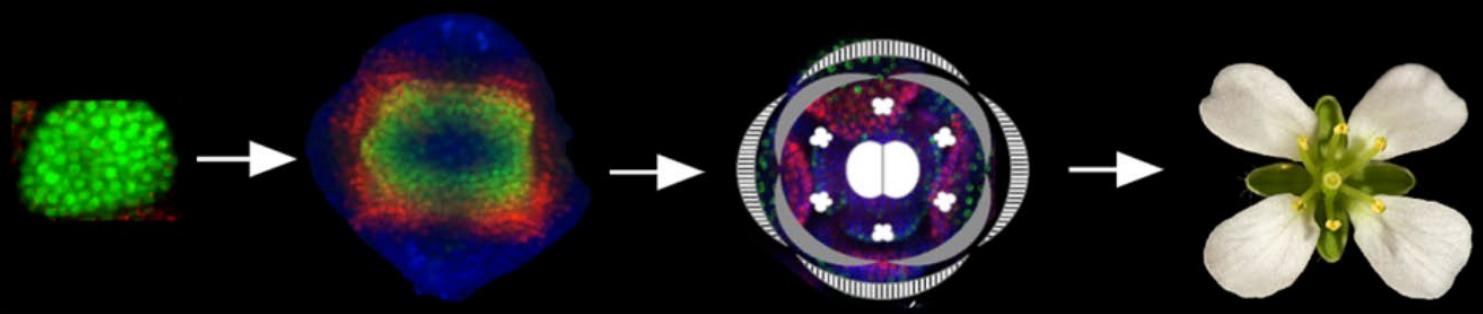
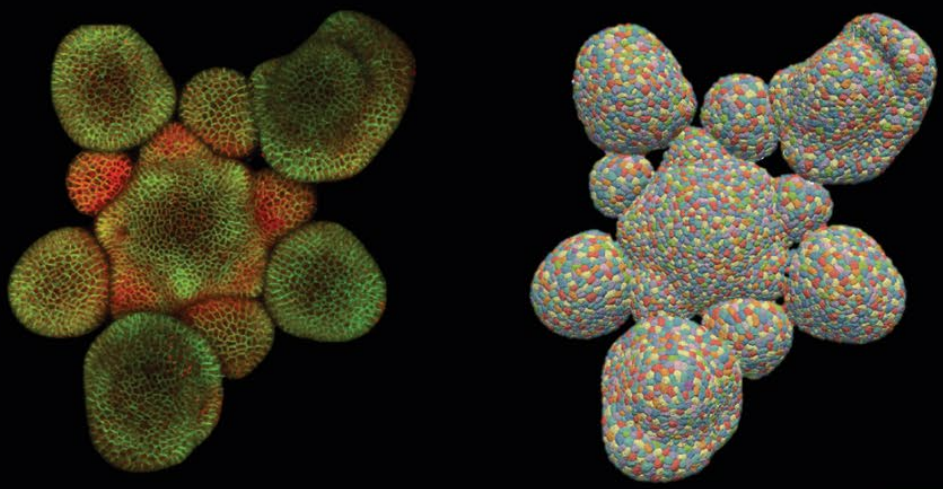


9th Plant Computational Biology Workshop

8 - 12 September 2025

Sainsbury Laboratory
University of Cambridge



THE SAINSBURY LABORATORY
UNIVERSITY OF CAMBRIDGE

Quantitative Plant Biology

Contents

Welcome

On behalf of the Organising Committee and the Sainsbury Laboratory Cambridge University (SLCU) we warmly welcome you to the 9th Annual Computational Biology Workshop. Sainsbury Laboratory Cambridge University (SLCU) and the Plant Reproduction and Development Lab, ENS Lyon jointly host the International Plant Computational Biology Workshop.

The annual meeting is spearheaded by members of the Computational Morphodynamics Group and aims to bring together scientists interested in modelling plant development and will feature invited speakers from multiple disciplines and those working on other model systems in life sciences.

The workshop features seminars based around a different theme each day and ample time for group discussions on current and future challenges in modelling development and morphogenesis. The meeting also includes more technical discussions and hackathons, where model developers aim to integrate software from different groups on image processing, meshing, and modelling.

Organising Committee

Amir Porat
Argyris Zardilis
Elise Laruelle
Henrik Jönsson
Renske Vroomans

Sponsor

This conference is sponsored by the Quantitative Plant Biology journal.

Special issue of Computational Morphodynamics

The organisers of this meeting are co-editing an issue dedicated to Computational Morphodynamics. Details of the call for papers.

General Information

Key contact

events@slcu.cam.ac.uk

Telephone
SLCU Switchboard/Reception: +44 (0)1223 761100
SLCU Security: +44(0)7780245369
SLCU Events Team: +44(0)1223 761121
Police/Fire/Emergency: 999 (when out in public)

Venue location

The Sainsbury Lab entrance is somewhat hidden. Our entry is down a driveway next to St Mary's School's Art Centre at 47 Bateman Street (What3words ref ///upon.elite.really.) The driveway next to the building leads to the main gates of the Lab. Please ring the Sainsbury Lab reception from the main gates. Our security team will let you through, after which, if you turn left, the Lab will be up the driveway on your right.

Directions from Cambridge train station

The Sainsbury Laboratory is located only 1 km, or 0.6 of a mile, from Cambridge Station. Head west along Station Rd | Turn right at Hills Road (A1307) | Turn left at Bateman Street | Turn left at the entrance (#47, before the 5th bollard).

Please do not try to enter the Botanic Garden to get to the Lab. Please use the 47 Bateman Street entrance only.

How to find us

Delegate registration

You may register at the Sainsbury Laboratory Atrium from 12:00pm on Monday 8 September. You must sign in and out at the registration desk every time you enter and leave the building – this is for health and safety to ensure everyone is safely out of the building in case of an emergency evacuation.

Name badges

Please collect your name badge at the sign-in desk and wear it while on site. Your name badge will contain the information you provided on how you wish to be addressed and your institute. The colour of the lanyard will indicate your photo consent preferences.

Luggage storage

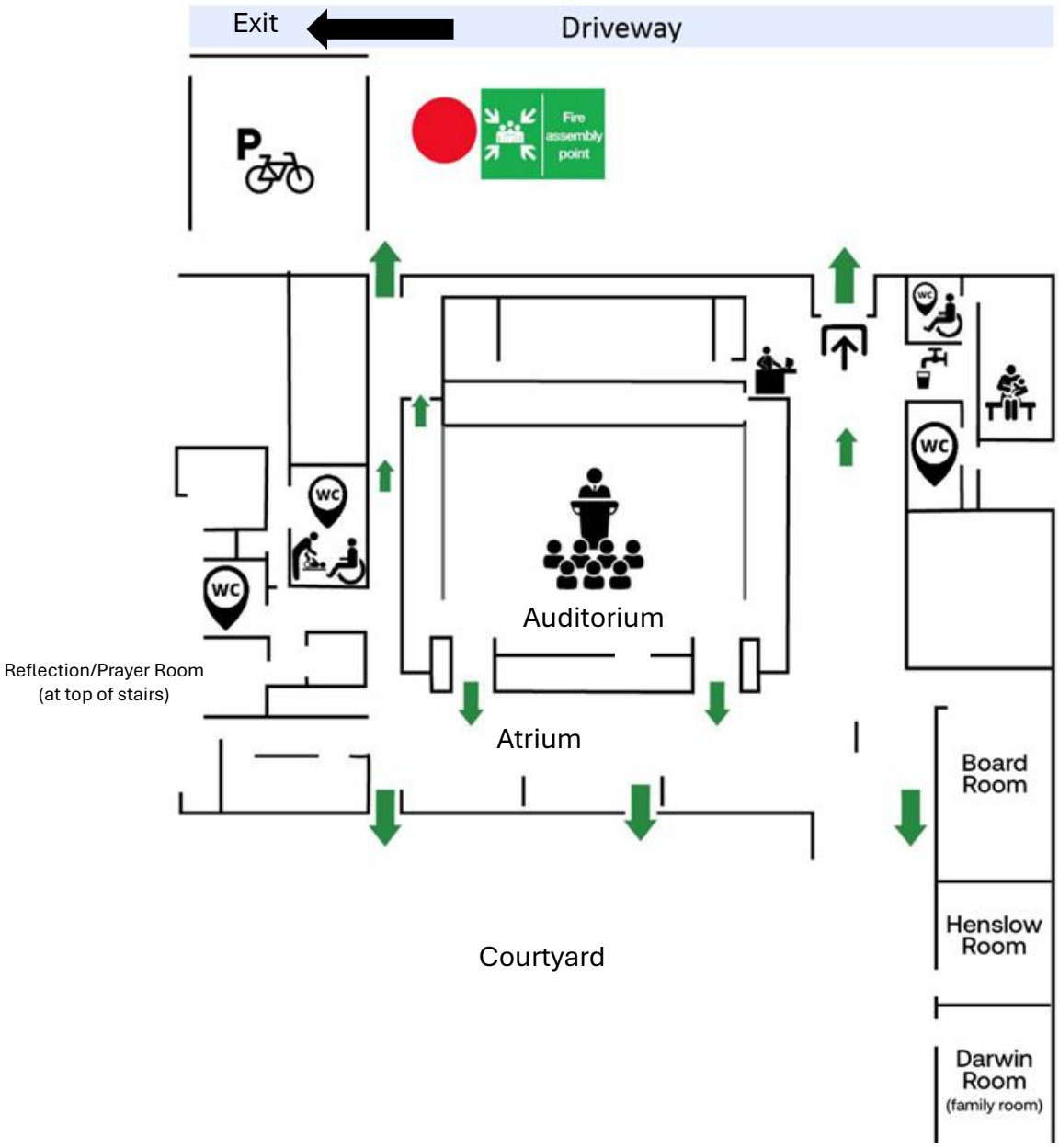
An unlocked area on one side of the auditorium is available to store luggage at SLCU. Please keep valuables with you, as the luggage area will be unsecured.

Posters

Please ensure you have the consent of all contributors to your poster to share the information on it and that you have appropriate copyright permissions in place. Your poster should be portrait orientation and B1 size (707 x 1000mm / 27.83 x 39.37 inches). We will provide poster boards and Velcro dots for your use.

First aid and fire safety

Please contact reception at SLCU should you require first aid assistance. A map indicating fire exits and mustering points is included in below.



Wi-Fi

You can access the free ‘UniOfCam-Guest' Wi-Fi network and follow the login instructions. Eduroam, the international Wi-Fi internet access roaming service for users in higher education, is also available in the building.

Prayer/Reflection Room

A dedicated room on the first floor is provided for prayer, meditation, reflection, and quiet time. There are prayer mats, and a meditation mat/cushion provided. This room can be found at the top of the stairs that are located near the kitchen.

Access to the Botanic Garden

Entry to the Garden is not permitted unless you enter during its opening hours (10:00-18:00) through its main gates and pay the relevant admission charge.

BYO Food

You will need to bring your own lunch on all days. There is an onsite cafe (Garden Café) that you can purchase food and drinks from. Please note that we have permission for delegates to visit the Garden Café, but not to enter the rest of the Cambridge University Botanic Garden unless you first purchase an entry ticket from the ticket booths at Trumpington or Hills Road.

There are also a number of bakeries, cafes and supermarkets along Hills Road that you can purchase lunch at.

Smoking

Smoking is only permitted in designated outdoor areas away from the building entrances. Please ask at reception for directions to the smoking area.

Parking

There is no car parking available at SLCU other than two spaces reserved for those who require disabled access. Please let us know if you require access to disabled parking. If you need to park in the area, full-day pay and display parking is available at the Cambridge Rail Station (0.7 miles) and Trumpington Road (0.3 miles), which are both reached via a relatively level sealed pathway.

Bicycle facilities

Bicycle parking is available in stands on-site.

Family resources

We have several onsite facilities and resources to support our meeting attendees and their families. Please contact us events@slcu.cam.ac.uk if you have any questions or suggestions for ways that we can support you during the meeting.

Lactation facilities

Breastfeeding is welcome in all public areas of the building. We also provide a private room for nursing and pumping with a separate fridge for milk storage (see building map for location).

Local attractions

Please find below links to a number of family-friendly attractions within walking distance of the meeting or accessible by public transport.

- University of Cambridge Museums and Botanic Garden
- Cambridge University Botanic Garden
- Museum of Archaeology and Anthropology
- The Fitzwilliam Museum
- Museum of Zoology
- Sedgwick Museum of Earth Sciences
- Museum of Classical Archaeology
- Kettle's Yard
- The Polar Museum
- Whipple Museum of the History of Science
- Centre for Computing History
- Cambridge Outdoor Market
- Cherry Hinton Hall Park

Professional and respectful etiquette

We are looking forward to many productive and invigorating discussions at the Computational Biology Workshop. To create a space that fosters open dialogue and where everyone feels welcomed, respected, and safe we expect that all participants will treat others with consideration and professionalism. To help create a meeting that welcomes free expression of ideas, please:

- Listen to the contributions of everyone with respect and appreciation.
- Be open to other participants' opinions. Critique ideas, not people.
- Give feedback constructively and with kindness.
- Share your thoughts and be mindful that time is limited, and others may wish to speak.

Programme 2025

All events take place in the SLCU Auditorium unless otherwise noted. Discussions will be held in various rooms (Auditorium, Board Room, Henslow Room and common areas)

Suggest Discussion Topics: Visit our Slido page to suggest and vote for discussion topics.

Day 1 – Mechanics

Monday 8 September 2025

12:45 Welcome

13:00 Invited Speaker: Osvaldo Chara – ForSys: Non-invasive inference of mechanical stress in static and dynamic tissues

14:00 Invited Speaker: Martine Ben Amar – Morpho-elasticity of thin living specimens: leaves and jellyfish embryos

15:00 Introduction and Organisation of Discussions

15:45 Coffee Break (Atrium)

16:00 Flash Talks

17:00 Poster Session (Atrium)

18:00 Drinks Reception (Atrium)

19:00 End

Day 2 – Patterning

Tuesday 9 September 2025

09:00 Presentation by *Quantitative Plant Biology* by Olivier Hamant (QPB Editor)

09:15 Invited Speaker: Kirsten ten Tusscher – The interplay between patterning and growth in shaping root architecture

10:15 Invited Speaker: David Rand – Dynamic landscape analysis: from dynamical system driven data analysis of single cell transcriptomics to predictive models of cellular decision-making with the early neural tube as an example

11:15 Discussions (various locations)

12:00 BYO Lunch (Atrium and Courtyard)

13:00 Short Talks from Sainsbury Laboratory

14:00 Discussions (various locations)

15:00 How to Get Published Workshop with QPB (Board Room) & Coffee Break (Atrium)

15:30 Technical Discussions (various locations)

18:00 Pizza (Courtyard)

Day 3 – Computer Graphics

Wednesday 10 September 2025

09:00 Invited Speaker: Eitan Grinspun – Talk Title TBC

10:00 Invited Speaker: Amir Vaxman – Discretization and representation of vector and flow fields

11:00 Coffee Break

12:00 BYO Lunch (Atrium and Courtyard)

13:00 Short Talks from John Innes Centre

14:00 Discussions (various locations)

15:00 Coffee Break (Atrium)

15:30 Technical Discussions (various locations)

18:00 Visit to a Cambridge Pub

Day 4 – Concepts

Thursday 11 September 2025

09:00 Invited Speaker: Yasmine Meroz – Plant Tropisms as a Window for Memory and Computation in Distributed Systems

10:00 Invited Speaker: James DiFrisco – The interplay between mechanics and genetics in the evolution of morphogenesis

11:00 Discussions (various locations)

12:00 BYO Lunch (Atrium and Courtyard)

13:00 Short Talks from RDP

14:00 Discussions (various locations)

15:00 Coffee Break

15:30 Technical Discussions (various locations)

18:00 Free Evening (separate private dinner for Invited Speakers)

Day 5 – AI

Friday 12 September 2025

09:00 Invited Speaker: Carola-Bibiane Schönlieb – Talk Title TBC

10:00 Invited Speaker: Ke Li – Large-Scale Foundation Models for Bioscience: From predictive modelling to biological design, towards AI scientists and future

11:00 Discussions (various locations)

12:00 BYO Lunch (Atrium and Courtyard)

13:00 Short Talks from IJPB + MPIPZ

14:00 Discussions (various locations)

15:00 Coffee Break

15:30 Technical Discussions (various locations)

18:00 Social Hour (Atrium and Courtyard)

Poster Abstracts

Learning a mechanical growth model of flower morphogenesis

Argyris Zardilis[1*], Alexandra Budnikova[1], Henrik Jönsson[1]

*argyris.zardilis@slcu.cam.ac.uk

[1]*Sainsbury Laboratory, University of Cambridge, Cambridge, UK*

Morphogenesis, the process by which organs take their shape, is a fundamental problem in biology and requires a complex combination of genetic, biochemical, and mechanical signals. The data that we collect for this process are usually multi-scale and multi-modal, typically image timeseries of tissue morphology and transcription data. As the data becomes larger and more diverse, the harder it becomes to gain meaningful understanding in terms of theoretical models. Here, and tackling this problem in the developing flower organ, we learn a mechanical model of growth starting from combined morphology and transcription data across the tissue by firstly learning and connecting independent representations for the two spaces and secondly refining the representation using the mechanical state of the tissue to learn a mechanical growth model. This approach can link multiple scales, in this case proposing the physical action of genes, and can act as a vehicle to accommodate diverse data and hypotheses in developmental biology of plants and beyond.

Coordination of cell cycle, cell growth and proliferation in the shoot apical meristem during floral transition

Chen, B.[1*], Casanova-Ferrer, P.[1], Coupland, G.[1], Formosa-Jordan, P.[1]

* bchen@mpipz.mpg.de

[1]Department of Developmental Biology, Max Planck Institute for Plant Breeding Research, Cologne 50829, Germany

The shoot apical meristem (SAM) undergoes dramatic morphological and functional changes during the floral transition. Its enlargement is referred to as 'doming'. However, the mechanisms that integrate cellular dynamics during the doming process remain elusive. Thus, this study explores the spatiotemporal patterns of cell cycle progression, cell growth, and proliferation, and investigates how these processes are coordinated during floral transition in the SAM of *Arabidopsis thaliana*, using confocal imaging and quantitative image analysis methods.

To track cellular dynamics with higher spatiotemporal resolution, we developed an optimised live-imaging method for the floral transition, which enables us to track the doming process. Using 3D segmentation and lineage tracking, we found that cell volume and proliferation increased in Layer 1 (L1) and L2 during doming. We also observed an increase in cell length, particularly in the rib zone, where cells differentiate into vascular tissue. Using the Plant Cell Cycle Indicator (PlaCCI) across different genotypes, we found G1-phase cells accumulate in the rib meristem and form a band-like structure, while G1 and S-early G2 markers are arranged in an interval pattern in wild-type plants. This pattern was more pronounced in the late-flowering *ft tsf* mutant, which exhibits a longer vegetative phase. This suggests that apical-basal zonation is coupled with higher proliferation and potential cell fate specification during the floral transition. Cell cycle analysis and live imaging revealed that cells with higher proliferation potential and mitotic activity are more prevalent in the SAM periphery and the boundary region between the primordia and the meristem.

The role of auxin transport through plasmodesmata in leaf vein patterning

David M. Holloway[1]*, Trausti K. Eiriksson[1,2] and Carol L. Wenzel[3]

*David_Holloway@bcit.ca

[1]*Mathematics Department, British Columbia Institute of Technology, Burnaby BC, Canada*
[2]*present address: Chemistry Department, University of Toronto, Canada*
[3]*Biotechnology Department, British Columbia Institute of Technology, Burnaby BC, Canada*

Veins are critical for the transport of water and nutrients within plant leaves and between the leaves and the rest of the plant. In leaf development, vein patterns are preceded by high-concentration localized tracks of the hormone auxin. Auxin regulates downstream genes involved in vascular differentiation. Proposals for the self-organizing mechanisms by which auxin canalizes from broad early distributions to later narrow prevascular tracks have been made for many decades and tested in mathematical models. Early concepts involving feedback on auxin flow have been adapted as more of the molecular biology is learned. Most models have focused on the feedback between auxin and PIN1, a membrane-bound protein involved in exporting auxin from cells. PIN mutations and interference with polar auxin transport (PAT) through PIN have strong effects on vein patterns. However, recent experiments show that even with PIN-dependent PAT presumably shut off, veins form and extend, albeit with altered patterning. This residual venation has a dependence on flow through plasmodesmata (PD) intercellular channels. We have developed a new mathematical framework for auxin flow via both PIN and PD. This produces better fits to data than prior PIN-only models, especially with respect to vein directionality and extension in reduced PIN transport conditions. Varying PD area recapitulates experimental results with PD mutants, in particular the loss of canalization at high PD permeability. The model points to several regulatory contributors involved in vein canalization, providing a new theoretical framework for characterizing the relative roles of PIN-dependent PAT and PD in regulating vein patterning in leaves.

Understanding the Biomechanics of Plant Tissues: Where to Place a New Cell Wall

Euan Smithers*[1], Mahwish Ejaz[1], Leo Serra[1], Elise Laruelle[1], Sarah Robinson[1]

*ets38@cam.ac.uk

[1]*Sainsbury Laboratory, University of Cambridge, Cambridge, UK*

How would you build a plant? Where to place the cell walls? Does this even matter? Due to turgor pressure, plant cell walls must resist substantial tensile stresses, and if not managed properly, they can lead to structural damage or an ineffective use of resources. Since plant cells are rigidly connected to one another, to resist this mechanical stress, precise control over the placement of new cell walls is vital for developing effective and efficient tissues. To explore how plants manage these stresses, we use interdisciplinary methods, such as mechanical perturbations on live tissues using an extensometer and performing finite element inflation simulations of different deformations. For this purpose, we have built up and improved existing modelling software to simulate plant tissues in 3D efficiently and with multiple layers. Through such methods, we have investigated the consequences of cell shapes and tissue structure across multiple scales. Our findings offer new insights into the role of cell division patterns, the prevalence of 3-way junctions (staggered like bricks in a wall), and why plant cells take certain shapes like rectangles. This research advances our understanding of how plants sense and respond to mechanical forces in their environment.

Understanding auxin-cytokinin antagonism in the regulation of phytohormone mediated SAM size plasticity

Heather M. McLaughlin[1]*, Henrik Jönsson[1]

*heather.mclaughlin@slcu.cam.ac.uk

[1]*The Sainsbury Laboratory, University of Cambridge (SLCU), Cambridge, UK*

The shoot apical meristem (SAM) contains a population of slowly dividing undifferentiated cells that give rise to all aerial organs, influencing the number of leaves and flowers produced. SAM size is regulated by the phytohormones auxin and cytokinin through largely distinct mechanisms. Auxin restricts SAM size by promoting differentiation at the periphery, whereas cytokinin promotes cell proliferation and meristem expansion. These pathways interact with the core CLAVATA3 (CLV3) and WUSCHEL (WUS) meristem regulators to maintain SAM activity. We aimed to better understand how auxin and cytokinin interact with each other and with the CLV3/WUS pathway to modulate SAM size. We quantified SAM/cell size phenotypes upon hormone applications and cotreatments in high-resolution imaging experiments. We further characterised phenotypes in auxin and cytokinin pathway mutants, observing an antagonistic relationship between these hormones in cell size regulation. Candidate regulators of cell/SAM size (genes antagonistically regulated by auxin and cytokinin) were identified by transcriptomics. Mutants in these genes were generated and analysed for cell and tissue-level phenotypes upon hormone treatments to assess their necessity for hormone-mediated SAM modulation. Mutants in clv3 were also assessed to understand the interaction between auxin, cytokinin and the core SAM regulatory feedback loop. Auxin partly rescued the clv3 mutants enlarged SAMs, suggesting that hormone-mediated SAM size control is partly CLV3 independent. Our findings reveal an additional antagonistic interaction between auxin and cytokinin in regulating SAM size through cell size modulation, contributing to our understanding of how hormonal interactions coordinate the regulation of stem cell niches in plant development.

Analysing stiffness in layered living systems to understand surface buckling patterns

Humberto Herrera-Ubaldo[1*], Chiara A. Airoldi[1], Robert Bellow[1], Chao Chen[2], Hongbo Fu[2], Carlos A. Lugo[1,3], Sarah Robinson[3], Alfred J. Crosby[2], Beverley J. Glover[1]

*hh585@cam.ac.uk

[1]*Department of Plant Sciences, University of Cambridge, Cambridge CB2 3EA, UK.*
[2]*Polymer Science and Engineering Department, University of Massachusetts Amherst, Amherst MA 01003, USA.*
[3]*Sainsbury Laboratory, University of Cambridge, Cambridge CB2 1LR, UK.*

Development of a living organism is a highly regulated process during which biological materials undergo constant change. *De novo* material synthesis and changes in mechanical properties of materials are key for organ development; however, few studies have attempted to produce quantitative measurements of the mechanical properties of biological materials during growth. Such quantitative analysis is particularly challenging where the material is layered, as is the case for the plant cuticle on top of the plant epidermal cell wall. Here, we focus on *Hibiscus trionum* flower petals, where buckling of the cuticle forms ridges, producing an iridescent effect. This ridge formation is hypothesised to be due to mechanical instability, which directly depends upon the mechanical properties of the individual layers within the epidermal cells. We present measurements of the mechanical properties of the surface layers of petal epidermal cells through atomic force microscopy (AFM) and the uniaxial tensile tester for ultrathin films (TUTTUT), across growth stages. We found that the wavelength of the surface ridges was set at the ridge formation stage, and this wavelength was preserved during further petal development, most likely because of the plasticity of the material. Our findings suggest that temporal changes in biological material properties are key to understanding the development of biological surface patterns. Now, we are studying how variation in the stiffness of the layers could explain the striation patterns observed in some mutant lines.

The physical, social and genetic dynamics of plant mitochondria: linking dynamics with mtDNA

Joanna M Chustecki [1*], Alora Q Schneider [1], Madeleine H Faber [1], Bara Altartouri [2], Alan C Christensen [1]

*joanna.chustecki@biology.ox.ac.uk

[1]School of Biological Sciences, University of Nebraska-Lincoln, Lincoln, Nebraska, USA.
[2]Department of Biochemistry and Center for Biotechnology, University of Nebraska-Lincoln, Lincoln, Nebraska, USA.

Plant cell mitochondria exhibit collective behaviours, with individuals moving rapidly and interacting. Mitochondrial populations are evenly spread across cellular space while forming efficient networks with high potential for exchanging contents. A framework of single-cell confocal microscopy, physical modelling and graph theory quantified behaviour and connectivity of the intracellular social network. This analysis can now include functional information on genetic contents and exchange across the population. Exogenous nucleotide staining and live imaging of *Arabidopsis* hypocotyl cells quantified mitochondrial subpopulations and potential mtDNA exchange events. By tracking individual organelles and their contents a detailed, quantitative, single-cell view can be taken. Cell segmentations and 3D image analysis counted individual mitochondria per cell, and those with/without mtDNA. We also introduced a genetically encoded photoconvertible fluorescent marker for mtDNA based on the bacterial H-NS binding protein. Plant mtDNA exhibits high rates of recombination. It is hypothesised that plant mitochondria retain individual, non-reticulated shapes partly to segregate genomic material. My previous work shows that genetic perturbation leads to altered physical dynamics, and live imaging with photoconversion of mtDNA allows direct testing of physical control over the genome. Using these tools will allow us to probe the link between physical control of colocalisation, positioning and genetic dynamics- particularly in relation to plant development and mtDNA inheritance to the next generation.

Connections
Lab website

- https://sites.google.com/view/licausi-lab/team

Socials

- https://bsky.app/profile/chusteckisci.bsky.social

https://x.com/ChusteckiSci

Quantitative analysis and modelling of temporal integration of auxin-signalling in the Arabidopsis Shoot Apical Meristem

John Thampi[1*], Hugo Caumon[1], Guillaume Cerutti[1], Christophe Godin[1], Teva Vernoux[1]

*john.thampi@ens-lyon.fr

[1]*Laboratory of Plant Development and Reproduction, Ecole Normale Supérieure de Lyon, France*

Plants have the capacity to grow and produce organs throughout their lifetime, producing robust, rhythmic, and often striking organ patterns - called phyllotaxis. As is typical in developmental systems, plants generate phyllotactic patterns from underlying spatiotemporal patterns of morphogens; in the shoot apical meristem of Arabidopsis thaliana, auxin is the primary morphogen responsible for the determination of robust spatial and temporal periodicity of organs. Accumulations of auxin have been shown to initiate new organ primordia and mathematical models of polar auxin transport have aided our understanding of this phenomenon. However, recent observations (1) suggest that there is stochasticity in auxin levels in individual cells and that cells integrate auxin information over time to initiate organs. We hypothesise that temporal integration is important in maintaining robust temporality of organogenesis and that this process is mechanistically regulated through chromatin accessibility driven by histone modification. In order to infer a phenomenological model of the process of temporal integration, we use a control systems approach (3) to analyse single-cell fluorescence microscopy data, and test its properties as an information processing system. We develop a mechanistic model of auxin-driven chromatin dynamics using Markov chains (2) to represent chromatin states and transitions. Our project aims to solidify and further our understanding of auxin as an organiser of dynamic positional information in the shoot apical meristem.

References

1. Carlos S Galvan-Ampudia, Guillaume Cerutti, Jonathan Legrand, Géraldine Brunoud, Raquel Martin-Arevalillo, Romain Azais, Vincent Bayle, Steven Moussu, Christian Wenzl, Yvon Jaillais, Jan U Lohmann, Christophe Godin, Teva Vernoux (2020) Temporal integration of auxin information for the regulation of patterning eLife 9:e55832

2. Eck E, Liu J, Kazemzadeh-Atoufi M, Ghoreishi S, Blythe SA, Garcia HG. Quantitative dissection of transcription in development yields evidence for transcription-factor-driven chromatin accessibility. Elife. 2020 Oct 19;9:e56429. doi: 10.7554/eLife.56429. PMID: 33074101; PMCID: PMC7738189.

3. M. Rivière, & Y. Meroz, Plants sum and subtract stimuli over different timescales, Proc. Natl. Acad. Sci. U.S.A. 120 (42) e2306655120, https://doi.org/10.1073/pnas.2306655120 (2023).

The mechanistic basis of trichome patterns and their diversity

Josep Mercadal[1]*, Pau Formosa-Jordan[1]

*jmercadal@mpipz.mpg.de

[1]Max Planck Institute for Plant Breeding Research, Cologne, Germany

Trichomes are specialized epidermal cells whose functions range from protecting plants from insect herbivores and UV light, increasing tolerance to freezing, to regulating plant water loss and temperature. During leaf development, trichomes emerge in periodic spatial patterns resulting from a complex network of regulatory interactions. However, understanding the key factors and mechanisms determining the spatiotemporal behavior of trichome patterns remains challenging due to the network's inherent complexity. While simple models of trichome patterning have been proposed, their mathematical properties have not been thoroughly explored and fall short of explaining the full diversity of trichome patterns observed in nature. Here, we use mathematical modeling and spatial analysis to show that simple models of trichome patterning already contain the essential ingredients for generating diverse patterns. Specifically, we demonstrate that cell-intrinsic bistability, together with lateral inhibition mediated by a mobile factor, is sufficient to reproduce the range of patterns observed in wild-type and trichome-specific mutants, including changes in trichome density, different pattern wavelengths, and the presence of trichome clusters. By analyzing the system through bifurcation theory, we map different patterning outcomes to distinct regions of parameter space, revealing how changes in regulatory interactions shape pattern diversity. Moreover, we explore the spatiotemporal dynamics of trichome initiation during leaf growth, revealing fundamental mechanisms of cell-type patterning in growing tissues. Our work provides a theoretical framework to understand the diversity of trichome patterns and their underlying mechanistic basis, highlighting how the intrinsic adaptability of the trichome network enables diverse developmental responses to changing environmental conditions.

Explaining a Franken-leaf: how violating boundaries leads to perturbation of cell growth direction

Maio, K.[1*], Cheng, J.[1], Lee, K.[1], Coen, E.[1], Sablowski, R.[1], Smith, R.[1]

*Kestrel.Maio@jic.ac.uk

[1]*Norwich Research Park, Colney Ln, Norwich NR4 7UH (John Innes Centre, Norwich, United Kingdom)*

The Arabidopsis thaliana leaf is characteristically flat and ovate. Two domains are required to form this shape: the adaxial and abaxial domains face towards and away from the meristem respectively. These two domains are mutually antagonistic – at the point where they meet, a boundary forms (termed the midplane), which informs polarity in leaf development and directs the development of the leaf blade. The development of this leaf shape is dependent on the careful coordination of growth. It relies upon high proximo-distal and medio-lateral growth as well as significantly lower growth in the adaxial-abaxial direction, about the boundary. This project explores whether ectopic boundary formation would be sufficient to induce tissue outgrowth from the leaf surface, by investigating shifts in adaxial–abaxial identity. This raises two hypotheses: a) that inducing an ectopic adaxial/abaxial sector would result in the development of a boundary, and b) that the formation of this boundary would redirect cell growth. The hat3athb4 double mutant is used as a model to explore these hypotheses. This mutant, which lacks two transcription factors regulating adaxial identity (HAT3 and ATHB4), develops tissue outgrowths from the adaxial surface. This project aims to determine whether these outgrowths result from mosaic loss of adaxial identity coupled with gain of abaxial identity, and how these identity changes interact with known boundary and margin genes, using a mixture of confocal microscopy, optical projection tomography, and computational modelling in GFtbox (MATLAB).

Sporopollenin chemical plasticity modulates pollen mechanics and resistance to hypoosmotic shock

Lei Xu[1*], Yifan Ju[1], Gui Yan[1], Anmei Zhu[1], Lei Li[2] and Yuchi He[1]

*lei.xu@hubu.edu.cn

[1]*School of Life Sciences, Hubei University, Wuhan, China*
[2]*State Key Laboratory of Protein and Plant Gene Research, School of Advanced Agricultural Sciences, Peking University, Beijing, China*

Sporopollenin, a structurally complex, chemically recalcitrant biopolymer, forms the outer exine layer of plant spores and pollen, protecting them from abiotic stress. Varying levels of phenolic constituents are incorporated as building blocks into sporopollenin in many species, but the structural and adaptive significance of sporopollenin decorated with phenolics remains unclear. Using an optimized alkaline hydrolysis method and NMR spectroscopy, we determined that plants have evolved the ability to incorporate phenolic compounds into sporopollenin in a phylogenetically ordered manner. Covalently linked phenolic constituents, including *p*-coumarate, ferulate, *p*-hydroxybenzoate and the canonical monolignol *p*-hydroxyphenyl (H) unit, occur in sporopollenin of vascular but not non-vascular plants. Evolutionary analyses showed that the metabolic scaffold for phenolic precursors evolved before the integration of phenolics into sporopollenin in tracheophytes. The conserved class III peroxidase PRX36, which is responsible for incorporating monolignol H unit into sporopollenin and contributes to maintaining pollen viability under hypoosmotic shock, co-evolved with p-hydroxyphenylation of sporopollenin in angiosperms, driving the prevalence of *p*-hydroxyphenylated sporopollenin. These findings provide an evolutionary framework for understanding genetic associations with sporopollenin chemical diversification and plant adaptation, and suggests a new way to genetically reconstruct sporopollenin biosynthesis in plants.

Integrative modelling of plant growth

Mélanie De Oliveira E Silva[1], Kalina Haas[1], Herman Höfte1, Alexis Peaucelle[1]

*melanie.de-oliveira-e-silva@inrae.fr

[1]Université Paris-Saclay, INRAE, AgroParisTech, Institut Jean-Pierre Bourgin (IJPB), 78000, Versailles, France

Understanding plant growth is crucial to predict crop yield evolution, a major challenge today. Plant growth is closely linked to the expansion of the cell wall, a complex network of polymers and proteins, fundamental to plant cell architecture. A key question is how can the cell wall expand without succumbing to the stress imposed by the turgor pressure. I will present advancements in a numerical model for growth and morphogenesis based on cell wall mechanical and biochemical characteristics, utilizing a nonlinear 3D finite element method. This model is currently developed in pavement cell and designed to have explicit dependency of variables on experimental data whenever possible. It is implemented in python. Special attention is given to technical aspects, such as model reliability, boundary conditions or mechanical formalism. The cell wall is defined as an isotropic, nearly incompressible, hyperelastic material. To model its expansion, a multiplicative decomposition of the deformation gradient is employed and adapted within a mixed formalism for this type of material. Through this model, we aim to explore the integration of various non-mutually exclusive growth mechanism as well as biochemical processes such as rapid regulatory mechanisms to simulate and potentially predict cell wall expansion.

Monitoring of Coffee Farms Using Computer Vision-Aided Intelligent System

Muhammad Noman[1*], Francisco Eron[1], Raphael Ricon de Oliveira[1], Antonio Chalfun-Junior[1]

*muhammad.noman@unimi.it

[1]Laboratory of Plant Molecular Physiology, Plant Physiology Sector, Department of Biology, Institute of Natural Science Federal University of Lavras, Lavras, MG, Brazil 37200-900

Earlier, researchers have employed computer vision-based automatic fruit detection to estimate coffee yield at the time of harvest, however, studies on the on-plant quantification of the coffee fruit are scarce. In this study, the latest version of the state-of-the-art algorithm YOLOv7 (You Only Look Once) was used for the first time. YOLOv7 was trained with 324 annotated images of fruit bearing coffee branches followed by its evaluation with 82 annotated images as validation data (supervised method) and then tested through raw images (unannotated) as test data. Meanwhile, the K-means models were trained which led to machine-generated color classes of coffee fruit for semi-supervised image annotation. Consequently, the developed model efficiently analyzed the test data with an mAP@.5 (mean average precision) of 0.89. Strikingly, our innovative semi-supervised method with an mAP@.5 of 0.77 for multi-class mode surpassed the supervised method which had mAP@.5 of only 0.60, leading to faster and more accurate annotation. While testing the yield estimation of the model in two plots, an average error of 3.78% was recorded between the predicted (pre-harvest) and ground truth (harvest) data for binary class mode. The average error for multi-class data was recorded as 3.87% for green, 3.445% for green-yellow, 5.09% for cherry-raisin, and 2.51% for dry fruits. This AI-based technology when integrated with other tools such as UAV would efficiently remotely monitor coffee field for informed decision about irrigation, fertilizer application and other measures of timely field management, hence advancing precision agriculture. Moreover, this machine learning intelligent model can be tailored for various other fruit farming.

Keywords: Coffee, precision agriculture, machine learning, artificial intelligence, digital phenotyping

Ubiquitous systems drift in the evolution of development

P.L. van der Jagt[1,2*], S. Oud[1,2], R.M.A Vroomans[1,2]

*plv21@cam.ac.uk

[1]*Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge, CB2 1LR, UK*
[2]*Department of Genetics, Downing Site, University of Cambridge, Cambridge, CB2 3EJ, UK*

Developmental systems drift (DSD) is a process where a phenotypic trait is conserved over evolutionary time, while the genetic basis for the trait changes. DSD has been identified in models with simpler genotype-phenotype maps (GPMs), however the extent of DSD in more complex GPMs, such as developmental systems, is debated. To investigate the occurrence of DSD in complex developmental GPMs, we constructed a multi-scale computational model of the evolution of gene regulatory networks (GRNs) governing plant meristem (stem cell niche) development. We found that, during adaptation, some regulatory interactions became essential for the correct expression of stem cell niche genes. These regulatory interactions were subsequently conserved for thousands of generations. Nevertheless, we observed that these deeply conserved regulatory interactions could be lost over the extended period of neutral evolution. These losses were compensated by changes elsewhere in the GRN, which then became conserved as well. This gain and loss of regulatory interactions resulted in a continual cis-regulatory rewiring in which accumulated changes caused changes in the expression of several genes. Using two publicly available datasets we confirmed the prevalence of cis-regulatory changes across six evolutionary divergent plant species, and showed that these changes do not necessarily impact gene expression patterns, demonstrating the occurrence of DSD. These findings align with the results from our computational model, showing that DSD is pervasive in the evolution of complex developmental systems.

Morphological Dynamics of the SAM and its relation to the stem cell niche during Floral Transition

Pau Casanova-Ferrer[1], Martina Cerise[1], Pau Formosa-Jordan[1], George Coupland[1]

*pcasanova@mpipz.mpg.de

[1]Department of Developmental Biology of Plants in the Max Planck Institute for Plant Breeding Research MPIPZ, Cologne, Germany

The floral transition converts the shoot apical meristem (SAM) from a leaf-producing vegetative state to a flower-producing inflorescence state. This switch is marked by a striking shape change: a small, flat SAM domes into a larger hemisphere, presumably to accommodate regularly spaced floral primordia. The cellular and regulatory mechanisms that drive this doming, however, remain unclear. We propose that doming arises from an internal reorganisation of the stem-cell niche maintained by the WUSCHEL (WUS)–CLAVATA3 (CLV3) feedback loop. To test this, we quantified SAM shape and gene-expression domains across the floral transition with 4D confocal imaging, automated segmentation and single-cell expression profiling. A parabolic fit to the meristem outline provides a robust morphological descriptor that can be compared across genotypes and stages. Our data reveal a transient vertical elongation of the WUS domain that precedes physical doming, while its lateral extent remains constant. In contrast, the CLV3 domain scales proportionally with overall SAM size. Remarkably, the high-expression overlap between WUS and CLV3 stays constant in volume throughout the transition, suggesting tight homeostatic control. Analyses of both loss- and partial gain-of-function *APETALA2* (AP2) mutants—candidates for modulating niche homeostasis—indicate that AP2 primarily affects transition timing and cell geometry rather than the fundamental WUS/CLV3 dynamics. We are now testing whether a minimal surface-signalling model, coupled to measured growth patterns, can reproduce these spatiotemporal changes without invoking additional regulators. Together, our results link niche-scale gene-regulatory dynamics to whole-meristem morphogenesis and provide a quantitative framework for modelling SAM shape control during developmental transitions.

Recurrent Emergence of Boundary Cell Types During Evolution of Floral Bullseye Pattern

Steven Oud [1, 2], Edwige Moyroud [1, 2] and Renske M.A. Vroomans [1, 2]

*so462@cam.ac.uk

[1]*Sainsbury Laboratory, University of Cambridge, Bateman Street, Cambridge, CB2 1LR, UK*
[2]*Department of Genetics, Downing Site, University of Cambridge, Cambridge, CB2 3EJ, UK*

Petal patterns contribute to the reproductive success of flowering plants by attracting pollinators and protecting reproductive organs from environmental factors. While some transcription factors (TFs) controlling pigment production and cuticle elaboration have been identified, little is known about the upstream developmental processes that first establish the petal regions where these regulators are active—the pre-patterning phase. Here, we developed a computational model of the evolution and development of petal patterns. We selected for gene regulatory networks (GRNs) that could generate the proximo-distal bullseye pattern of *Hibiscus trionum* petals, which resulted in robust patterning dynamics and a variety of bullseye proportions. We found that the evolution of these bullseye patterns was often accompanied by the spontaneous emergence of a third cell type at the boundary between the proximal and distal regions with a unique gene expression profile. These bullseye boundary cells appeared in the majority of simulations despite not being explicitly selected for, and we validated their presence experimentally in *H. trionum* petals. Although boundary cell types could emerge spontaneously without apparent function, our results indicate they were more often important for pattern formation and more evolutionarily stable when gene expression was noisy. This suggests that this emergent cell type contributes to reproducible bullseye formation by buffering against developmental variability. Altogether, these results illuminate the early steps of petal pattern formation and demonstrate how novel cell types arising spontaneously and repeatedly from selection on other features can help achieve developmental robustness.

Detection and validation of EST-SSR markers associated with sugar yield in sugarcane

S. Divakar[1], Ashutosh Singh[2*], Ratnesh Kumar Jha[2.1], D. N. Kamat[3]

*ashutosh@rpcau.ac.in

[1] Department of AB&MB, CBSH, Dr. Rajendra Prasad Central Agricultural University (RPCAU), Samastipur, Bihar, India 848125.
[2, 2.1] Centre for Advanced Studies on Climate Change, Dr. Rajendra Prasad Central Agricultural University (RPCAU), Samastipur, Bihar, India 848125.
[3] Sugarcane Research Institute, Dr. Rajendra Prasad Central Agricultural University (RPCAU), Samastipur, Bihar, India 848125.

Sugarcane (Saccharum spp.) is a widely grown crop that meets approximately 87% of global demand for sugar. The impact of changing climatic conditions on sugarcane growth, productivity, and metabolism results in reduced sucrose accumulation in sugarcane. Owing to its polyploidy and complex genetic nature, it is difficult to identify and map genes related to complex traits such as sucrose content. An association mapping was employed to identify genes or markers for marker-assisted selection. EST-SSR primers were obtained from in silico studies and their functionality was assessed using Blast2Go software. Thirty EST-SSR primers linked to sugar content were chosen and validated through association analysis. A total of 70 F1 diverse genotypes were phenotyped for various parameters of sucrose accumulation along with the two control lines. The results demonstrated significant variation among genotypes in sugar yield traits, including Brix value, purity, and sucrose content. Correlation studies indicated significant associations between the Brix%, sucrose content, and sucrose recovery. To prevent false-positive associations, association analysis was conducted using a mixed linear model. The analysis revealed that the SEM 407 marker was significantly linked to the Brix% and sucrose content. The SEM 407 primers were putatively associated with diphosphate-fructose-6-phosphate 1-phosphotransferase, which is linked to Brix% and sucrose content. This functional marker could be used for marker-assisted selection in sugarcane breeding programs, potentially expediting the improvement of sugar yield traits.

KEYWORDS: *sugarcane, EST-SSR, sugar content, association mapping, sucrose, marker-assisted selection*

Identifying rare cell types in the Arabidopsis Root from single cell RNA-sequencing data

Suchetana Mitra[1,3*],Silvia Grigolon[3], Olivier Martin[1,2]

* suchetana.mitra@universite-paris-saclay.fr

[1]Université Paris-Saclay, CNRS, INRAE, Univ Evry, Institute of Plant Sciences Paris-Saclay (IPS2), 91405, Orsay, France;
[2]Université Paris-Cité, CNRS, INRAE, Institute of Plant Sciences Paris-Saclay (IPS2), 91405, Orsay, France;
[3]Sorbonne Université, CNRS, Institut de Biologie Paris-Seine (IBPS), Laboratoire Jean Perrin (LJP), 75005 Paris, France;

The *Arabidopsis* root provides an excellent model to study cell fate determination, as its stereotypical cell files divide along a single axis and undergo progressive differentiation. Recent high-quality single-cell atlases of the *Arabidopsis* root transcriptome have enabled detailed profiling of differentiated cell types and their continuous transcriptional changes. However, these studies largely overlook the stem cells that give rise to these files, as they are rare, lack clear marker genes, and are challenging to isolate. Anatomical studies nevertheless reveal a well-defined spatial organization of root stem cells surrounding the “quiescent center,” which regulates stem cell activity without itself dividing. My research aims to characterize the transcriptomes of these distinct cell populations within the root stem cell niche. Identifying the gene expression profiles that distinguish these states will highlight candidate transcription factors and regulatory interactions underlying fate decisions. In parallel, I am applying spatial reconstruction approaches, including optimal transport methods, to align single-cell transcriptomes with the known architecture of the root. This integration bridges molecular profiles with spatial context, providing insights into how cell states are maintained and coordinated within the niche. Ultimately, my long-term goal is to develop a dynamic gene regulatory network model that explains root stem cell states, their spatial constraints, and the stepwise transitions underlying differentiation.

The spatial organisation of coral-algae symbiosis

Sutherland, A.1,2, Xiong, F.1,2, McLaren, S.1,2*

*sbm35@cam.ac.uk

[1]The Gurdon Institute, University of Cambridge
[2]Department of Physiology, Development and Neuroscience, University of Cambridge

How do different organisms interact to unlock new possibilities for life? The diverse capabilities of multicellular organisms stem from the spatial organisation of specialised cells. Unlike the classic paradigm of gradually specified and relatively fixed spatial cell arrangements, corals gain new specialised cell organisations by integrating algal symbionts into their cells, acquiring the ability to access nutrients from photosynthesis. This symbiosis enables corals to survive in nutrient-poor environments, unlocking the existence of the planet's most biodiverse ecosystems - coral reefs. However, the photosynthetic basis of this symbiosis is highly sensitive to the physical environment and breaks down under light and heat stress in an event called 'bleaching'. Some coral-algal partnerships persist whilst others collapse under environmental change, raising the question - how do corals and algae build a symbiosis for survival in a given environment? Using a combination of high-resolution imaging, molecular biology approaches and mechanical perturbations we reveal that algal symbionts are not passively accommodated but dynamically patterned within the host. We show that symbionts localise to the tentacles during host morphogenesis and that this organisation can be remodelled under altered environmental conditions. Using a combination of experimental biology and computational approaches, we are investigating how symbiont spatial organisation in the host is regulated and whether it can be modulated to adapt to different environmental conditions. Overall, our work aims to reveal fundamental principles of how interacting organisms dynamically shape each other's biology to survive in demanding ecological niches and has potential implications for coral reef ecosystem conservation.

A method for estimating Young's modulus of maize stalks using torsional vibration mode

Tomobe Haruka*[1], Nakashima Taiken[2], Kato Yoichiro[3]

*tomobe.haruka.58m@gmail.com

[1]*Saitama University, Japan,*
[2]*Hokkaido University, Japan*
[3]*The University of Tokyo, Japan*

Lodging in crops has been a limiting factor for crop yields. Accurate and high-throughput measurement of Young's modulus of stalks is necessary to produce varieties with high resistance to lodging in cereal crops. Recently, high-throughput techniques have been developed to measure Young's modulus of stalks. Among these methods, the method for estimating Young's modulus of a stem from the wave velocity of ultrasonic waves propagating in the longitudinal direction of the stalk is faster than existing methods. Still, the obtained Young's modulus is inconsistent with that obtained by destructive testing. Theoretically, it shows that it is difficult to obtain an accurate Young's modulus using existing methods, where a Young's modulus is obtained from the traveling time of a set of first arrivals of longitudinal waves due to the dispersion characteristics of the longitudinal waves. We hypothesized that a Young's modulus is robustly obtained using a set of the first arrival of torsional waves, which do not have dispersion. The experimental results show that the Young's modulus obtained from the torsional waves is almost equivalent to that obtained from the bending tests, which supports the hypothesis. Future research will construct the analytical dispersion characteristics of the stalk with the pith and the rind for non-destructively measure the internal structure with the elastic waves.

What are rules for division orientation in plant apical meristems?

Zhenglin, W.[1*], Robert, B.[2], Jordi, C.[3], Enrico, C.[3], Richard, S.[1]

*Zhenglin.wang@jic.ac.uk

[1]*Department of Computational and Systems Biology, John Innes Centre, Norwich NR4 7UH, UK;*
[2]*Department of Plant Sciences, University of Cambridge, Downing Street, Cambridge CB2 3EA, UK;*
[3]*Department of Cell and Developmental Biology, John Innes Centre, Norwich NR4 7UH, UK.*

The shoot apical meristem (SAM) and root apical meristem (RAM) of Arabidopsis thaliana are both regions of continuous cell division, yet they give rise to distinct cell file patterns. Cell division orientation dictates how new cell walls are placed, and the accumulation of repeated divisions with specific orientations over time accounts for the overall tissue organization and distinct cell file patterns. Within the past decades, three main theories have been introduced to predict the cell division orientation in living organisms: shortest wall rule, principal growth direction, and polarity. However, their applicability across different meristem cells remains unclear. In my project, SAM and RAM serve as model systems to test whether a universal mechanism governs division orientation or if distinct rules operate in different developmental contexts. For investigating the underlying mechanisms of cell division, 2D and 3D computational models based on the cell division of RAM and SAM also provide insights into this process. Although most previous work has focused on formative divisions creating new cell types and layers, here I focus on the symmetric cell divisions that create more files. The work aims to understand how the geometric properties of dividing cells will predict the division plane and whether this prediction can be affected by other factors, like polarity, isotropic or anisotropic growth.

Connections

- MorphoGraphX (https://morphographx.org/)