosynthetic pathway for production of arborinane-type triterpenes. An orthologous cluster was also identified in common wheat and its ancestral

species, which is elicited by fungal pathogens, suggesting that the triterpene products may play a role in plant defence. Further characterization of these and other novel triterpene gene clusters that we have identified in the grasses will ultimately provide a broad view of triterpene biosynthesis and chemical diversity in this group of plants.

9. PRECISION NUCLEOTIDE EDITING IN SUGARCANE FOLLOWING HOMOLOGY DIRECTED REPAIR OF TARGETED DNA

Mehmet Tufan Oz[1,2,3], Ratna Karan[1], Aldo Merotto[1], Fredy Altpeter[1,2]
[1]University of Florida, USA, [2]Center for Advanced Bioenergy and Bioproducts Innovation, USA, [3] Earlham Institute

Genome editing tools such as CRISPR/Cas9 enable precise targeting and introduction of double strand DNA breaks which are proceeded by cellular repair mechanisms, such as NHEJ or HDR. Highly efficient NHEJ generates an abundance of random insertions and deletions (indels). Frameshift mutations associated with these indels of unspecified size and sequence might result in loss of function phenotypes of agronomic importance. Gain of function mutations, on the other hand, generally require precise nucleotide editing in the target gene and replacement of inferior alleles. This can be accomplished with the aid of a homologous repair template and the cellular HDR mechanism.

We present a highly efficient HDR mediated precision nucleotide editing in multiple alleles of the *acetolactate synthase* (ALS) gene in the highly polyploid sugarcane which confer herbicide resistance. Faithful transmission of superior *ALS* alleles with introduced target mutations at 574 and/or 653 amino acid locations to vegetative progenies was confirmed with amplicon sequencing using Sanger chain termination, PacBio SMRT sequencing and evaluation of herbicide resistance.

Acknowledgements: This material is based upon work supported by the U.S. Department of Energy, Office of Science, Office of Biological and Environmental Research (Award Number DE-SC0018420).

10. BREEDING FOR EARLY MATURITY AND IN SILICO IDENTIFICATION OF EARLINESS RELATED GENES IN PEANUT (ARACHIS HYPOGAEA L.)

Sammiya Jannat[1,3], Mahmood Ul Hassan[1], Asad Hussain Shah[2], Gabriela Toledo-Ortiz[3]
[1]University of Rawalpindi, Pakistan, [2]University of Kotli, Pakistan,[3]Lancaster University

Peanut (*Arachis hypogaea*) is one of the world's most important legume and oilseed crops due to its high nutritive and economic values. Climate changes including seasonal shifts, rain pattern change, droughts and high temperature highly influence the cropping pattern and productivity. In the rainfed areas of Pakistan, peanut is the only cash crop with immense economic importance, and is badly affected by these changes. In the present research, twenty early maturing lines from USDA and four (4) local high yielding varieties have been screened in the field on the basis of their germination time, days to first and 50% flowering and yield related attributes. Maturity was further characterized by harvesting the crop at different stages and counting mature and immature seed numbers. Then four (4) selected early maturing, adaptable exotic lines were subjected to crossing with three (3) local varieties, using the line x tester mating design and the F1 generation was produced. Significant results were obtained in terms of gene action and heritability on parental and F1 analysis on the

basis of morphological data. The homologs of genes associated with earliness including genes from FT family, *CONSTANS* like genes and *Phytochrome A, B* and *E* like were blasted in PeanutBase from soyabean and Arabidopsis. The the genes with more than 90 percent similarity on the basis of nucleotide and protein alignment were identified from the peanut data base for the expression analysis using qPCR.

11. DISSECTING MERISTEM REGULATION IN MARCHANTIA POLYMORPHA GEMMAE WITH SINGLE-CELL RNA SEQUENCING AND HIGH THROUGHPUT MICROSCOPY

Marius Rebmann[1], Mihails Delmans[1], Susana Sauret-Gueto[1], Marta Tomaselli[1], Linda Silvestri[1], Paul Coupland[2], Alicja Szalapak[1], Emanuele Orsini[1], Jim Haseloff[1]
[1]University of Cambridge, [2]Cancer Research UK

Plant growth is localised in meristematic regions where a precise balance of cell proliferation and differentiation is maintained by a network of transcription factors, signalling molecules and phytohormone gradients. Recent advances in genome editing pave the way for rational re-design of plant development, potentially transforming the development of new crop varieties. However, our understanding of the genetic programs underpinning development is fragmented and identifying novel regulators in traditional model systems and crops remains challenging due to their morphological and genetic complexity. The Marchantia gemma could provide a simple testbed to attempt predictable engineering of growth, but little is known about meristem regulation in Marchantia. Here we present the use of single cell RNA sequencing combined with high throughput imaging for genome wide identification of meristem regulators in Marchantia gemmae.

12. MORPHOLOGICAL AND MOLECULAR ASSESSMENT OF GENETIC DIVERSITY IN DIOSCOREA SPECIES

Saheed Alarape[1, 2], Rasheed Awodoyin[1], Ben Faloye[2], Michael Abberton[2]
[1]University of Ibadan, Nigeria, [2]International Institute of Tropical Agriculture, Nigeria

Yams are starchy root staples and a primary source of income in West Africa. Yam is a multi-species and vegetatively propagated crop and an economically important staple food for more than 300 million people in low income food-deficit countries of the tropics. Knowledge of the new collections is essential to harness its full potential for food and income for the poor farmers and as well increase the genepool for yam crop improvement. Therefore, understanding the genetic diversity among the newly collected yam accessions will enhance breeding programs' decisions. This study was carried out to assess the morphological and molecular characteristics of newly collected *Dioscorea* species for genetic diversity. One hundred accessions of yam which comprised of 83 *Dioscorea rotundata* accessions, 16 *Dioscorea praehensilis* and 1 *Dioscorea cayenensis* were obtained from Benin Republic. A field experiment was conducted in IITA, Ibadan in the 2018 cropping season, in a Randomized Complete Block Design (RCBD) with two replications. Morphological characterisation of the young and mature stems was done using yam descriptors. The quantitative data were subjected to inferential statistics while the qualitative data were subjected to descriptive statistics using SAS version 9.4. The results revealed a high morphological variability in the

yam accessions. This can provide a novel insight into the genetic diversity and population of yam accessions which can enhance its utilisation in pre-breeding programs and future conservation.

13. ESSOILDB: A SEMANTIC KNOWLEDGE BASE FOR SYNTHETIC PHYTOCHEMISTRY

Vineeta Lamba[1], Manish Kumar[1], Shruthi M[1,2], Ambarish Kumar[1], Peter Murray-Rust[3, 4], Gitanjali Yadav[1,4]
[1]National Institute of Plant Genome Research (NIPGR), India, [2]Ramaiah Institute of Technology, India, [3]ContentMine Ltd, Cambridge, [4]University of Cambridge

Terpenes are major components of phytochemical biosynthetic pathways and volatile terpenes (billions of tons emitted annually [1]) mediate specialised adaptations in the plant kingdom such as defence and communication. Terpenes also have many industrial uses (e.g. biofuels, feedstocks, fragrance and flavour and medicinal chemistry). Elucidation of product preferences for terpene synthase (TPS) by correlating the genome to terpenome, would pave the way for rational design of novel TPS enzymes, an important opportunity for synthetic biology and the bioeconomy.

The Essential Oils Database (EssoilDB) [2] has collected systematic knowledge from the scholarly literature for plants and their volatile organic profiles. We report a new version of the database based on Linked Open Data, especially Wikidata. EssoilDB contains references to ~2000 plants and ~8000 compounds which are now being normalised and made semantic through links to Wikidata and other authorities. We used Taxise [3] to disambiguate binomial plant names with 99.9% success. The compounds are being identified through OPSIN [4] , Wikidata[5], ChEBI and other sources. EssoilDB also includes observational parameters such as PlantPart, DevelopmentalStage and GeoLocation.

The new EssOilDB knowledgebase will be part of public Linked Open Data and so can be linked into chemical pathways such as WikiPathways. The resultant knowledge graph allows enrichment (drugs, invasive species, climate) and generalisations (such as “Africa”, “Monoterpenes”, “Conifers” even though these do not occur in the original article). EssoilDB can be an important information component in emerging AI in synthetic biology.

[1] https://www.ncbi.nlm.nih.gov/pmc/articles/PMC4370762/ [2] http://www.nipgr.ac.in/Essoildb/
[3] https://cran.r-project.org/web/packages/taxize/index.html [4] http://opsin.ch.cam.ac.uk/
[5] https://www.wikidata.org/wiki/Wikidata:Main_Page [6] https://www.ebi.ac.uk/chebi/

14.ADDGENE - A UNIQUE NON-PROFIT ORGANIZATION ACCELERATING SCIENCE.

Benoit Giquel
Addgene

Addgene (http://www.addgene.org) is a nonprofit organization whose mission is to accelerate research and biomedical discovery by facilitating access to useful research materials and information. To fulfill this mission, Addgene maintains a repository that distributes >70,000 plasmids contributed by scientists coming from more than 3,500 different labs all over the world. The repository stores, quality controls, and annotates the data associated with the plasmids. Addgene also provide ready-to-use viral particles produced

from select plasmids deposited in the repository. Researchers can use these viral particles directly in their experiments, thereby skipping the viral production process and accelerating their research.

Addgene's repository contains many plasmid tools that were specifically designed for Plant Biology. This includes tools for plant systems such as Arabidopsis, wheat, maize, rice, tomato, and a variety of other species, ranging from genome engineering and gene regulation to fluorescent proteins. In addition to individual plasmids, our collection also contains tools kit for easily creating plant expression vectors or for the use of the CRISPR technique.

Addgene advocates for open science and all plasmid data is made freely available to the public on our website. Addgene is also building a variety of educational resources, including protocols, videos, podcasts, blog posts, and eBooks that are accessible for free. These educational materials cover topics from basic biology to career development for an audience ranging from undergraduate biologists to tenured professors. By providing these services, Addgene's goal is to create a lasting resource for research and discovery around the world.

15. TRYOSINE-ENRICHED METABOLISM AND THE EVOLUTION OF A NOVEL TYROSINE-DERIVED METABOLITE

Hester Sheehan
University of Cambridge

Betalains are pigmented tyrosine-derived specialized metabolites that, in plants, are restricted to a single order, the *Caryophyllales*. Betalains are mutually exclusive with the otherwise ubiquitous anthocyanin pigments. Betalains are produced via a simple metabolic pathway that begins with tyrosine and requires the action of as little as three enzymes, a cytochrome P450 (CYP76AD1), a 4,5-dopa-extradiol dioxgenase (DODA), and a glucosylation enzyme, to produce the two classes of betalain pigments – betaxanthins (yellow/orange) and betacyanins (red). Over the past five years, we have assembled a dataset of transcriptomes for over 350 species, which together with over 10 sequenced genomes, covers 32/39 families and over 30% of the 752 genera in the order *Caryophyllales*. We have utilised this comparative dataset to identify lineage-specific gene radiations, step-wise gene duplications, neo-functionalisation events, and genome rearrangements that underpin the emergence of the betalain pathway. More recently we have described a previously unknown novel isoform of the enzyme arogenate dehydrogenase that has lost feedback inhibition, and which is driving the unusual phenomenon of tyrosine-rich metabolism in *Caryophyllales*. We provide evidence that tyrosine-derived betalain pigmentation has evolved directly as a result of this unusual tyrosine-rich adaptive landscape.

16. DEMONSTRATING A MATERIAL MAKING PROCESS THROUGH THE CULTIVATION OF MYCELIUM GROWTH

Dilan Ozkan
Newcastle University

Today, mycelium is used in many different ways: As packaging in industry; as acoustic panels; wall insulation; bricks in buildings; as a textile or as a raw material in designed objects such

as furniture. The purpose of this research is to explore the ways to cultivate mycelium as a living building material that has its own tendencies. Going beyond the limitations of linear moulding techniques and developing a method that guides the mycelium growth will help designers to, as Richard Sennett says, always be a step ahead of the material. The first phase of the study involves experimentation by paying close attention to any factors that might cause a difference in the behaviour of mycelium, to understand its properties and nature. After having understood its act, the research will continue by the cultivation of mycelium growth. Design of an automated system that enables to reach the intended growth, by anticipating its reactions, is going to be the end product and the final phase of this investigation. In this study, rethinking about architectural fabrication that focuses on revealing potentials of living organisms such as autonomy, self-assembly or responsivity, can demonstrate a new approach in material making processes and geometries.

17. OPEN ENZYMES FOR AN EQUITABLE BIOECONOMY

Chiara Gandini[1, 2], Jenny Molloy[1,2], Harry Akligoh[2]
[1]University of Cambridge,[2]Open Bioeconomy Lab

Enzymes are essential workhorses of molecular biology, enabling us to perform PCR, do cloning, study genes expression and synthesize complex molecules. However, access to enzymes is a major impediment to scientists in the global South and in low resourced settings like DIYBio labs, local biotechnology companies, small and medium-sized enterprises setting up biological manufacturing facilities or for practical education in biotechnology for the many.

A collection of genes that encodes for off-patent enzymes routinely used in molecular biology protocols will be made freely available under an Open Material Transfer Agreement. For each of the enzymes a tailored low-cost quality-assured protocol will be developed for their robust expression, purification (if needed) and formulation. The prototyping of genetic constructs for protein expression will be implemented through synthetic biology approaches such as the recently developed high-throughput Loop assembly. In addition, cell-free expression systems will be investigated not only as a useful tool for high-throughput prototyping of protein purification through an in-house 3D printed platform but also as a valuable tool that offers the prospect of shipping and storing a cell-free 'factory' at ambient temperature.

The open enzyme collection is a project within the Open Bioeconomy Lab, which addresses the accessibility of reagents in low-resourced contexts by providing a toolkit for local manufacture of enzymes.

18. BIOSYNTHESIS OF SILVER SILVER NANOPARTICLES USING CARICA PAPAYA AQUEOUS SEED EXTRACT FOR BIOMEDICAL APPLICATION

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The aim of this study was to perform greensynthesis of siler nanoparticles (AgNPs) from the seed extract of *Carica papaya*, a medicinal plant which is widely used across Cameroon. Synthesized AgNPs were analysed by UV-Visible spectroscopy, X-ray diffraction (XRD), Fourier transform infrared spectroscopy (FTIR), Scanning electron microscopy (SEM) and

Energy dispersive spectroscopy. The results have confirmed that green synthesis of AgNPs leads to the fabrication of sphere-shaped particles with a diameter of 9,6nm. Furthermore, these AgNPs were subjected to antioxidant (H^2O^2 scavenging and phosphomolybdate method), anti-inflammatory (against protein denaturation) and antimicrobial studies (against *Pseudomonas aeruginosa* and *Saphylococcus aureus*).

We obtained a MIC of 37.89 and same for the MBC in the case of *Staphylococcus aureus* and 75.78 as MIC and 37.89 as MBC in the case of *Pseudomonas aeruginosa*. The protein denaturation test gave an IC50 of 35.037 and the H^2O^2 scavenging method gave IC50 of 233.38 and phosphomolybdate method, 289.22 µg/ml. *Carica papaya* are available through out the year in Cameroon and the ecofriendly approach of synthesis coupled with its bioactivity has demonstrated its potential as a novel biomaterial which can be used for various biomedical applications.

19. APPLICATION OF BACTERIAL CELLULOSE FOR ARCHITECTURAL MATERIAL SYSTEMS AND DESIGN

Sunbin Lee, Martyn Dade-Robertson, William Willats, Meng Zhang
Newcastle University

This research aims to examine living matter in architecture to realise a living architectural membrane. This is conducted by exploring bacterial cellulose and works towards in vivo self-growing material assembly in guided growth control of bacteria cells. In nature, cells are alive and environmentally responsive and are able to produce structural materials such as cellulose. Cellulose is the basic primordial material that forms the basis of organisms and plant systems. All natural materials have multifunctionally graded material properties within a single structure by combining cellulose with various materials that have different properties, including softness, hardness, permeability and transparency. Bacterial cellulose, which is a non-fuel and biodegradable material, indicates a higher strength through hardness than cellulose found in nature due to the higher density. The high water-retention level of bacterial cellulose and its mechanical properties enable its utilisation in a wide variety of fields such as biomedical devices, electronics, tissue engineering, and furniture and fabrics on multiple scales from nano to macro. Unlike the life cycle of typical non-living building materials, bacterial cellulose, as a living architectural material, can be utilised to architectural building materials by continuously providing nutrition for bacterial synthesis. It can also be combined with multiple materials such as chitin to control its stiffness, flexibility, and transparency. This can be applied to membrane structures, building cladding materials. In order to regulate the precisely guided growth of the bacterial cellulose, bacteria cells and nutrition will be provided computationally at certain points on bacterial cellulose surfaces continuously utilising a robotic arm.

20. SYNTHESIS OF NANO COMPOSITE MATERIALS FROM PLANT VIRUS

Sachin Shah, George Lomonossoff
John Innes Centre

Plant viral nanostructures offer new templates for the synthesis of metallic nanotube and nano cage structures. These nano scale structural assemblies can be serve in nanodevices, batteries, catalysis and therapeutics. Icosahedral biological nanostructures, such as cowpea mosaic virus (CPMV) and tubular structures such as Trp-RNA attenuation protein (TRAP) and tobamoviruses (TMV and ToMV), can act as templates for materials such as metals and metal oxides. We are investigating the plant rod shaped virus, non-infectious in animals, tobacco mosaic virus (TMV). Each viral particle consists 2130 identical coat proteins arranged in a hollow, helical tubular motif around a single genomic 6400 base strand of RNA. The outer and inner diameters of this nanotube are 18 nm and 4 nm, respectively, and it is 300 nm in length. The external and internal surfaces of plant virus consist of addressable active hydroxyl, carboxyl and amine functional groups. These functionalities are utilized for *in situ* nucleation of inorganic materials. Nanoparticles consisting of iron oxides have been generated on wild type TMV using wet chemistry. Dialyzed virions in aqueous suspension were mixed with aqueous Fe(II) and Fe(III) salts under controlled pH conditions generating coating with a ≈ 50 nm thick ion oxide layer. After removal of virus, high-resolution 3D-TEM tomography images of synthesised iron oxide nanotubes showed a central hollow channel running along their lengths and showed the metallic porous wall of tube. These hollow tubular nanostructures could be useful in nano-electronics and as electrode materials for batteries.

21. IMPROVING NITROGEN USE EFFICIENCY BY INCREASING CROP CONTROL OF NITRIFICATION

Maria Hernandez-Soriano[1], Simon Griffiths[2] ; Anne Osbourn[1], Tony Miller[1]
[1]John Innes Centre, [2]Crop Genetics, John Innes Centre, Norwich Research Park

Approximately half of the world food production is supported by the application of nitrogen (N) fertilizers to crops but ~50% is transformed by soil microbes (through nitrification/denitrification) and lost to the environment by leaching/gaseous emissions. Synthetic nitrification inhibitors only suppress microbial nitrification for a few days and are highly toxic. Potential alternatives are biological nitrification inhibitors (BNIs) exuded from the roots of certain varieties of plants. While modern varieties of wheat do not demonstrate BNI activity, some historic varieties have shown evidence of BNI activity. However, there is scant data available for soil systems. Selected wheat landraces including those with demonstrated ability to reduce nitrification rates are being grown seasonally in an experimental field site and in the greenhouse.

We use three complementary methodologies to measure nitrification rates in soil rhizosphere where wheat landraces are growing: a colorimetric method to determine potential nitrification rate by measuring ammonium and nitrate concentration; nitrate-selective sensors continuously monitor nitrate concentration after the addition of ammonium fertilizer; bioluminescent reporter bacteria to discriminate nitrification activity. This information will be used to: i) identify quantitative trait locus (QTL) associated with particular phenotypic

traits, e.g the production of metabolites such as nitrification inhibitors; ii) identify secondary metabolite pathways associated with BNI compound production in wheat, with the aim of introducing the trait into modern elite varieties.

22. LIVING BIO-COMPOSITE MATERIALS AS ARCHITECTURAL FABRICS

Assia Stefanova
Newcastle University Architecture, Planning & Landscape

Within modern applications, microorganisms are often combined with organic and inorganic substrates to increase their resilience, protect them from sudden environmental changes, as well as to maximize their performance and reduce the amount of space needed for them to function. Within the context of the built environment the ability to attach microorganisms onto substrates opens up the possibility of integrating and sustaining metabolic functions within the various layers of the building fabric. The term bio-composite is used in this context in relation to minimal moisture environments created by a substrate and photosynthetic organism for the purposes of CO2 fixation. The study tests a range of pottery clays (Crank ES50, Crank ES65, White Fleck, Porcelain) as substrates for sustaining *Chlorella vulgaris* a single cell photosynthetic green algae species that is affected by nutrients, amount of CO2 available and access to sunlight. Photosynthetic efficiency could reach up to 20% in *Chlorella* species compared to the typical 1% in land plants. *Chlorella vulgaris* is a preferred species for the purposes of CO2 fixation and is a promising candidate for cultivation on clay as it is a resilient species able to withstand stress factors. The study tests five different nutrient levels of BG11 growth medium that is absorbed into the clay. The study demonstrates the ability of the clay substrate to sustain and encourage growth over a 14 day period.

23. PROTEOMICS ANALYSIS PIPELINE USING R FOR PROTEOMICS

Marielle Vigouroux[1], Jan Sklenar[2], Govind Chandra[1], Laurent Gatto[3,4]
[1]John Innes Centre,[2]The Sainsbury Laboratory, Norwich, [3]University of Cambridge, [4]de Duve institute, Belgium

While the throughput of mass spectrometers used in proteomics has increased in recent years, data processing workflows are still a recognised bottleneck. Available proprietary and open-source software require a significant amount of manual intervention and processing is very slow for large datasets. There is therefore a need for a highly configurable tool that could be used for different types of experiments and would provide reproducible results. We have developed a proteomics data analysis pipeline using the existing RforProteomics Bioconductor package as an alternative to existing, commercial software with the view of improving automation and visualization of results.

24. THE EARLHAM DNA FOUNDRY: AN AUTOMATION PLATFORM FOR SYNTHETIC BIOLOGY

Jose Antonio Carrasco Lopez
Earlham Institute

The Earlham Institute's DNA Foundry has been established to provide the UK bioscience community with access to high-throughput laboratory automation. In particular, to provide

access to automated workflows for the design, building and testing of engineered organisms. To date, we have automated the fabrication of plasmid constructs at high throughput. This allows us to scale from small to large projects, generating 100's of constructs a week. We use a modular setup that harnesses an automated biobank complemented by a suite of liquid handling robots to array source plates, assemble larger constructs from standard DNA parts and perform downstream microbiological workflows. These include the delivery of DNA to biological organisms ('chassis'), high throughput plasmid DNA purification, NGS, and interrogating the function of delivered DNA by rapid, quantitative phenotyping. Our platforms also enable us to automate tasks such as media screening and optimisation, strain-screening, anaerobic and microaerophilic fermentations and high-throughput protein expression.

25. COMMUNITY RESOURCE FOR WHEAT AND RICE TRANSFORMATION

Allan Kouidri, Charline Soraru, Sarah Bowden, Melanie Craze, Emma J. Wallington
NIAB, Cambridge

The NIAB Crop Transformation facility has a proven track record in the transformation of a number of important crop species, including cereals such as wheat, barley and rice. The BBSRC BBR fund has recently awarded funding to NIAB for The Community Resource for Wheat and Rice Transformation. This project makes our wheat transformation platform freely available to academic plant science researchers in the UK for another five years and now also includes rice transformation.

We are keen to engage with wheat researchers and also with researchers working with genes from model species to test their hypotheses in wheat and rice. This will enable new genes to be evaluated more quickly in crops essential to food security worldwide, and allow researchers to amass crucial data which can be used as a basis to seek follow-on funding through traditional funding routes.

Efficient expression of genes in any system requires that regulatory elements are chosen for their temporal or spatial expression. Currently there are an insufficient number of such elements characterised for use in wheat or rice, which leads to difficulty in transferring multigene traits or complex pathways into these crops and limits the potential of the technology. Repetition of sequences within a T-DNA can lead to instability and deletion of regions prior to integration into the plant genome, or to subsequent gene silencing within the plant. We will characterise gene expression profiles with 50 different regulatory elements in stable wheat and rice transgenic lines. These will include both promoter and terminator sequences, fused to a reporter gene such as GUS or fluorescent proteins as appropriate. Annual calls for applications for the funded resource will be publicised on our website www.niab.com/pages/id/90/Crop_Transformation. To register your interest in updates by email please contact emma.wallington@niab.com

26. DIVERSITY AND SIGNIFICANCE OF MEDICINAL FLORA OF LOWER HIMALAYAS IN AZAD KASHMIR

Asad Hussain Shah, Afnan Altaf, Sobia Shabbir, Summun Zahid, Tahira Nawaz, Sammaya Jannat
University of Kotli Azad Jammu and Kashmir, Pakistan

Azad Jammu and Kashmir has been blessed with a repository of medicinal plants distributed near the plains of Punjab to the tops of Himalayan Mountains. This diversity comes due to the diverse climatic conditions prevailing in the area from sub tropical to temperate forests. The presented paper comprises of research on selected medicinal plants, (*Hippophae rahmnoides L), (Elaeagnus umbellate T), (Zanthoxyum almatum)*, *(Berberis lyceum R)* and *(Casearia tomentosa)*. These important medicinal plants have been popular for their ethnobotanical properties in the state of Azad Jammu and Kashmir and were tested for their anti bacterial, anti diabetic, anti coagulant, anti oxidant activities, insecticidal, and mosquitoes repellent properties using in-vitro methods. Sea buckthorn (*Hippophae rhamnodies L*) has been found excellent multipurpose plant species to be used in pharmaceutical, cosmetic and agriculture industry. Autumn olive (*Elaegnus umbellatae*) and (*Berberis Lycium*) have shown significant results for anti-diabetic and anti coagulant activities and have potential to be utilized for development of drugs for human use. The acetone extract of (*Zanthoxylum alamatum*) fruit has shown mosquito repellent properties. Similarly (*Casearia tomentosa*) has shown promising results to be utilized in development of Bio-pesticides in future.

27. FOCUS STACKING PHOTOGRAPHY OF CLARINET REEDS. HOW DOES MICROSCOPIC STRUCTURE AFFECT MUSICAL QUALITY?

Jennifer Deegan

I am taking close-up photographs of clarinet reeds to find out why it is that some are better than others at playing certain types of music than others. Some clarinet reeds are particularly good at producing resonant high notes, while others are very good for crossing the break legato. With careful adjustment, individual players can make good reeds even better. Clarinet reeds are made from the stems of the grass, *Arundo donax*.

There is some anecdotal knowledge in the clarinet-playing community of how reeds can be adjusted to improve musical performance, and about how different reeds of different commercial brands might vary in performance. Likewise there is good scientific knowledge of the subject within corporate research groups, but this information is kept secret. I am collaborating with the musicians on the "The Clarinet BBoard" website to look at whether my photography and their musical knowledge together could help to unravel some of the secrets in this area, and make the information available publically availabe for new learners.

I would be very interested to be in touch with possible collaborators from the grass research community and from the music community. I was previously an academic scientist and I am now a volunteer scientist on parenting career break, learning the clarinet alongside my musical son.

28. THE EXPRESSION OF JAPANESE ENCEPHALITIS VIRUS ENVELOPE GENE IN GREEN COS

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[1]Thammasat University, Rangsit Center, Thailand, [2]John Innes Centre

The expression of Japanese encephalitis virus (JEV) envelope gene in green cos leaf was a project undertaken at the John Innes Centre during 6 September to 20 October 2018 and is one of the projects of the research training program at the John Innes Centre during long vacation every year since 2010 until now. The summary of this research is as follows. The production of envelope protein of the JEV in green cos by using the envelope gene expression by 8 epitopes (MEP: multiepitope) of Japanese encephalitis virus vaccine strain SA14-14-2 that provides the highest immune response against JEV. After incorporated the envelope gene into pEAQ-HT vector, we cloned genes in Escherichia coli and Agrobacterium tumefaciens, respectively, then expressed the envelope protein of JEV in green cos leaves. The result can be seen in photographs of green cos leaves by both visible light camera and ultraviolet light camera. Further research should include the analysis and identification by chemiluminescence immunoassay and by the Matrix-assisted Laser Desorption/Ionization Time of Flight (MALDI-TOF). Further purification of the envelope protein expression of JEV in green cos that will be benefited for the production of envelope protein of the JEV plant-based vaccine.

ABOUT OPENPLANT

OpenPlant is a joint initiative between the University of Cambridge, John Innes Centre and the Earlham Institute, funded by the BBSRC and EPSRC as part of the UK Synthetic Biology for Growth programme.

Synthetic Biology offers the prospect of reprogrammed biological systems for improved and sustainable bioproduction. While early efforts in the field have been directed at microbes, the engineering of plant systems offers even greater potential benefits. Plants are already cultivated globally at low cost, harvested on the giga-tonne scale, and routinely used to produce the widest range of biological materials, from fibres, wood, oils, sugar, fine chemicals, drugs to food.

There is urgent need to improve our ability to reprogram crop metabolism and plant architecture in the face of global threats from new pathogens, climate change, soil degradation, restricted land use, salinity and drought. The next generation of DNA tools for "smart" breeding of crop systems should be shared - to promote global innovation and equitable access to sustainable bioeconomies.

OpenPlant is:

- developing new tools and methods for plant synthetic biology,
- providing mechanisms for open sharing of standardised resources,
- applying these tools to world-leading projects in trait development, and
- facilitating interdisciplinary exchange, outreach and international development.

The initiative promotes interdisciplinary exchange, open technologies and responsible innovation for improvement of sustainable agriculture and conservation.

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