2017 FASEB Mechanisms in Plant Development Meeting Summary

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A systems biology approach to understanding development

The 2017 FASEB meeting "Mechanisms in Plant Development" launched with a keynote by **Philip Benfey** (Duke University, USA) about the current understanding of root development. He presented an analysis of the dynamics of the *SHORTROOT* (*SHR*) - *SCARECROW* (*SCR*) - *CyclinD6* (*CYCD6*) signaling network during root stem cell specification and the effects of specific carotenoid derivatives on lateral root prepatterning. Further, he proposed a minimal gene regulatory network consisting of epidermis-expressed *SHR* and *MYB36* combined with CIF2 peptide treatment, which is sufficient for endodermis differentiation and Casparian Strip formation. Finally, he presented a new root phenotyping system for direct monitoring of maize root architecture in an agricultural field setting.

Next, **Neelima Sinha** (University of California, Davis, USA) discussed mechanisms of resistance to the parasitic plant dodder (*Cuscuta spp.*) in tomato. Using transcriptomics and whole genome resequencing in resistant and susceptible cultivars of tomato (*S. lycopersicum*), she mapped loci conferring resistance to dodder infection. Furthermore, she discussed the roles of lignin deposition in cortex cells for dodder resistance. She outlined a signaling cascade involving NBS-LRR proteins as well as MYB and AP2-type transcription factors that controls the expression of genes involved in lignin biosynthesis in response to dodder infection.

Finishing the first session, **Anthony Bishopp** (University of Nottingham, UK) presented mathematical approaches to explain vascular patterning in the root. His models suggest that vascular patterning can be established independent of initial asymmetry in auxin concentrations. Instead, a model solely based on spatial constraints and root growth are sufficient to enable vascular pattern in its final form to emerge from a simple genetic network, explaining the vast diversity seen in different flowering plants.

Alternations between generations

The first session on Monday was under the theme ***Alternations between generations*** and started off with **Thomas Dresselhaus** (University of Regensburg, Germany) presenting fascinating work on a number of small signaling peptides that regulate pollen tube attraction and other aspects of fertilization in Arabidopsis and maize. He finished by presenting a recent transcriptome study regarding zygotic genome activation in developing maize embryos showing that 10% of genes are active a few hours after fertilization.

Next, **Rita Groß-Hardt** (University of Bremen, Germany) explained how the phytohormone ethylene regulates polytubey during pollen tube reception by triggering disintegration of the non-

receptive synergid. In addition, she discussed the developmental consequences associated with the attraction of supernumerary pollen tubes.

The next speaker, **Stewart Gillmor** (CINVESTAV, Mexico), discussed contrasting findings concerning the ratio of maternal and paternal transcripts during early embryo development. He highlighted his recent paper showing delayed paternal rescue of zygotic patterning mutants, and presented a new, comprehensive hybrid embryonic transcriptome suggesting a maternal gene expression bias in young Arabidopsis embryos.

Then, **Duarte Figueiredo** (Uppsala BioCenter, Sweden) highlighted the recently published work on the role of auxin in seed coat development. Auxin is produced in the endosperm and exported to the integuments in an AGL62-dependent manner, where it seems to repress Polycomb Complex genes and thus allows for seed coat formation.

Sharon Kessler (Purdue University, USA) presented recent work on the importance of the subcellular localization of MLO proteins during pollen tube reception. Additionally, she discussed ongoing work to understand the molecular basis of natural variation in fertility, resistance to powdery mildew, and ovule number.

Moritz Rövekamp (University of Zurich, Switzerland) unraveled the ancient function of the *Cr*RLK1L family in cell elongation during vegetative development by studying the single family member Mp*FERONIA* in the liverwort *Marchantia polymorpha*. He summarized preliminary results suggesting an additional role for Mp*FERONIA* in sexual reproduction.

Finally, **Siobhan Braybrook** (The Sainsbury Laboratory, UK) discussed cell wall adaptations of brown algae to different tidal zones. She presented her studies on the re-hydration of artificial cell walls and embryo development in Fucus – and highlighted the importance of charged cell wall polysaccharides for marine plant survival.

Short Range Signaling

Developmental mechanisms are often regulated by release of signaling molecules or mechanical forces and perception of these signals by neighboring cells. The afternoon session of the meeting on ***Short Range Signaling*** was opened by **Dolf Weijers** (Wageningen University, the Netherlands) discussing new players in early embryo development. Weijers showed that polarly-localized SOK proteins influence the direction of cell divisions during early embryo development. In addition, using a whole-genome approach to determine the transcription patterns along the ontogeny axis of the root, his lab found that the main patterns are expressed in two opposing gradients. He proposed the idea that in the root meristem cells gradually switch from undifferentiated to differentiated cells.

Elizabeth Haswell (Washington University in Saint Louis, USA) introduced the role of mechanotransduction and mechanosensitive ion channels in development. In Arabidopsis ten genes encode proteins closely related to the canonical MscS mechanosensitive ion channel from E. coli. Haswell showed that one of these Arabidopsis genes, MSL8, protects pollen grains from the osmotic shocks intrinsic to their development and showed that it serves as a mechanoreceptor.

The next speaker of this session, **Joop Vermeer** (University of Zurich, Switzerland) focused on cell volume control in endodermal cells overlying the emerging lateral root. He used live cell imaging to observe the cytoskeleton dynamics during lateral root growth through the endodermal cell layer. Vermeer showed that during this process microtubule arrays (visualized with MAP4) rapidly reorganise in the surrounding tissues and that a specific Arabidopsis MAP protein was induced in these cells.

Keiko Torii (University of Washington, USA) took us through the enigmas of receptor-ligand-based mechanisms defining stomata development. Torii discussed the autocrine role of EPF1 peptide in the meristemoid cells as well as ERECTA-LIKE1 receptor distribution in different cell types and its correlation with cell-specific identity.

The next talk by **Ora Hazak** (University of Lausanne, Switzerland) was dedicated to the role of the first differentiating root vascular tissue called protophloem in sensing of CLE peptides. Protophloem is a dynamic continuously differentiating tissue providing the sugars and hormones necessary for the maintenance of the root meristem. Her findings show that this tissue is responsible for the sensing of high levels of CLE peptides that results in locking of the protophloem in an undifferentiated state and later in the suppression of the root growth.

Nathanaël Prunet (Caltech, USA), presented the results of a collaborative work with Toshiro Ito and Frank Wellmer on the developmental origin of the phenotype of the Arabidopsis superman mutant, whose flowers show an increase in stamen number. Prunet nicely showed that flower patterning associates with auxin depletion and cytokinin accumulation at the boundaries between floral whorls and organs. He could demonstrate that this balance is inverted at the boundary between whorls 3 and 4 in the superman mutant. Prunet and collaborators showed that auxin biosynthetic genes are direct targets of SUPERMAN; they proposed that disinhibition of local auxin biosynthesis at the boundary between stamens and carpels is the cause of the superman phenotype.

Juan-Jose Ripoll (University of California, San Diego, USA) helped us to understand fruit growth processes. After fertilization fruit undergoes a dramatic increase in size that is essential to nourish and protect the growing seeds inside. Ripoll exploited Arabidopsis thaliana as a working platform and combined modeling, live imaging technologies and molecular genetics to follow the mechanisms that regulate fruit size and shape.

Antia Rodrigues-Villalon (ETH Zurich, Switzerland) closed the session with a discussion of the role of phosphoinositide homeostasis in vascular tissues development. During differentiation, vascular conductive cells fully (in xylem) or partially (in phloem) lose their organelles and

cytoplasm to become conductive tissues. Rodrigues-Villalon showed that imbalance in phosphoinositide homeostasis at the plasma membrane suppresses differentiation both in xylem and phloem conductive cells by affecting vacuolar biogenesis.

Pluripotency and regeneration

Rüdiger Simon (University of Düsseldorf, Germany) opened the ***Pluripotency and regeneration*** session by discussing incoherent feedback loops active during the regulation of shoot apical meristem development in Arabidopsis. From genetic studies and fluorescence microscopy he identified previously uncharacterized members of the CLE peptide family that potentially restrict meristem size from the periphery of the *CLAVATA3* domain.

Next, **Michael Scanlon** (Cornell University, USA) presented genetic and genomic analyses of maize leaf development. He showed the genetic dissection of the *narrow sheath* (*ns*) mutant, which results from mutations in two *WOX3* transcription factor genes, *NS1* and *NS2*. From RNA-seq and ChIP-seq experiments on laser microdissected shoot apices he concluded that *NS1* is expressed in the pre-primordial margins and functions in recruiting the lateral domain of the maize leaf.

Agata Burian (University of Silesia, Poland) then proposed a microRNA-mediated signaling pathway that regulates axillary meristem development in Arabidopsis. Using live imaging she visualized miRNA expression patterns at the position of future axillary meristems that suggest roles of miRNAs in the timing of axillary meristem release.

Akira Iwase (RIKEN, Japan) started the second half of the session, with a discussion on wound-induced cellular reprogramming by the AP2/ERF transcription factor *WOUND INDUCED DEDIFFERENTIATION 1* (*WIND1*). He presented ChIP-seq and RNA-seq experiments that identified direct *WIND1* target genes, which may contribute to restoring pluripotency at sites of wounding.

Next, **Ken Birnbaum** (New York University, USA) talked about mechanisms of tissue reorganization during regeneration, using wounded Arabidopsis root tips as an experimental model. He used single-cell transcriptomics and time-lapse microscopy to show that patterning of the root stem cell niche is re-established across groups of cells rather than from a cryptic stem cell niche, and that this re-establishment of cellular organization is preceded by the rapid expression of *MONOPTEROS* (a root specification gene) independent of auxin.

Remko Offringa (Leiden University, the Netherlands) presented a molecular switch for rejuvenation and polycarpy in flowering plants that is regulated by members of the AT-HOOK MOTIF CONTAINING NUCLEAR LOCALIZED (AHL) protein family. He showed that enhanced AHL expression rejuvenates axillary meristems in the Arabidopsis inflorescence and allows Arabidopsis plants to flower and set seed multiple times. He concluded his talk with a discussion on the potential to exploit rejuvenation biology for increased crop productivity.

Laura Ragni (University of Tübingen, Germany) closed the session with a presentation about periderm development in the Arabidopsis hypocotyl and root. She discussed roles for Programmed Cell Death (PCD) and abscission during periderm establishment, and further presented data showing that periderm development is not affected when lateral root development is compromised.

Gene Regulatory Networks

From roots to fruits, **the gene regulation and regulatory networks session** showed how NGS technologies are addressing fundamental plant developmental questions in diverse plant species; including topics such as: (1) How roots cope with a "harsh world", (2) How fruits decide which tissue develops into the flesh, (3) What defines fruit shape? (4) How the plant hormone, auxin does so much, and (5) Why different mutations in the same gene generate diverse phenotypes.

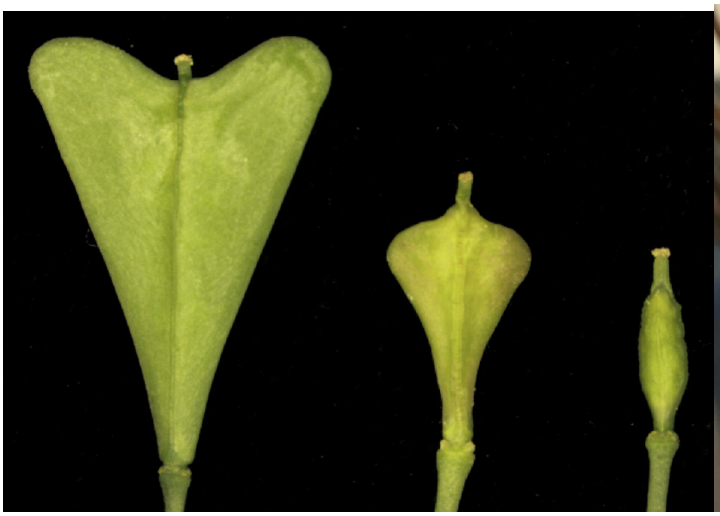
Siobhan Brady (University of California, Davis, USA) focused on how tomato roots develop the exodermis, a lignified and suberinised layer in the root. Using cell type specific sequencing technologies, they identified an evolutionary shift in cell-type specific expression, resulting in exodermis cells' monopolizing suberin related genes. During drought these suberin genes are upregulated in commercial tomato varieties (*Solanum lycopersicum*), but not in the drought-tolerant wild tomato (*Solanum pennelli*), highlighting exodermis suberinization as a possible target for drought tolerance.

The "inside-out" fruit of strawberry was the focus of the talk by **Zhongchi Liu** (University of Maryland, USA). Strawberry fruit flesh develops from the inflorescence stem tip, leaving the maturing achenes, seed-containing ovaries, on the outside. Classical experiments demonstrated that strawberry fruit flesh development is regulated by auxin released by the seed-containing ovaries, but the molecular mechanism of communication between the seed and the maternal tissue was unclear. RNAseq and tissue specific auxin measurements, identified bidirectional communication involved in the specification of which tissue becomes the fruit flesh; the endosperm and seed coat produce auxin transported into the stem tip, and there is a novel role for FT in flesh to seed communication.

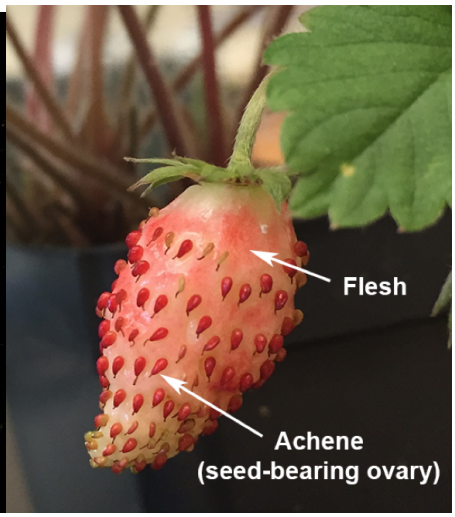
Next, **Lars Ostergaard** (John Innes Centre, UK) described how computational modelling and genetics explain the development of heart shaped fruits in Shepherds Purse (*Capsella rubella*) and the elongated fruits of *Arabidopsis thaliana.* The FRUITFULL (FUL) gene is required for growth during the post-germination phase and *ful* mutants have similar phenotypes in both species. They have also identified several additional fruit shape defective mutants by TILLING in *Capsella* such as *heartless, heartbreak* and *braveheart*.

Andrea Gallavotti (Rutgers University, USA) presented research on auxin-dependent transcriptional regulation in maize. Using DAP-seq and ATAC seq, they have identified binding sites for many Auxin Responsive Factors (ARFs), genome-wide. Many known activating and repressing ARFs bind upstream of the same genes (some 60% of ARF target genes), suggesting cooperative or competitive binding may generate auxin's diverse effects.

Jeff Long (University of California, Los Angeles, USA) explored how different mutations in the same HD ZIP III transcription factors have diverse phenotypic effects in *Arabidopsis*. Using inducible expression, ChIPseq, and ChIP re-ChIP, they described complex regulatory interactions with transcription factor homo- and heterodimers with both, shared and unique binding sites upstream of important developmental genes, especially in the cytokinin pathway.



Capsella wild type and two *fruitfull* mutant alleles



A maturing fruit of the wild strawberry studied in the Zhongchi Liu lab

Patterning mechanisms

The session on **Patterning mechanisms** opened with a talk by **Teva Vernoux** (ENS de Lyon, France), who discussed the problem of robustly patterning organs at the periphery of the shoot apical meristem (SAM). Combining experiments and computational modeling he showed how spatial-temporal fluctuations in auxin signaling filters out noise to confer robustness on organogenesis, and highlighted a role for the CLAVATA3 domain boundary in the regulation of this process.

Next, **Marcus Heisler** (University of Sydney, Australia) discussed how phyllotactic patterning in the SAM is limited to the periphery of the meristem. He showed that organs are centered on a small gap between the expression domains of REVOLUTA and KANADI where auxin signaling is maximised, and highlighted how the configuration of this boundary region in the SAM cues both the placement of organs and their dorsoventrality. He also showed that wound-induced auxin depletion in the SAM rearranges the REV and KAN1 expression domains, leading to a new explanation for the influence of wounding on leaf dorsoventrality.

Continuing the theme of patterning boundaries, **Annis Richardson** (University of California, Berkeley, USA), explained how the understanding of boundary formation in grasses has been impeded by the dearth of mutants with organ boundary defects. She then presented *fused leaf 1*

(fsl1), a maize mutant with a range of phenotypes related to defective organ boundary formation and maintenance, and summarized work towards identification of the causal mutation in *fsl1.*

Next, **Dominique Bergmann** (Stanford University, USA) outlined an integrated picture of stomatal patterning and the establishment of polarities in these lineages. She presented recent work by postdoc Anne Vatén identifying a regulatory circuit involving cytokinin, several cytokinin-regulated CLE peptides and response regulators (A-ARRs), as well as the stomatal transcription factor SPEECHLESS, which provides a means to adaptively regulate stomatal lineages.

Expanding on the theme of tissue polarities **Catherine Mansfield** (John Innes Centre, UK) presented work investigating coordinated polarities in the leaf, focusing on BREAKING OF ASYMMETRY IN THE STOMATAL LINEAGE (BASL) a protein which polarly localizes to one edge of the cell during stomatal patterning. She showed that broad induction of BASL expression in a developing leaf has coordinated cellular polarities across the entire organ that appear to be independent of the stomatal lineage, consistent with the existence of an intrinsic tissue-wide polarity.

The talk of **Aman Husbands** (Cold Spring Harbor, USA) followed and returned to the topic of robustly patterning boundaries, focusing on Class III HD-ZIP (HD-ZIPIII) proteins and the role of the StAR-related transfer (START) domain these proteins contain. Using PHABULOSA as a representative protein for the family, he discussed work showing how the START domains – in complex with a so far unidentified ligand – confer switch-like behavior to HD-ZIPIII proteins while simultaneously increasing their transcriptional potency.

Finishing the session, **Baoqing Ding** (University of Connecticut, USA) discussed the molecular underpinnings of periodic pigment spot patterning in monkeyflowers (*Mimulus*) by reaction-diffusion. Mutant analysis and transgenic experiments show that these patterns are likely produced by diffusion and reaction of a compound activating anthocyanin formation (a R2R3-MYB activator) and a compound repressing the activator (a R3-MYB repressor), leading to the periodic activation of pigmentation.

Evolution and comparative development

All the investigators in this exciting session generated new molecular, genetic tools in diverse plant model systems to understand the development of complex, ever-evolving plant forms.

Miltos Tsiantis (Max-Planck Institute for Plant Breeding Research, Germany) studies leaf morphological diversity in *Cardamine hirsuta*, a relative of *Arabidopsis thaliana* with compound leaves. A computational model of leaf margin development with feedbacks between CUPSHAPED COTELYDON (CUC) transcription factors and the hormone auxin, suggested that changes in transport of auxin by PINFORMED (PIN) efflux carriers and the growth repressive activity of CUCs could generate diverse lobed and compound leaf shapes. Accordingly, the *C. hirsuta REDUCED COMPLEXITY* (*RCO*) gene encoding an *HD-ZIP-I* can reinforce local growth repression by CUCs thus

creating compound leaves in *C. hirsuta*. *RCO* was lost in *A. thaliana* and when transformed back into this species it was sufficient to increase leaf complexity but not to cause complete *Cardamine*-like leaf development— although leaf physiology was altered indicating a potentially adaptive role. The latter was supported by finding positive selection signatures in *RCO*. Tsiantis suggested that few strong-effect regulators of leaf shape (like RCO) act with additional small effect genes to cause leaf margin diversity. He detailed efforts to isolate those and study their effects on growth

Elena Kramer's talk (Harvard University, USA) explored the genetic basis of the petal spur, a unique floral structure in columbines. SEM of young petals showed that anisotropic growth contributes to the length of the final petal spur, with sustained cell elongation in *Aquilegia* species correlating with longer spurs. Transcriptomic profiling of developing petals, followed by inducible gene silencing by VIGS and *in situ* hybridization, show that division coordination by a TCP transcription factor is necessary for normal spur growth, and the function of STYLISH (SHI/STY) homologs is necessary for nectary development at the spur tip. QTL mapping of spur length in interspecies populations has identified a single mendelian locus that controls the presence and absence of spurs. Nonetheless, the genetic architecture of spur morphology may involve multiple loci, not shared between all columbine species.

Knowing that floral traits such as color, scent, and shape work together to attract pollinators, **Cris Kuhlemeier** (University of Bern, Switzerland) explored the genetics underlying the complex evolutionary history accompanying changes in pollinator preferences in petunia. QTL mapping of crosses between pollinator types (*P. secreta*, bee pollinated and *P. exerta*, bird pollinated) identified alleles of MYB transcription factor ANTHOCYANIN2 (AN2) as key to the evolution of bee pollination in *P. secreta*. Both species evolved from an ancestor carrying a pseudogene version of AN2 caused by a frame-shift deletion, leading to a white, hawkmoth-pollinated flower. However, in *P. secreta*, AN2 was 'resurrected' by an additional, codon-restoring deletion. Loci for UV floral display mapped to regulatory sequences of flavonol biosynthesis, together suggesting that somewhat simple molecular changes can underlie significant phenotypic and ecological niche changes.

Yoan Coudert (CNRS / Natural History Museum Paris, France) used the leafy shoot axis of the model bryophyte, *Physcomitrella patens,* to understand gametophytic branching. Unlike flowering plant sporophytes, where polar auxin transport and *PIN* genes are required to regulate lateral outgrowth, computational models of branch patterning in moss suggest that apolar auxin transport best explains observed architectures. Supporting this hypothesis, mutants in *P. patens* and manipulation of cell-cell diffusion rates show that the PIN auxin efflux carriers are minor contributors to architecture in *P. patens*, suggesting that not all plant architectures require polar auxin transport and alternative mechanisms exist in basal land plants.

Devin O'Connor (Sainsbury Laboratory, Cambridge University, UK) examined the function of closely-related PINFORMED (PIN) auxin efflux carriers in *Brachypodium distachyon*. Using fluorescent fusion proteins, Devin saw that Sister-of-PIN1 (SoPIN1), an efflux protein lost in *Arabidopsis* but conserved in most flowering plants, is expressed in the epidermis of the meristem and localizes asymmetrically towards auxin maxima. PIN1 paralogs BdPIN1a and BdPIN1b,

however, express subepidermally in the developing vascular trace, transporting auxin away from lateral organs. Heterologous expression and complementation in Arabidopsis using the Brachypodium PINs showed that the SoPIN1 and PIN1 clades are not functionally equivalent. Loss of *SoPIN1* in *Brachypodium* is sufficient to give a phenotype like PINFORMED1 in *Arabidopsis*, whereas *PIN1* paralogs *BdPIN1a* and *BdPIN1b* together cause an internode elongation defect, suggesting that multiple auxin efflux carriers in *Brachypodium* may together perform the functions of *Arabidopsis* PIN1.

The RCO expression domain in *Cardamine hirsuta*

Virus-induced gene silencing (VIGS) in the columbine flower (*Aquilegia sp.*)

Growth dependent morphogenesis

Adrienne Roeder (Cornell University, USA) launched the session by presenting a fluctuation-based patterning mechanism in *Arabidopsis* sepals (outermost floral organs). Sepals curvature is influenced by randomly patterned giant cells that form through endoreduplication. Giant cell formation requires the AtML1 transcription factor which has a linear, dosage-dependent role based on mutant and transgenic lines. Time-lapse imaging of *YFP-AtML1* revealed that AtML1 expression fluctuates in sepal cells. Mathematical modelling of this, suggests that a specific threshold of AtML1 needs to be surpassed during the G2-phase of the cell cycle to allow endoreduplication and subsequent giant cell formation.

Ari Pekka Mahonen (University of Helsinki, Finland) presented elegant work describing how cambium stem cells are formed post-embryonically in the *Arabidopsis* root. Cell lineage tracing revealed that only pericycle and procambial cells in contact with xylem precursors contribute to the formation of cambium. Single cell lineage tracing and ablation experiments showed that the central

cell layer acts as an "organizer" upon which the division capacity of adjacent cells depends. Conditional mutants also revealed a developmental module consisting of auxin, auxin response factors, HD-ZIP III transcription factors and WOX-like transcription factors required for radial cambium formation, secondary growth and correct patterning in the root.

Carolyn Rasmussen (University of California, Riverside, USA) presented a probabilistic mathematical model to predict 3D division plane orientation in plant cells. Time-lapse imaging of young maize leaves expressing a tubulin-marker line allowed for visualization of division plane (pre-prophase band) establishment and the division itself. The iterative model, seeking minimal division wall area and integration of preprophase band orientation predicts the correct transverse division 97% of the time in-silico (compared to 95% in-vivo), which is much closer to reality than previously published 2D models.

Pilar Cubas (Centro Nacional de Biotecnologia, Spain) presented work on identifying gene regulatory networks that regulate axillary bud dormancy. Both developmental and environmental cues can promote or inhibit bud outgrowth and are integrated by *BRANCHED1* (*BRC1*), an inhibitor of bud growth. Transcriptomics analyses in repressed and activated buds in wild-type and *brc1* plants identified three HD-ZIP I transcription factors, which together with *BRC1* induce ABA biosynthesis in dormant buds triggering outgrowth. The triple mutant has a bushy phenotype when grown under shade conditions, which usually inhibit lateral growth and promote apical dominance.

Sebastian Soyk (CSHL, USA) presented recent work on the negative epistasis effects of MADS-box transcription factors on tomato yield. When stacking a trait that was selected during domestication and is linked to bigger fruit size with the "jointless" locus that facilitates mechanical harvesting, tomato inflorescences became highly branched and semi-sterile. Using a combination of natural alleles and CRISPR engineering, this can be overcome, resulting in a continuum of inflorescence branching, where some hybrid combinations produced single-branched inflorescences and significantly higher yields.

Hernan Lopez-Marin (Max-Planck Institute for Plant Breeding Research, Germany) reported on the identification of the *super determinant (sde)* mutant that fails to properly initiate axillary meristems in tomato. The SDE gene shows similarities to PRC1-like components but lacks the canonical RING domain. He proposes that a non-canonical PRC1 complex establishes competence for axillary meristem initiation.

Finally, **Katy Guthrie** (University of Missouri - Columbia, USA) presented work on the *Suppressor of sessile spikelet 2* (*Sos2*) mutant, which suppresses the second spikelet formation specific to the maize clade of grasses. She showed that the *Sos2* mutation seems to have roles in inflorescence, spikelet and flower meristems, and that the *Sos2* mutation could partially suppress the indeterminate meristem mutation *ramosa2*.

Environmental Adaptations

The final session of the meeting on Environmental Adaptations kicked off with a talk by **Stacy Harmer** (University of California, Davis, USA), who introduced us to Sunflower as a model system for studying circadian rhythms. Before dawn, sunflower inflorescences re-orient themselves to face east in preparation for the rising sun. Harmer demonstrated that this ability to anticipate sunrise is dependent upon a spatio-temporal separation of auxin responses between day and night across the East and West halves of the sunflower stem. Notably, she was able to show that inflorescence orientation impacts temperature-dependent pollen shedding, which has a significant influence on the frequency of pollinator visits and yield.

The next talk was by **Daniel Chitwood** (Independent Researcher), who talked about a new method for measuring topology, called Persistent Homology, can be used to compare diverse 2-dimensional and 3-dimensional shapes. He presented several studies using persistent homology, including comparisons between roots and shoots, grape rachises from the core grape diversity collection in Geneva, NY, and a massive "leaf morphospace" that was generated from 182,707 leaves from different seed plant families. Surprisingly, he was able to show that there is predictive value to these measurements; 30% of the leaves in this massive leaf morphospace could be accurately assigned back to their respective plant families.

Next, **Jessica Guseman** (USDA-ARS Appalachian Fruit Research Station, USA) shed light on how environmental signals are integrated into the molecular control of shoot architecture in Arabidopsis and Prunus species. TAC1 and LAZY1 (members of the IGT gene family members) work together to influence branch angles. Guseman demonstrated that each of the IGT genes responds differently to light treatments and mutant combinations with core components of the light signaling pathway. Further work investigating how light influences the IGT family will help us to understand complex architecture problems in trees, for example – how understory branches respond to shading from the top of the tree.

Next, **Ben Holt** (Associate Professor at the University of Oklahoma, USA) took us through a rigorous series of experiments looking into the functional specificity for how the CONSTANS (CO) DNA binding complex regulates expression of the floral promoting factor FT. Using three-dimensional protein structures, chromatin modeling, and amino acid sequence alignments between the CO DNA binding complex and its functional analog, the Nuclear Factor-Y complex, Holt was able to pinpoint specific residues of the CO DNA binding domain that specify the enhancer element binding capacity of this complex.

Salehin Mohammad (University of California, San Diego, USA) spoke next on the connection between AUX/IAA signaling and glucosinolate biosynthesis. Mohammad used RNA-sequencing, glucosinolate profiling (with LC-MS), and genetic stacking, to delineate a signaling pathway that connects IAA5, IAA6, and IAA19 with the regulation of aliphatic glucosinolate biosynthesis. Surprisingly, he was able to demonstrate that mutants in this pathway are drought sensitive, suggesting a new role for aliphatic glucosinolates in abiotic stress tolerance.

The meeting concluded with an illuminating talk by **Heike Lindner** (The Carnegie Institute of Washington, USA) on the phenotyping capacity of GLO-Roots, a robotic system that uses a luciferase reporter system to track root architecture over time. Underground environmental pressures (for example water availability and nutrient composition) have the ability to shape root architecture over evolutionary time. Lindner is leveraging the geographic and genetic diversity of Arabidopsis to perform a GWAS for environmentally selected root architectural traits across a collection of ecotypes.

Conference attendance summary:

The 15th FASEB meeting "Mechanisms in Plant Development" 2017 took place once again at the Vermont Academy in Saxons River, VT. The organizers Prof. Doris Wagner (University of Pennsylvania), and Prof. Marja Timmermans (University of Tübingen) invited 26 speakers (including the keynote) representing the international "who is who" in plant developmental biology. With an almost equal ratio of 46% to 54% female and male speakers, respectively, this meeting represents an outstanding example for gender equality in science. One interesting fact, however, was that the vast majority of the invited female speakers were from US Universities (8 vs. 3 from Europe, 1 from Japan), whereas the vast majority of European invited speakers were male (9 vs. 3 from US, 1 from China/substituted by Australian). Unfortunately, 3 invited speakers could not attend the meeting and were substituted by equally qualified scientists. To promote visibility of early career researchers, 30 short talks were selected from submitted abstracts. 15 of those talks were given by PIs in pre-tenure stages of their career (7 female, 8 male), 3 by grad students (2 female, 1 male), and 12 by postdocs (4 female, 8 male, representing roughly the ratios of submitted abstracts). The outstanding program and the unrivaled reputation of this bi-annual meeting attracted 145 international attendees (54.5% male and 45.5% female) with 57.2% attendees coming from US Universities and research institutions, 32.6% from Europe, and the rest from other countries all over the world. Of the 119 attendees that disclosed their ethnic background, 12% were from underrepresented minorities (hispanic/latino, black/african american, native american/pacific island), 27% were asian, and 61% were caucasian. The FASEB Diversity Resource program aims at increasing access to research careers and create research training opportunities for ethnically and socio-economically underrepresented groups.

One special feature of this conference is and has always been that speakers present a good amount of unpublished data to receive input and opinions from other experts in the field. In addition, all 145 attendees were invited to bring posters, and evening poster sessions in a relaxed environment gave the opportunity for very fruitful discussions and great interactions between young researchers and established PIs. An additional poster session was dedicated to grad students to promote visibility and guarantee interaction with more established scientists. Two "meet the speakers" lunches and the newly established "career development" lunch with topics as diverse as "how to publish your science" to "science and social responsibilities" encouraged interactions across different career stages. Overall, the friendly, enthusiastic, encouraging and inclusive

environment of this conference is a shining example of how conferences should be and offers diverse role models for young scientists.

During the election of the organizers for the 2019 meeting, the community of plant developmental biologists once again proved how progressive it is, and voted Kenneth Birnbaum (New York University) and Jill Harrison (University of Bristol) as the next organizers. We are excited for the next FASEB meeting “Mechanisms in Plant Development” 2019 at St. Bonaventure University and we thank the Vermont Academy for being a great host of the past FASEB meetings.