PROGRAMME AND ABSTRACT BOOK

ADVANCES IN PLANT REPRODUCTION – FROM GAMETES TO SEEDS

30 JUNE – 1 JULY 2018
FIRENZE FIERA CONGRESS
AND EXHIBITION CENTRE,
FLORENCE, ITALY

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SOCIETY FOR EXPERIMENTAL BIOLOGY

ADVANCES IN PLANT REPRODUCTION – FROM GAMETES TO SEEDS

ORGANISED BY:
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CATERING

Lunch and refreshments during the satellite meeting are included in your registration fee and will be served in the breakout area located on the ground floor of Palazzo Affari.

CERTIFICATE OF ATTENDANCE

Delegates requiring a certificate of attendance should visit the SEB registration desk on their departure or by email from admin@sebiology.org

VENUE

Firenze Fiera Congress and Exhibition Centre
Piazza Adua, 1, 50123, Firenze FI, Italy
Tel: +39 055 49721
Web: www.firenzefiera.it/en/

The scientific sessions will be taking place in room Adua 1 located on the first floor in Palazzo Affari.

WI-FI INTERNET ACCESS

Internet access is available during the meeting and free of charge. Log in details will be available at the registration desk.

LIABILITY

Neither the Society for Experimental Biology nor the Firenze Fiera Congress and Exhibition Centre will accept responsibility for damage or injury to persons or property during the meeting. Participants are advised to arrange their own personal health and travel insurance.

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**Please note: The SEB will be taking photos during the event for promotional purposes. If you have any concerns, please visit the SEB registration desk.*

POSTER SESSIONS

The poster sessions will be taking place in the breakout area between 16:45 – 17:45 on 30 June and 16:45 – 18:00 on 1 July. Poster presenters are invited to hang their poster on arrival (Velcro will be provided) and are asked to remove their posters by 18:00 on 1 July. Any posters left behind will be disposed of.

REGISTRATION

The registration desk will be open during the hours of the meeting and a SEB staff member will be on hand during the refreshment and lunch breaks should you require any assistance.

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We're looking to increase the conversation at the meeting using:
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PROGRAMME

SATURDAY 30 JUNE

08:45 REGISTRATION

09:30
Welcome and introduction
Sílvia Coimbra
Meeting organising committee

SESSION 1 OVULE DEVELOPMENT – GERMLINE DEVELOPMENT AND FUNCTION

CHAIR: SÍLVIA COIMBRA

10:00
Prof Lucia Colombo
Università degli Studi di Milano, Italy
Molecular mechanisms controlling ovule development in Arabidopsis
PS18.1

10:30
Dr Matthew R Tucker
The University of Adelaide, Australia
Activating the female germline during Arabidopsis and barley ovule development
PS18.2

11:00 REFRESHMENT BREAK/POSTERS

11:30
Dr Daphné Autran
IRD - University of Montpellier, France
Role of early ovule architecture in female germ cell fate establishment
PS18.3

11:45
Miss Sara C M Pinto
Sexual Plant Reproduction and Development lab, Faculty of Sciences, University of Porto, Portugal
Deciphering the cellular communication during early ovule development
PS18.4

12:00
Dr Malgorzata Gutkowska
Institute of Biochemistry and Biophysics PAS, Poland
Rab-dependent vesicular traffic is indispensable for maternal control of male and female gametophyte development but not for embryo development of *Arabidopsis thaliana*
PS18.5

12:15
Sebastien Andreuzza
University of Cambridge, United Kingdom
Elucidating the genetic and developmental controls of germline formation and differentiation in plants
PS18.6

12:30 LUNCH/POSTERS

13:45
Dr Aureliano Bombarely
Virginia Tech, United States
Genetic insights of the modification of the reproduction mechanisms during plant domestication
PS18.7

14:15
Dr Concha Gomez-Mena
CSIC, Spain
Overexpression of the tomato *SPOROCYTELESS* ortholog alters reproductive development
PS18.8

14:30
Miss Cindy Callens
University of Nottingham, United Kingdom
The effects of heat stress on the reproductive organs of European barley varieties
PS18.9

PROGRAMME

SESSION 2 POLLEN GERMINATION AND POLLEN TUBE GROWTH - FERTILIZATION AND POLYSPERMY BLOCK

CHAIR: LUCIA COLOMBO

14:45
José Feijó
University of Maryland, United States
Ion homeostasis and reproduction: molecular basis and integrative mechanisms
PS18.10

15:15
Dr Marta A Mendes
University of Milan, Italy
Synergid cell death in Arabidopsis, a role for Cytokinin
PS18.11

15:30
Pecha Kucha
Miss Jessy Silva (PS18.12), Rosanna Petrella (PS18.13), Mr Ricardo B Lopes (PS18.14), Mário L Costa (PS18.15)

15:40 REFRESHMENT BREAK/POSTERS

16:15
Ana Marta Pereira
Universitá degli Studi di Milano, Italy
Lost highway: a pistil & pollen tube love story
PS18.16

16:30
Amal J Johnston
Jacobs University, Germany; University of Heidelberg, Germany
A higher-order transcription factor network governs egg cell differentiation and stress homeostasis in *Arabidopsis*
PS18.17

16:45 POSTER SESSION 1

17:45 END OF DAY 1

SUNDAY 1 JULY

08:30 REGISTRATION

CHAIR: CRISTINA FERRANDIZ

09.00
Dr Pilar S Testillano
Biological Research Center CIB-CSIC, Spain
Microspore embryogenesis: unravelling the determinant factors of cell totipotency for crop improvement
PS18.18

09:30
Prof Sílvia Coimbra
Faculdade de Ciências Universidade do Porto, Portugal
AGPs as markers for phragmoplast assembly during *Quercus suber* microsporogenesis
PS18.19

09:45
Dr Maria Manuela R Costa
BioISI University of Minho, Portugal
Chromatin remodelling during the progamic phase of *Quercus suber*
PS18.20

SESSION 3 EMBRYOGENESIS AND ENDOSPERM DEVELOPMENT - SEED AND FRUIT DEVELOPMENT

CHAIR: SIMONA MASIERO

10:00
Cristina Ferrandiz
Instituto de Biología Molecular y Celular de Plantas, CSIC-UPV, Spain
A stylish story of carpel evolution
PS18.21

PROGRAMME

10.30
Dr Varvara E Tvorogova
Saint Petersburg State University, Russia
MtWOX9-1 gene in the somatic embryogenesis in *Medicago truncatula*
PS18.22

10:45
Pecha Kucha
Mr Márcio FM Couto (PS18.23), Mr Luís F C Póvoas (PS18.24), Dr Mara Cucinotta (PS18.25), Dr Silvia Manrique (PS18.26)

10:55 REFRESHMENT BREAK/POSTERS

11:30
Mr Meisam Nazari
Georg-August University of Göttingen, Germany
Response of soybean and common bean seeds to ultrasound
PS18.27

11:45
Ms Ana Lopes
Faculdade de Ciências da Universidade do Porto, Portugal
Stay stick: how to fit each tile in the SEEDSTICK TF control frame?
PS18.28

12:00
Prof Simon J Hiscock
Department of Plant Sciences, University of Oxford, United Kingdom
Stigma surface components and their role(s) in sexual plant reproduction
PS18.29

12:30 LUNCH/POSTERS

CHAIR: PILAR TESTILLANO

13:45
Dr Emidio Albertini
Dept. of Agricultural Food and Environmental Sciences, University of Perugia, Italy
APOSTART: a candidate gene involved in embryo progression and parthenogenesis
PS18.30

14:15
Dr Martina Juranic
CSIRO Agriculture and Food, Australia
Too many mothers in a gamma-irradiated mutant of apomictic *Hieracium praealtum*
PS18.31

14:30
Duarte D Figueiredo
Swedish University of Agricultural Sciences and Linnean Center for Plant Biology, Sweden
Auxin regulates endosperm cellularisation in Arabidopsis
PS18.32

14:45
Dr Clément Lafon Placette
Department of Botany Charles University in Prague, Czech Republic
Evolution of hybridisation barriers along Arabidopsis lineages: the case of hybrid seed lethality
PS18.33

15:00
Mr Buzi Raviv
Ben Gurion University, Israel
Novel insights into the function of dead organs enclosing embryos of angiosperms
PS18.34

15:15 REFRESHMENT BREAK/POSTERS

PROGRAMME

🕓 **15:45**
Dr Simona Masiero
University of Milan, Italy
A FRUIT-TALK
PS18.35

🕓 **16:15**
Ms Elina A Potsenkovskaya
Saint Petersburg State University, Russia
NF-Y genes in *Medicago truncatula* somatic embryogenesis
PS18.36

🕓 **16:30** CLOSING REMARKS AND DISCUSSION

🕓 **16:45** POSTER SESSION 2 AND FAREWELL PORT WINE TASTING

🕓 **18:00** CLOSE OF MEETING

POSTER SESSIONS 30 JUNE AND 1 JULY

Miss Jessy Silva
Faculdade de Ciências da Universidade do Porto, Portugal
Unravelling the importance of FLA5 (Fasciclin-like Arabinogalactan Protein 5) in Arabidopsis reproduction
PS18.12

Rosanna Petrella
University of Milan, Italy
BASIC PENTACYSTEINE PROTEINS control septum formation during carpel development in *Arabidopsis thaliana*
PS18.13

Mr Ricardo B Lopes
Faculty of Sciences of the University of Porto, Portugal
Development and characterisation of knock-down RNAi and promoter-induced GUS expression lines for Arabinogalactan Protein 20 (AGP20) in *Arabidopsis thaliana*
PS18.14

Mário L Costa
Faculdade de Ciências da Universidade do Porto, Portugal
Fasciclin-like Arabinogalactan Proteins expression pattern during seed development is highly conserved across species
PS18.15

Mr Márcio FM Couto
Faculty of Sciences of the University of Porto, Portugal
Fasciclin-like arabinogalactan proteins involved in plant reproduction: an analysis from *Quercus* to *Arabidopsis*
PS18.23

Mr Luís F C Póvoas
Department of Biology Faculty of Sciences of the University of Porto, Portugal
Expression of allergens in *Betula pendula* pollen under atmospheric pollution influence
PS18.24

Dr Mara Cucinotta
Dipartimento di Bioscienze, Università degli Studi di Milano, Italy
VPS13 is involved in the miRNA-dependent translational repression pathway required for ovule development in *Arabidopsis thaliana*
PS18.25

Dr Silvia Manrique
Universitá degli Studi di Milano, Italy
Regulation of sporogenesis through auxin-dependent pathways
PS18.26

Amal J Johnston
Jacobs University, Germany; University of Heidelberg, Germany
BYEPASS - A robust and versatile homology-(in)dependent multi-fragment assembly for functional transgenesis
PS18.37

Amal J Johnston
Jacobs University, Germany; University of Heidelberg, Germany
Boechera revisited: developmental heterochrony and epigenetically coordinated transcriptional rewiring underlie apomixis
PS18.38

ADVANCES IN PLANT REPRODUCTION – FROM GAMETES TO SEEDS

PS18.1 MOLECULAR MECHANISMS CONTROLLING OVULE DEVELOPMENT IN ARABIDOPSIS

SATURDAY 30 JUNE 2018 **10:00**

LUCIA COLOMBO (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), ANDREA GUAZZOTTI (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), MARA CUCINOTTA (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), ALEX CAVALLERI (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), VERONICA GREGIS (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY)

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Ovules are highly complex structures that upon double fertilization develop into seeds. The determination of ovule identity and number is therefore essential to ensure progeny. We have investigated the role of auxin and cytokinins and their cross talk in the determination of ovule number and ovule development. One of the transcription factors that play an important role in ovule development is the Auxin Response Factor Monopteros (MP). We have created two CRISPR CAS9 *mp* mutant alleles to study the role of MP during ovule development. The mutants have been fully characterised and the data presented. Furthermore the network controlled by MP and the transcriptional and post-transcriptional regulation of MP during ovule development will be discussed.

PS18.2 ACTIVATING THE FEMALE GERMLINE DURING ARABIDOPSIS AND BARLEY OVULE DEVELOPMENT

SATURDAY 30 JUNE 2018 **10:30**

MATTHEW R TUCKER (THE UNIVERSITY OF ADELAIDE, AUSTRALIA), LAURA G WILKINSON (THE UNIVERSITY OF ADELAIDE, AUSTRALIA), DAYTON C BIRD (THE UNIVERSITY OF ADELAIDE, AUSTRALIA), WENG H LEONG (THE UNIVERSITY OF ADELAIDE, AUSTRALIA)

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Female gamete formation in flowering plants initiates in the ovule, where a pool of somatic cells give rise to a single germline cell. Germline establishment is a fundamental prerequisite for seed development, but is poorly understood due to the location of progenitor cells deep within the flower. We have been investigating this process in dicot and monocot models using cell-type specific methodologies. Our approach is providing novel molecular, compositional and morphometric insight into the mechanistic basis and evolutionary conservation of germline formation, and identifying potential targets for crop improvement strategies.

PS18.3 ROLE OF EARLY OVULE ARCHITECTURE IN FEMALE GERM CELL FATE ESTABLISHMENT

SATURDAY 30 JUNE 2018 **11:30**

DAPHNÉ AUTRAN (IRD - UNIVERSITY OF MONTPELLIER, FRANCE), CÉLIA BAROUX (UNIVERSITY OF ZÜRICH, SWITZERLAND), ETHEL MENDOCILLA-SATO (UNIVERSITY OF ZÜRICH, SWITZERLAND), ELVIRA HERNANDEZ-LAGANA (IRD - UNIVERSITY OF MONTPELLIER, FRANCE), THOMAS VAIN (IRD - UNIVERSITY OF MONTPELLIER, FRANCE), GABRIELLA MOSCA (UNIVERSITY OF ZÜRICH, SWITZERLAND), DANIEL GRIMANELLI (IRD - UNIVERSITY OF MONTPELLIER, FRANCE), CÉLIA BAROUX (UNIVERSITY OF ZÜRICH, SWITZERLAND)

@ DAPHNE.AUTRAN@IRD.FR

During plant early ovule development, the somatic-to-reproductive transition establishes the female germ cell initial or MMC, committed to meiosis. Despite considerable progress in deciphering genetic and epigenetic contributions to MMC fate establishment, we lack a precise description of the associated morphogenetic events in the ovule primordium. This question can now be addressed thanks to the advent of non-invasive, high-resolution 3D imaging and image processing techniques, combined to functional approaches. In addition, with its relatively simple structure, consisting of c.a. 10 cells at emergence and c.a. 100 cells at mature MMC stage, the Arabidopsis ovule primordium offers an attractive 3D object to create tissue models capturing informative patterning rules. Our first results suggest that cell division and growth patterns are dynamic during early ovule development. Genetic alteration of anisotropic cell growth and cell geometry lead to defects in the regionalisation of cell divisions and to the formation of multiple MMCs. Conversely, mutations in different pathways known to alter MMC unicity also change cell proliferation patterns. We further hypothesize that auxin response and signalling may contribute patterning instructions influencing MMC fate.

PS18.4 DECIPHERING THE CELLULAR COMMUNICATION DURING EARLY OVULE DEVELOPMENT

SATURDAY 30 JUNE 2018 **11:45**

SARA C M PINTO (SEXUAL PLANT REPRODUCTION AND DEVELOPMENT LAB, FACULTY OF SCIENCES, UNIVERSITY OF PORTO, PORTUGAL), MATTHEW TUCKER (PLANT DEVELOPMENTAL GENETICS LAB, UNIVERSITY OF ADELAIDE, AUSTRALIA), SÍLVIA COIMBRA (BIOSYSTEMS AND INTEGRATIVE SCIENCES INSTITUTE, FACULTY OF SCIENCES, UNIVERSITY OF PORTO, PORTUGAL)

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The European consortium SEXSEED (H2020-MSCA-RISE-2015) was conceived to increase the knowledge on seed development. Its main goal is to assemble the regulatory network controlled by *SEEDSTICK (STK)*, a D-class MADS box transcription factor. *STK* is considered the master regulator of ovule and seed development. During ovule development, *STK* is expressed early on, when the ovule is a finger-like structure, and along all development. However, *STK* known functions are related with successful fertilization and post-fertilization events. We aimed at understanding how *STK* controls early ovule development. Morphological and genetic analysis of *stk* ovules, point that regulates female germline development, notably, by interfering with cellular identity perhaps through an epigenetic mechanism.

It is known that *STK* directly regulates the expression of two *(REM)* transcription factors to confer identity to the synergids and antipodals in the embryo sac. Analysing previously obtained MMC and nucellus microarray data we propose that *REM24* may be regulated by *STK* during early ovule development, influencing germline development. Gene expression analysis shows that *STK* can regulate *REM24* expression. We wish to understand whether *REM24* is the molecular puzzle piece fitting STK in the genetic model of germline development. Therefore, *rem24* mutants are being characterised in order to establish a relation with *STK* and the female germline formation pathway.

PS18.5 RAB-DEPENDENT VESICULAR TRAFFIC IS INDISPENSABLE FOR MATERNAL CONTROL OF MALE AND FEMALE GAMETOPHYTE DEVELOPMENT BUT NOT FOR EMBRYO DEVELOPMENT OF *ARABIDOPSIS THALIANA*

SATURDAY 30 JUNE 2018 **12:00**

MALGORZATA GUTKOWSKA (INSTITUTE OF BIOCHEMISTRY AND BIOPHYSICS PAS, POLAND), JOANNA ROJEK (UNIVERSITY OF GDANSK, POLAND), JULITA NOWAKOWSKA (UNIVERSITY OF WARSAW, POLAND), MARTA WNUK (INSTITUTE OF BIOCHEMISTRY AND BIOPHYSICS PAS, POLAND), MALGORZATA LICHOCKA (INSTITUTE OF BIOCHEMISTRY AND BIOPHYSICS PAS, POLAND), JERZY BOHDANOWICZ (UNIVERSITY OF GDANSK, POLAND), EWA SWIEZEWSKA (INSTITUTE OF BIOCHEMISTRY AND BIOPHYSICS PAS, POLAND)

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Eukaryotic cells rely on accuracy and efficiency of vesicular traffic. Key molecules providing specificity of formation of a vesicle and subsequently its recognition and fusion with the acceptor membrane are Rab proteins. Rabs are anchored to membranes by covalently linked geranylgeranyl group(s). This posttranslational modification is catalyzed by Rab geranylgeranyl transferase (RGT).

We discovered that *Arabidopsis* plants with mutations in the gene encoding beta subunit of RGT *(rgtb1)* have seriously disordered female gametogenesis and this effect is of maternal origin. Decreased Rab geranylgeranylation leads to mislocalization of PIN-1 protein around growing gametophyte followed by defective auxin responses. Additionally large callose deposits result in ovule degeneration. Male gametogenesis is disturbed as well in *rgtb1* plants leading to almost-complete sterility of the pollen. Deposits of callose and abnormal exine sculpturing are observed. Defects in male gametogenesis result from aberrant tapetum structure and function on maternal plant. Surprisingly, pollination of *rgtb1* mutant with WT pollen gives normally developing heterozygous embryos and only minor malformation of the seeds. The plants germinate and grow normally. This suggests that communication between maternal plant and developing gametophytes relies strongly on vesicular traffic. On contrary, proper Rab cycling in maternal plant is dispensable for developing embryo.

This work was supported by Polish NCN grant UMO-2016/21/D/NZ3/02615 to MG.

PS18.6 ELUCIDATING THE GENETIC AND DEVELOPMENTAL CONTROLS OF GERMLINE FORMATION AND DIFFERENTIATION IN PLANTS

SATURDAY 30 JUNE 2018 **12:15**

SEBASTIEN ANDREUZZA (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM), ARTEMIS PERRAKI (UNIVERSITY OF CAMBRIDGE, UNITED KINGDOM)

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Sexual reproduction relies on the formation of specialised sex cells, the gametes, which give rise to a new individual upon fertilisation. Gametes differentiate from precursors that acquire a reproductive fate, the germ cells, and which undergo meiosis to produce haploid cells with re-assorted genetic material. Because of the difficulty to access germ cells, we know very little about the genetic and developmental mechanisms in plants that control their formation and differentiation - which ultimately governs fertility. Here we present our preliminary results in developing a method to isolate male and female germ cells on a large scale, for direct characterisation in the model plant *Arabidopsis thaliana.* In parallel, we also take a classical genetic approach, and identified a new function critical for male meiosis. Our preliminary work paves the way to elucidate the regulatory mechanisms of plant germline differentiation, which should lead to innovative applications for plant breeding programmes.

PS18.7 GENETIC INSIGHTS OF THE MODIFICATION OF THE REPRODUCTION MECHANISMS DURING PLANT DOMESTICATION

SATURDAY 30 JUNE 2018 **13:45**

AURELIANO BOMBARELY (VIRGINIA TECH, UNITED STATES), TOMAS HASING (VIRGINIA TECH, UNITED STATES), SILVIA MANRIQUE (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), CHENMING CUI (VIRGINIA TECH, UNITED STATES), LUCIA COLOMBO (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), DAVID HAAK (VIRGINIA TECH, UNITED STATES), DAVID ZAITLIN (UNIVERSITY OF KENTUCKY, UNITED STATES)

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Domestication can be defined as the process of adapting wild plants and animals for human use. The usability of these species is linked to the selection of specific traits such as flower morphology, fruit size or yield. The selection of these traits can affect directly and indirectly the plant reproduction mechanisms. For example, the selection of subtle phenotypic variations such as flower colour can produce a switch in the pollinator. Other traits such as fruit size can be associated to polyploidy, that in some cases such as triploid bananas, causes sterility and the abolition of the sexual reproduction. Florist's gloxinia *(Sinningia speciosa)* is an excellent model to study plant domestication using genomic tools. This herbaceous perennial species from the Gesneriaceae family is endemic to the Atlantic coastal forest of southeastern Brazil. John Fyfe developed the first hybrid in 1845 and since then, the intense breeding has produced a wide range of different phenotypes, mainly affecting the flower morphology and corolla colour. Selection of actinomorphic flowers and double corollas where stamens or nectaries have been transformed in petals are the main examples of phenotypes affecting plant reproduction in this species. The QTL analysis of a F2 wild (with zygomorphic flowers) x domesticated (with actinomorphic flowers) population combined with the re-sequencing of 21 different accessions revealed that a mutation in the Cycloidea gene is responsible for actinomorphic/radial flowers.

PS18.8 OVEREXPRESSION OF THE TOMATO *SPOROCYTELESS* ORTHOLOG ALTERS REPRODUCTIVE DEVELOPMENT

SATURDAY 30 JUNE 2018 **14:15**

CONCHA GOMEZ-MENA (CSIC, SPAIN), EDELIN M ROQUE (CSIC, SPAIN), Mª JESUS LOPEZ-MARTIN (CSIC, SPAIN), MARICRUZ ROCHINA (CSIC, SPAIN), LUIS A CAÑAS (CSIC, SPAIN), JOSE PIO BELTRAN (CSIC, SPAIN)

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HYDRA gene, the ortholog of the *SPOROCYTELESS/NOOZLE* gene from Arabidopsis (Rojas-Gracia *et al.*, 2017) is involved in the initiation of the sporogenesis and the control of fruit set in tomato. Seedless fruit production is obligate in *hydra* mutants and fruit initiation seems to occur as a consequence of the premature activation of hormonal promoting signals usually originated after pollination and fertilization of the mature ovule. To further analyse the role of *HYDRA/SlSPL* during reproductive development we generated tomato plants that overexpressed this gene. The ectopic expression of *HYDRA/SlSPL* during vegetative development strongly reduced plant size. However, leaf number, leaf shape and plant architecture was not altered by the overexpression of this gene in vegetative tissues. During reproductive development *HYDRA/SlSPL* overexpression modifies flower morphology and reduces plant fertility resulting in a low number of fruits that contain small seeds. Based on these results, we are investigating a possible role for *HYDRA/SlSPL* in the regulation cell size or cell division during gametophyte development.

PS18.9 THE EFFECTS OF HEAT STRESS ON THE REPRODUCTIVE ORGANS OF EUROPEAN BARLEY VARIETIES

SATURDAY 30 JUNE 2018 **14:30**

CINDY CALLENS (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM), MATTHEW R TUCKER (UNIVERSITY OF ADELAIDE, AUSTRALIA), DABING ZHANG (SHANGHAI JIAO TONG UNIVERSITY, CHINA), ZOE A WILSON (UNIVERSITY OF NOTTINGHAM, UNITED KINGDOM)

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Barley *(Hordeum vulgare)* is a widely grown cereal crop that is mainly grown for stock feed, malting and brewing. Abiotic stress is one of the major causes of reduction in crop yield. Many of our cereal crops will need to be redesigned to survive new extremes, with all major climate change models predicting an increase in temperature in the future. It is important to determine key stages of inflorescence development in different cultivars when floral organs are most vulnerable to heat stress. The stages of floret development when meiosis and mitosis occur in the reproductive organs have been shown to be vulnerable to abiotic stresses in species such as rice *(Oryza sativa)*, maize *(Zea mays)* and wheat *(Triticum aestivum)*. In this study, we examined three commercial European barley varieties in control and high temperature conditions to investigate the effects on reproductive development. Using a combination of fertility assays, 3-dimensional modelling, cytology and immunolabelling, we describe the effect of heat stress on floret development and identify cultivar-specific variations in stress response. This enabled us to determine the key stages of inflorescence development in different cultivars when floral organs are most vulnerable to heat stress. This information will be used to identify and generate barley cultivars that are less susceptible to heat stress at specific stages of floral development.

PS18.10 ION HOMEOSTASIS AND REPRODUCTION: MOLECULAR BASIS AND INTEGRATIVE MECHANISMS

SATURDAY 30 JUNE 2018 **14:45**

JOSÉ FEIJÓ (UNIVERSITY OF MARYLAND, UNITED STATES)

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Ion homeostasis has been implicated at various of reproductive success. We focus on Ca^{2+} and pH signalling on the pollen tubes. I will report on molecular mechanisms and quantitative studies of the choreography of these two ions during chemotropic responses to show the relevance of the ionic status of the pollen in the perception and signalling of external cues and correct pollen tube targeting.

PS18.11 SYNERGID CELL DEATH IN ARABIDOPSIS, A ROLE FOR CYTOKININ

SATURDAY 30 JUNE 2018 **15:15**

MARTA A MENDES (UNIVERSITY OF MILAN, ITALY), GIADA CALLIZAYA TERCEROS (UNIVERSITY OF MILAN, ITALY), LUCIA COLOMBO (UNIVERSITY OF MILAN, ITALY)

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Fertilization in flowering plants is complex and requires a series of coordinated events involving the male and female gametophytes to ensure successful seed production. In the female gametophyte the two synergid cells are responsible both for the attraction and reception of the pollen tube - the male gametophyte. Once the pollen tube penetrates the receptive synergid, it ceases growth and enters a programmed leading to cell death; this allows the release of the two sperm cells into the receptive synergid – which also undergoes a similar process of cell death. Two REM transcription factors, VAL and VDD, both targets of the ovule identity MADS-box complex SEEDSTICK-SEPALLATA3, form a complex that can control the expression of the cytokines oxidase/dehydrogenase CKX7. The correct maintenance of cytokinin levels is required for the receptive synergid to die, allowing sexual fusion to take place.

PS18.16 LOST HIGHWAY: A PISTIL & POLLEN TUBE LOVE STORY

SATURDAY 30 JUNE 2018 **16:15**

ANA MARTA PEREIRA (UNIVERSITÁ DEGLI STUDI DI MILANO, ITALY), ANA LOPES (UNIVERSIDADE DO PORTO FACULDADE DE CIÊNCIAS, PORTUGAL), SÍLVIA COIMBRA (UNIVERSIDADE DO PORTO FACULDADE DE CIÊNCIAS, PORTUGAL), SIMONA MASIERO (UNIVERSITÁ DEGLI STUDI DI MILANO, ITALY)

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Flowering plants bear immotile sperm cells, which must be transported along the pistil tissues to reach the embryo sac inside the ovule, to achieve double fertilization. The pollen tube (PT) is responsible for transporting and delivering this passive cargo. Along its journey through the pistil, it travels along the stigma, the style transmitting tract (TT) and the funiculus. In Arabidopsis thaliana the TT is the main road for PT growth before it turns abruptly in the direction of an unfertilized ovule. The pistil tissues provide support, nutrition, and guidance for the growing PTs.

Any defect in the development of these tissues may lead to a deficient PT growth and a low seed set. AGPs are signalling molecules crucial for PT guidance and successful fertilization. They are abundant constituents of the PT pathway and are known to be involved in different reproductive processes. We have shown that at least one specific AGP, JAGGER, is important during the PT reception at the embryo sac. jagger mutant ovules are able to attract more than one PT due to a failure in synergid degeneration. Transcriptomic data comparing jagger and wild-type pistils have shown misregulation of some genes, which are being studied. Besides this function, JAGGER is expressed in other pistil tissues. Its function in these tissues and the involvement of AGPs in PT growth is under analysis.

PS18.17 A HIGHER-ORDER TRANSCRIPTION FACTOR NETWORK GOVERNS EGG CELL DIFFERENTIATION AND STRESS HOMEOSTASIS IN *ARABIDOPSIS*

SATURDAY 30 JUNE 2018 **16:30**

AMAL J JOHNSTON (JACOBS UNIVERSITY, GERMANY; UNIVERSITY OF HEIDELBERG, GERMANY), OLGA J KIRIOUKHOVA (JACOBS UNIVERSITY, GERMANY; UNIVERSITY OF HEIDELBERG, GERMANY), PALLAVI PAWAR (UNIVERSITY OF HEIDELBERG, GERMANY), GEETHA GOVIND (UNIVERSITY OF HEIDELBERG, GERMANY), PRAMOD PANTHA (LOUISIANA STATE UNIVERSITY, UNITED STATES), RENÃÉ LEMCKE (UNIVERSITY OF HEIDELBERG, GERMANY), DANAÃÉ S LARSENA (UNIVERSITY OF HEIDELBERG, GERMANY), ALAGARSAMY M RHAHUL (UNIVERSITY OF HEIDELBERG, GERMANY), JUBIN N SHAH (UNIVERSITY OF HEIDELBERG, GERMANY), CHATHURA WIJESINGHEGE (LOUISIANA STATE UNIVERSITY, UNITED STATES), YUE ZHOU (MAX-PLANCK-INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), WILHELM GRUISSEM (ETH ZURICH, SWITZERLAND), FRANZISKA TURCK (MAX-PLANCK-INSTITUTE FOR PLANT BREEDING RESEARCH, GERMANY), MAHESHI DASSANAYAKE (LOUISIANA STATE UNIVERSITY, UNITED STATES)

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Egg cell is the maternal precursor from which the entire organism emerges upon fertilization and ensuing embryogenesis, and its ontogeny requires tightly coordinated genetic control involving transcription factors and complex regulatory networks. We describe here interplay between evolutionarily conserved onco-protein homologs consisting of a core transcriptional repressor RETINOBLASTOMA RELATED (RBR) and redundant MYB proteins that orchestrate egg cell differentiation and development in the model plant *Arabidopsis*. In addition to the RBR-MYB duo, we show that a family of RWP-RK-domain containing MONO-AMNIOTIC TWIN EGGS (MATE), and LEAFY COTYLEDON1 (LEC1), both plant-specific transcription factors, participate during egg cell differentiation and reproductive stress response. RBR physically interacts with MYBs, MATEs and LEC1, and it also binds to most of these loci. Deregulation of RBR, MYBs and MATEs led to proliferating egg cells in support of their requirement to prevent parthenogenesis of the sexual eggs. Cross-regulation among these factors, and transcriptional repression by RBR and Polycomb Repressive Complex 2 (PRC2)-mediated histone H3K27 trimethylation, govern egg development and expression of zygotic polarity genes of the WUSCHEL RELATED HOMEOBOX family. The proposed regulatory model connecting these major hubs will be highly relevant for in-depth dissection of sexual or parthenogenetic egg cell development.

PS18.18 MICROSPORE EMBRYOGENESIS: UNRAVELLING THE DETERMINANT FACTORS OF CELL TOTIPOTENCY FOR CROP IMPROVEMENT

SUNDAY 1 JULY 2018 **09:00**

PILAR S TESTILLANO (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN), MARÍA-TERESA SOLÃÍS (CIB-CSIC AND COMPLUTENSE UNIV. OF MADRID UCM, SPAIN), EDUARDO BERENGUER (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN), IVETT BÁRÁNY (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN), YOLANDA PÉREZ-PÉREZ (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN), ELENA CARNEROS (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN), MARÍA C RISUEÑO (BIOLOGICAL RESEARCH CENTER CIB-CSIC, SPAIN)

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Under specific stress treatments, isolated microspores can be reprogrammed *in vitro* towards embryogenesis, producing doubled-haploid embryos and plants, useful biotechnological tools in plant breeding as source of new genetic variability, fixed in homozygous plants in only one generation. Stress-induced microspore embryogenesis is also an excellent system to study cell reprogramming, totipotency and embryogenesis. Our recent investigations in two model crop species, *Brassica napus* and *Hordeum vulgare*, have revealed that the stress treatment inducing embryogenesis also caused cell death, together with activation of autophagy and cystein proteases. *In vitro* treatments using autophagy inhibitors reduced cell death levels and, consequently, increased the efficiency of *in vitro* microspore embryogenesis, indicating a role for autophagy in microspores death. Results have also shown that microspore reprogramming, totipotency and embryogenesis initiation were epigenetically regulated, and associated with global DNA hypomethylation, *MET1 DNA* methyltransferase down-regulation, and low levels of histone H3K9 dimethylation. Treatments with epigenetic modulators like azacytidine (DNA demethylating agent) and BIX-01294 (inhibitor of H3K9 methylation) promote microspore reprogramming, leading to higher proportion of embryogenesis initiation. Endogenous auxin has been revealed as a determinant factor of embryogenesis induction since de novo auxin biosynthesis, its activity and polar transport were required for microspore embryogenesis initiation, while their pharmacological inhibition drastically reduced embryo formation. The findings provide new insights into the mechanisms underlying microspore embryogenesis initiation and progression. They also open up new intervention pathways to improve the efficiency of *in vitro* embryogenesis systems for their exploitation in crop improvement and breeding programs.

PS18.19 AGPS AS MARKERS FOR PHRAGMOPLAST ASSEMBLY DURING *QUERCUS SUBER* MICROSPOROGENESIS

SUNDAY 1 JULY 2018 **09:30**

MÁRIO COSTA (FACULDADE DE CIÊNCIAS UNIVERSIDADE DO PORTO, PORTUGAL), SÍLVIA COIMBRA (FACULDADE DE CIÊNCIAS UNIVERSIDADE DO PORTO, PORTUGAL),

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Quercus suber L., is an evergreen tree native to the Mediterranean basin region, and is mostly found stretching from the Estremadura region of Spain to the Ribatejo and Alentejo regions of Portugal. Arabinogalactan proteins (AGPs) are highly glycosylated hydroxyproline rich cell membrane bound GPI-anchored proteins. AGPs have been for long associated with several aspects of plant development including cell proliferation and survival, pattern formation, reproduction and growth. Previous studies during microsporogenesis in Q. *suber* and Arabidopsis showed an intimate connection between AGPs and the gametophytic cells differentiation. AGPs disruption in both Arabidopsis and *Nicotiana tabacum*, was shown to disturb the cortical microtubular organization. Zygote and proembryo cells of *N. tabacum in vitro* cultures subjected to β-glucosyl Yariv (βGlcY) reagent, an exogenous AGP inhibitor, presented an increase of aberrant division and endosomes distribution patterning on the cell plate, related to the reduction of AGPs. During *A. thaliana* microsporogenesis AGPs were shown to integrate the cell plate formation, being detected after the convoluted sheets stage, suggesting that AGPs may play a determinant role in the cell division patterning by affecting the cell plate localization and formation. Immunolocalization of AGPs and pectins in several development stages of *Q. suber* anthers was performed revealing that during the short period encompassed between meiosis initiation and tetrad formation, JIM13 and JIM8 AGP epitopes could be found labelling the cytoplasm, vesicular structures and newly formed cell walls. This finding may be one more link connecting AGPs to cell division and microspore differentiation.

PS18.20 CHROMATIN REMODELLING DURING THE PROGAMIC PHASE OF *QUERCUS SUBER*

SUNDAY 1 JULY 2018 **09:45**

MARIA MANUELA R COSTA (BIOISI UNIVERSITY OF MINHO, PORTUGAL), TERESA RIBEIRO (BIOISI UNIVERSITY OF MINHO, PORTUGAL), HELENA SILVA (BIOISI UNIVERSITY OF MINHO, PORTUGAL), LEONOR MORAIS-CECÍLIO (LEAF INSTITUTE OF AGRONOMY UNIVERSITY OF LISBON, PORTUGAL)

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Flower development is a complex process, which determines species reproductive success. Chromatin states associated with distinct epigenetic marks have been correlated with the development of floral tissues. Trees of Quercus genus are monoecious with a long progamic phase (delayed fertilization), and commonly with biennial fructification. *Q. suber* is unique as it has both biennial and annual cycles of fructification, being a good model to study both reproductive habits in the same background. Here we describe some chromatin remodelling events during the long progamic phase in *Q. suber* annual and biennial flowers. Fluorescence immunodetection marks related to transcription activity (H3K4me3 and H3K18ac) and to transcription silencing (5-mC and H3K9me2) were assessed in different stages of the progamic phase. In all the studied stages, an increasing gradient of all epigenetic marks was detected from the stigma to the abscission zone. In general, the marks associated with active transcription were more widely distributed with a stronger signal than the marks associated with gene silencing. In this work, we also used the genomic resource generated by the Portuguese Cork Oak ESTs Consortium to identify *Q. suber* homologues of epigenetic modifying enzymes and established their phylogenetic relationships. Expression of these genes was evaluated by qRT-PCR. This work evidences that the progamic phase in *Q. suber* either in annual or in biennial flowers is a long and complex process involving chromatin remodelling in several tissues.

PS18.21 A STYLISH STORY OF CARPEL EVOLUTION

SUNDAY 1 JULY 2018 **10:00**

MCRISTINA FERRANDIZ (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), AFRICA GOMARIZ-FERNANDEZ (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), VICTOR ZÚÑIGA-MAYO (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), CHLOÈ FOURQUIN (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), VERÓNICA SÁNCHEZ-GERSCHON (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), PATRICIA BALLESTER (INSTITUTO DE BIOLOGÍA MOLECULAR Y CELULAR DE PLANTAS. CSIC-UPV, SPAIN), STEFAN DE FOLTER (LANGEBIO CINVESTAT-IPN, MEXICO)

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Fruits are a major evolutionary acquisition of Angiosperms, essential to protect the developing seeds and to ensure seed dispersal. Fruit patterning and fruit traits such as form, size or texture, depend in great extent from carpel patterning, the ovule-bearing floral organs. Carpels form the gynoecium, organised in a structure of functional modules with specific roles. Our long-term goal is to understand how these modules are specified and spatially distributed in the developing gynoecium, and what is the molecular basis of the morphological and functional diversity found between species. A number of transcription factors (TFs) with a role in carpel patterning have been identified in *Arabidopsis thaliana*. While genetic pathways directing dehiscence zone formation have been well characterised, the regulatory networks directing patterning of most of the other functional modules in the gynoecium, like style and stigma, are poorly understood. Here we will present data that suggest that TFs directing carpel morphogenesis may specify module identity according to the different composition of multimeric complexes in a restricted spatial domain. Moreover, we will show how most of the functions of the major TFs involved in the specification of the style and the stigma in Arabidopsis are also conserved in distant dicot species, as well as protein-protein interactions among them. Our results, in the context of extensive phylogenetic studies carried out by other groups, suggest that carpel-specific functional domains may have evolved by the assembly of these complexes at the origin of Angiosperms.

PS18.22 *MtWOX9-1* GENE IN THE SOMATIC EMBRYOGENESIS IN *MEDICAGO TRUNCATULA*

SUNDAY 1 JULY 2018 **10:30**

VARVARA E TVOROGOVA (SAINT PETERSBURG STATE UNIVERSITY, RUSSIA), NIKITA S KURMAZOV (SAINT PETERSBURG STATE UNIVERSITY, RUSSIA), ELINA A POTSENKOVSKAYA (SAINT PETERSBURG STATE UNIVERSITY, RUSSIA), LUDMILA A LUTOVA (SAINT PETERSBURG STATE UNIVERSITY, RUSSIA)

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Somatic embryogenesis in vitro is widely used in biotechnology, for example, for agrobacterial transformation or artificial seeds production. In this regard, search for new stimulators of somatic embryogenesis can be useful. In our study, a gene coding for transcription factor MtWOX9-1 in the model object *Medicago truncatula* was shown to be involved in the somatic embryogenesis, which was confirmed by the qPCR and promoter:GUS analysis. More importantly, its overexpression led to the remarkable increase in the somatic embryogenesis capacity and was associated with changes in expression levels of several genes associated with somatic embryogenesis.

It is well known that expression of *WOX* family genes can be regulated by peptide hormones from CLE family by means of positive or negative feedback loops. In our study, we identified several *CLE* genes, which are up- or downregulated by *MtWOX9-1* overexpression. We plan to check if some of these peptides can also stimulate or repress *MtWOX9-1* expression.

PS18.27 RESPONSE OF SOYBEAN AND COMMON BEAN SEEDS TO ULTRASOUND

SUNDAY 1 JULY 2018 **11:30**

MEISAM NAZARI (GEORG-AUGUST UNIVERSITY OF GÖTTINGEN, GERMANY), POURIA SADEGHIANFAR (GEORG-AUGUST UNIVERSITY OF GÖTTINGEN, GERMANY)

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Soybean *(Glycine max L.)* and common bean *(Phaseolus vulgaris)* are two of the most important legumes for human consumption. Their seeds contain a hard and impermeable coat resulting in poor germination and decreased yield. This study was performed to break the coat-induced dormancy of soybean and common bean seeds by ultrasound technique. The treatments included 0 (control), 10, 20, and 30 min exposure to ultrasound, each treatment consisting of four replicates. The results indicated that ultrasound significantly increases the germination rate of soybean and common bean seeds ($p<0.05$). However, only the germination percentage of soybean seeds significantly increased by ultrasound. The highest germination rates were observed after 20 and 30 min exposure of common bean and soybean seeds to ultrasound, respectively. The treatment 30 min exposure to ultrasound led to the highest germination percentage (75%) for soybean seeds. The highest (1467.21 μm^2) cotyledon cell area of common bean seeds was related to 20 min exposure to ultrasound. It is concluded that ultrasound could enhance the germination rate of soybean and common bean seeds as well as the germination percentage of soybean seeds. The underlying mechanisms for this could have been the creation of micro-pores and micro-cracks by ultrasound on the seed coat resulting in a higher amount of water imbibed by the seed. It is plausible that higher water imbibed after treating the seeds by ultrasound has led to a faster release of α-amylase enzyme, a quicker starch hydrolysis, and improvement of seed germination rate.

PS18.28 STAY STICK: HOW TO FIT EACH TILE IN THE SEEDSTICK TF CONTROL FRAME?

SUNDAY 1 JULY 2018 **11:45**

ANA LOPES (FACULDADE DE CIÊNCIAS DA UNIVERSIDADE DO PORTO, PORTUGAL), ANA MARTA PEREIRA (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), RICARDO FERRAZ (FACULDADE DE CIÊNCIAS DA UNIVERSIDADE DO PORTO, PORTUGAL), PATRÍCIA SOUSA (FACULDADE DE CIÊNCIAS DA UNIVERSIDADE DO PORTO, PORTUGAL), LUÍS G PEREIRA (FACULDADE DE CIÊNCIAS DA UNIVERSIDADE DO PORTO, PORTUGAL), MARTA MENDES (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), SIMONA MASIERO (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), LUCIA COLOMBO (UNIVERSITÀ DEGLI STUDI DI MILANO, ITALY), SÍLVIA COIMBRA (FACULDADE DE CIÊNCIAS DA UNIVERSIDADE DO PORTO, PORTUGAL)

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The plant organogenesis charming process embodies structures of refined control of gene expression. The final shape of a single tissue relies deeply on its cell wall and genes involved in its modification; act downstream of transcription factors (TF). Inside a seed, the seed coat shelters its embryo further influencing its mechanisms of dormancy, dispersal and longevity. In Arabidopsis, after fertilization, the seed coat raises from the ovule inner and outer integuments, during a rapid growth transformation of cell division and expansion. SEEDSTICK (STK), one of the major MADS-box TF that regulates ovule and seed differentiation, revealed its direct target genes, by RNA and CHIP sequencing analysis, specifically arabinogalactan proteins (AGPs), long time involved in important plant development processes, like cell proliferation, pollen tube growth and seed germination. Cytokinin oxidase/dehydrogenase (CKX) genes were also found as STK targets. CKX enzymes are responsible for most cytokinin catabolism and for this phytohormone irreversible degradation. Cytokinin intervenes in cell division, differentiation and proliferation. Since STK is a TF controlling ovule and seed integument identity, its direct target genes - AGP24, AGP31, CKX6 and CKX7 - are being studied, to unravel their function during these stages. Plants expressing the GUS reporter under the control of AGP24, AGP31, CKX6 and CKX7 promoter genes, were examined by histochemical localization of β-glucuronidase activity. We aim to validate the STK regulation of these players, understand their role during seed development and clarify the possible crosstalk between STK, these sugar signalling molecules and cytokinin.

PS18.29 STIGMA SURFACE COMPONENTS AND THEIR ROLE(S) IN SEXUAL PLANT REPRODUCTION

SUNDAY 1 JULY 2018 **12:00**

SIMON J HISCOCK (DEPARTMENT OF PLANT SCIENCES UNIVERSITY OF OXFORD, UNITED KINGDOM), ADORACIÓN ZAFRA (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN CSIC GRANADA, SPAIN), JUAN D REJÓN (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN CSIC GRANADA, SPAIN), ALEXANDRA M ALLEN (SCHOOL OF BIOLOGICAL SCIENCES UNIVERSITY OF BRISTOL, UNITED KINGDOM), JUAN DE DIOS ALCHÉ (ESTACIÓN EXPERIMENTAL DEL ZAIDÍN CSIC GRANADA, SPAIN)

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The pollen-pistil interaction comprises a pre-zygotic molecular 'courtship' between the haploid male gametophyte and the diploid maternal tissues of the sporophyte, the outcome of which determines largely whether or not seed will be produced. Molecules regulating intraspecific self-incompatibility have been well characterised in a number of species, but molecules mediating 'compatibility' within and between species remain poorly understood. These molecules regulate the earliest stages of the pollen-pistil interaction: pollen capture, pollen adhesion, pollen germination and pollen tube penetration of the stigma. Many diverse molecules have been implicated in these processes, including arabinogalactan glycoproteins, esterases, peroxidases, hydrolases and small cysteine-rich proteins. More recently, transcriptome sequencing of stigmas has identified numerous stigma-specific proteins that may be involved in pollen-stigma interactions. Here I will assess the potential role of a range of candidate proteins identified by transcriptome analysis of stigmas from *Senecio* and olive – two species with dry stigmas. I will then discuss the apparently ubiquitous accumulation of reactive oxygen species (ROS) in angiosperm stigmas and their possible role(s) in the early stages of the pollen-stigma interaction and in defence, again referring to specific studies in *Senecio* and olive.

PS18.30 APOSTART: A CANDIDATE GENE INVOLVED IN EMBRYO PROGRESSION AND PARTHENOGENESIS

SUNDAY 1 JULY 2018 **13:45**

EMIDIO ALBERTINI (DEPT. OF AGRICULTURAL FOOD AND ENVIRONMENTAL SCIENCES UNIVERSITY OF PERUGIA, ITALY), DOMENICO AIELLO (DEPT. OF AGRICULTURAL FOOD AND ENVIRONMENTAL SCIENCES, UNIVERSITY OF PERUGIA, ITALY), GIANPIERO MARCONI (DEPT. OF AGRICULTURAL FOOD AND ENVIRONMENTAL SCIENCES, UNIVERSITY OF PERUGIA, ITALY) DEL ZAIDÍN CSIC GRANADA, SPAIN)

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Apomixis is a naturally occurring mode of asexual reproduction in flowering plants, resulting in embryo formation without meiosis or egg fertilization. Seed derived progenies are genetically identical to the maternal parent. In crop species, apomixis would enable the instantaneous fixation of the complete genome of the best plants. In *Poa pratensis* we isolated a gene, APOSTART.

To understand its function, we are now characterising Arabidopsis APOSTART members. In particular, PpAPO1shares high homology with Arabidopsis protein At5G45560, thus renamed *AtAPO1* and with *EDR2*. In order to verify if *AtAPO1* and *EDR2* have additive/redundant roles we generated and analysed the *atapo1-2/edr2* double mutants. Double mutants germinated slower and plants appeared smaller than wt. High phenotypic variability was found between and within mutant lines. The reason for this variability could be found in polyploidy or epigenetic changes. Double mutant plants appear smaller than the parental lines, interestingly also the double mutant developing siliques are smaller. Manual dissection of double mutant siliques show that seed development is compromised in *atapo1-2/edr2*. Microscopic analyses show that all seeds contain embryos, 30% of which show delayed/ arrested development. We performed a comparison of DNA methylation between double mutants and wt for *AtAPO* promoter regions and for their reduced representation whole genomes. On the other hand, polyploidy was investigated both by checking the chromosome number of some genotypes and by flow cytometry. Overall results in terms of methylation analysis and ploidy in Arabidopsis double mutants will be reported and critically discussed.

PS18.31 TOO MANY MOTHERS IN A GAMMA-IRRADIATED MUTANT OF APOMICTIC *HIERACIUM PRAEALTUM*

SUNDAY 1 JULY 2018 **14:15**

MARTINA JURANIC (CSIRO AGRICULTURE AND FOOD, AUSTRALIA), STEVEN HENDERSON (CSIRO AGRICULTURE AND FOOD, AUSTRALIA), SUSAN D JOHNSON (CSIRO AGRICULTURE AND FOOD, AUSTRALIA), ANDREW SPRIGGS (CSIRO AGRICULTURE AND FOOD, AUSTRALIA), ANNA M KOLTUNOW (CSIRO AGRICULTURE AND FOOD, AUSTRALIA)

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Hieracium praealtum is predominately a facultative aposporous apomict which also forms a small percentage of seed sexually. The development of the sexual female germline initiates and is usually terminated after enlargement of one or more aposporous initial (AI) cells differentiating from sporophytic tissue surrounding megaspores undergoing meiosis. An unreduced aposporous female gametophyte forms by mitosis and both embryo and endosperm form without fertilization. A collection of gamma irradiated deletion mutants of *H. praealtum* had previously identified two independent and dominant loci controlling apomixis in *H. praealtum, LOSS OF APOMEIOSIS (LOA)* and *LOSS OF PARTHENOGENESIS (LOP)*. They are required for AI cell initiation and fertilization-independent seed development, respectively. A unique deletion mutant lacking LOA *(m119)* was found to have multiple enlarged cells within the ovule. These cells were confirmed to have megaspore mother cell (MMC)-like identity using anti-AGP (arabinogalactan) and anti-callose antibodies and DIC microscopy. Furthermore, the multiple MMCs in the apomixis mutant ovule were able to enter and complete meiosis producing a tetrad of four megaspores. Subsequent sexual development ceased. These results suggest that in the apomict processes limit MMC formation to a single cell as has been observed in sexual species. Transcriptomes of apomict and mutant ovules were analysed in order to find pathways that could be involved in regulating numbers of MMCs formed.

PS18.32 AUXIN REGULATES ENDOSPERM CELLULARISATION IN ARABIDOPSIS

SUNDAY 1 JULY 2018 **14:30**

DUARTE D FIGUEIREDO (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT BIOLOGY, SWEDEN), RITA A BATISTA (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT BIOLOGY, SWEDEN), CLAUDIA KÖHLER (SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT BIOLOGY, SWEDEN)

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The development of a seed in flowering plants starts with a double fertilisation event that leads to the formation of two fertilisation products: the embryo and the endosperm. The endosperm is an ephemeral tissue that nourishes the growing embryo, similar to the placenta in mammals. In most angiosperms endosperm development starts as a syncytium, where nuclear divisions are not followed by cytokinesis. The timing of endosperm cellularisation largely varies between species and the event triggering this transition remains unknown. In our work we show that increased auxin biosynthesis in the endosperm prevents its cellularisation, leading to seed arrest. Auxin-overproducing seeds phenocopy paternal-excess triploid seeds derived from hybridisations of diploid maternal plants with tetraploid fathers. Concurrently, auxin-related genes are strongly overexpressed in triploid seeds, correlating with increased auxin activity. Reducing auxin biosynthesis and signalling re-establishes endosperm cellularisation in triploid seeds and restores their viability, highlighting a causal role of increased auxin in preventing endosperm cellularisation. We propose that auxin determines the time of endosperm cellularisation and thereby uncovered a central role of auxin in establishing hybridisation barriers in plants.

PS18.33 EVOLUTION OF HYBRIDIZATION BARRIERS ALONG ARABIDOPSIS LINEAGES: THE CASE OF HYBRID SEED LETHALITY

SUNDAY 1 JULY 2018 **14:45**

CLÉMENT LAFON PLACETTE (DEPARTMENT OF BOTANY CHARLES UNIVERSITY IN PRAGUE, CZECH REPUBLIC), FILIP KOLÁŘ (DEPARTMENT OF BOTANY CHARLES UNIVERSITY IN PRAGUE, CZECH REPUBLIC), ROSWITHA SCHMICKL (DEPARTMENT OF BOTANY CHARLES UNIVERSITY IN PRAGUE, CZECH REPUBLIC), IDA M JOHANNESSEN (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY, DEPARTMENT OF BIOSCIENCES, UNIVERSITY OF OSLO, NORWAY), KARINA S HORNSLIEN (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY, DEPARTMENT OF BIOSCIENCES, UNIVERSITY OF OSLO, NORWAY), MOHAMMAD F ALI (DEPARTMENT OF PLANT BIOLOGY SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT, SWEDEN), KATRINE N BJERKAN (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY DEPARTMENT OF BIOSCIENCES UNIVERSITY OF OSLO, NORWAY), JONATHAN BRAMSIEPE (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY, DEPARTMENT OF BIOSCIENCES, UNIVERSITY OF OSLO, NORWAY), BARBARA M GLÖCKLE (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY, DEPARTMENT OF BIOSCIENCES, UNIVERSITY OF OSLO, NORWAY), CAROLIN A REBERNIG (DEPARTMENT OF PLANT BIOLOGY, SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT, SWEDEN), ANNE K BRYSTING (CENTRE FOR ECOLOGICAL AND EVOLUTIONARY SYNTHESIS DEPARTMENT OF BIOSCIENCES UNIVERSITY OF OSLO, NORWAY), PAUL E GRINI (SECTION FOR GENETICS AND EVOLUTIONARY BIOLOGY DEPARTMENT OF BIOSCIENCES UNIVERSITY OF OSLO, NORWAY), CLAUDIA KÖHLER (DEPARTMENT OF PLANT BIOLOGY SWEDISH UNIVERSITY OF AGRICULTURAL SCIENCES AND LINNEAN CENTER FOR PLANT, SWEDEN)

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Hybrid seed lethality, a long-known hybridisation barrier in angiosperms, has undergone a regain of scientific interest in the past years. This resulted in a clarification of its developmental and molecular basis: impaired differentiation of the endosperm and the deregulation of its transcriptome involving well-known regulators such as *AGAMOUS-LIKE* transcription factors are consistently found in recent studies. Nevertheless, the genetic cause for this type of reproductive isolation, its rate of evolution and its role in regulating gene flow between wild populations remain unresolved. In a recent work, we showed that endosperm defects in hybrid seeds between *Arabidopsis lyrata* and *A. arenosa* were consistent with observed gene flow between these species, suggesting an important role of this reproductive barrier in the speciation process between *A. lyrata* and *A. arenosa*. We also showed that hybrid seed lethality has a dosage basis similar to interploidy hybrid seed defects, and its genetic basis is variable even within one species. We are now interested in identifying the genetic loci involved in this barrier and test for their evolution along Arabidopsis lineages.

PS18.34 NOVEL INSIGHTS INTO THE FUNCTION OF DEAD ORGANS ENCLOSING EMBRYOS OF ANGIOSPERMS

SUNDAY 1 JULY 2018 **15:00**

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In angiosperms, the embryo is dispersed from the mother plants surrounded by remnants of the mother reproductive organs such as indehiscent fruits and seed coats. For instance, in dicots, the integument layers will form the seed coats; in wild grasses, the dispersal units consist of the caryopsis surrounded by the dead floral bracts. The maternally derived organs (MDO) of grasses are undesired in agriculture but their adaptive value has not been fully explored. We investigated the proposal that the MDO of seeds and dispersal units have been evolved to function more than just means for physical embryo protection. We showed that dead MDO of various plants store and release upon hydration active hydrolases including nucleases and chitinases, which maintain activity years after the mother plant dies. Proteome and ICP analysis revealed multiple oxidative and pathogenesis stress related proteins and nutrients that are released upon hydration. Further analysis showed that although germination from the intact dispersal unit of wild emmer wheat was delayed, post germination growth was better than that of separated caryopses. In some of the studied dicot species, seed coats and pericarps exhibited microbial growth control activity of the seed coat extracts, even after years of storage in uncontrolled conditions. Thus, our study show that the dead, MDO enclosing the embryo store important factors that can engineer the micro environment of the germinating seed; support seed longevity and serve as a first line of defence during germination and increase seedling establishment.

PS18.35 A FRUIT-TALK

SUNDAY 1 JULY 2018 **15:45**

SIMONA MASIERO (UNIVERSITY OF MILAN, ITALY), STEFANO ROSA (UNIVERSITY OF MILAN, ITALY), CHIARA MIZZOTTI (UNIVERSITY OF MILAN, ITALY), SARA FORLANI (UNIVERSITY OF MILAN, ITALY), CAROLINA COZZI (UNIVERSITY OF MILAN, ITALY)

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Given the fundamental nature of both the dietary and biological significance of fruit, molecular dissection of fruit growth and maturation has considerable interest. The yield and quality factors associated with fruits are of key importance to agricultural production, future improvements of fruit characteristics will rely on the comprehension of the mechanisms controlling fruit development and maturation. Here we report our efforts to shed light into the molecular networks controlling fruit development in the model plant *Arabidopsis thaliana*. In order to identify genes whose products control Arabidopsis fruit development and maturation, a transcriptome analysis by RNA-deep-sequencing has been performed, comparing wild-type (WT) siliques, devoid of seeds, at 3, 6, 9 and 12 DPA, thus covering all the phases of silique development and maturation. The bioinformatics and statistical analysis of the data led to the identification of about thousand genes differentially expressed between early and late stage of silique development. Among all the different clusters, we are currently exploring the role of the NAC transcription factors. Our data strongly indicate that NAC proteins participate to the homeostasis of gibberellins and other hormones. Auxins, gibberellins, cytokinins, abscisic acid, and ethylene have been implicated at various stages of fruit development, to better understand their role in Arabidopsis siliques growth and maturation we have measured GA and ABA content at 3, 69 and 12 DPA Arabidopsis fruits.

PS18.36 NF-Y GENES IN *MEDICAGO TRUNCATULA* SOMATIC EMBRYOGENESIS

SUNDAY 1 JULY 2018 **15:45**

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Somatic embryogenesis is a specific type of plant reproduction. Investigation of somatic embryo development *in vitro* can be very useful as a model for studying zygotic embryogenesis and regeneration as a whole. As a consequence, search for the new regulators of somatic embryogenesis is important.

MtNF-YB10 is a close homolog of *Arabidopsis thaliana LEC1* gene, well-known regulator of zygotic and somatic embryogenesis. Both of them encode proteins belonging to the NF-YB family, which, together with NF-YA and NF-YC subunits, form heterotrimeric NF-Y transcription factor. Plant genomes contain genes coding for several NF-YA, B and C proteins, which theoretically can combine in multiple NF-Y trancription factors.

We found that *MtNF-YB10* expression increases during somatic embryogenesis in *Medicago truncatula*. Furthermore, mutants with *MtNF-YB10* loss of function have changed somatic embryogenesis capacity. In our study, we search for NF-YA and C subunits which can work together with MtNF-YB10 in somatic embryogenesis. Now we have demonstrated that expression levels of *MtNF-YC3* and *7*, as well as *MtNF-YA3* and *8*, increase during somatic embryogenesis. Our next step is to check the interaction between NF-YB10 and these subunits using modified yeast two-hybrid system and BiFC analysis.

This work was supported by RSCF grant 16-16-10011, RFBR grant 17-04-01708 A and the grant of SPbU Alumni Association.

POSTER SESSIONS 30 JUNE AND 1 JULY

PS18.12 UNRAVELLING THE IMPORTANCE OF FLA5 (FASCICLIN-LIKE ARABINOGALACTAN PROTEIN 5) IN ARABIDOPSIS REPRODUCTION

SATURDAY 30 JUNE 2018

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The fasciclin-like arabinogalactan proteins (FLAs) are a subclass of 21 members that belong to the arabinogalactan protein (AGP) family in *Arabidopsis thaliana*. FLAs are a heterogeneous group characterised by having one or two fasciclin-like domains and one or two AGP-like glycosylated regions in their polypeptide core. They are widely distributed in various cells and tissues and are implicated in plant growth and development, yet only few FLA genes in *Arabidopsis* have been identified and functionally characterised. This study is focused on fasciclin-like arabinogalactan protein 5 (FLA5). FLA5 has 2 PRO-rich domains flanking a fasciclin domain and a glycosylphosphatidylinositol (GPI) anchor. FLA5 is a target of the transcription factor SEEDSTICK, which regulates the development of the ovule and the seed. Since seeds are essential units for plant propagation and the first step in their development is the formation of ovules, it is very important to study the genes involved in the reproductive process. Therefore, to increase our knowledge about the role of FLA5, the objective of the present work was to study a *fla5* RNA interference knock-down line and access its localization by GFP/GUS promoter analysis.

PS18.13 BASIC PENTACYSTEINE PROTEINS CONTROL SEPTUM FORMATION DURING CARPEL DEVELOPMENT IN *ARABIDOPSIS THALIANA*

SUNDAY 1 JULY 2018

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The GAGA binding proteins BASIC PENTACYSTEINE PROTEINS (BPCs) are transcription factors, present in several plant species. The Arabidopsis BPCs family is composed of seven members that have been divided in three different classes, based on their protein sequence similarity (Meister *et al.*, 2004). BPCs are ubiquitously expressed in the plant and analysis of the mutants reveal a redundant function in different stages of plant development (Monfared et al., 2011). Mutation of the five BPCs affects a wide range of processes i.e. fruit development. Analysis of the mutant reveal that the fruit, smaller in size, has defects in the formation of the septum, an important structure that divides the ovary in two halves and play an crucial role during fertilization; in particular, we detect a defect in the fusion of the septum, following by a lack of differentiation of the transmitting tract cells, important for the correct growth and guidance of the pollen tube from the style to the ovary. Sequence analysis of the promoter region of genes involved in septum development identify

SPATULA (SPT) as a putative BPCs target. qRT-PCR analysis show a strong downregulation of *SPT* in the *bpc* quintuple mutant. Our results confirm a role of BPCs in septum development, most likely by the regulation of SPT and provide insight into the transcriptional regulatory networks that control fruit development in Arabidopsis.

PS18.14 DEVELOPMENT AND CHARACTERISATION OF KNOCK-DOWN RNAI AND PROMOTER-INDUCED GUS EXPRESSION LINES FOR ARABINOGALACTAN PROTEIN 20 (AGP20) IN *ARABIDOPSIS THALIANA*

SATURDAY 30 JUNE 2018

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AGP20 belongs to a large family of proteins rich in hydroxyproline and highly glycosylated, the Arabinogalactan Proteins (AGPs). Preliminary results from our lab, resulting from the expression pattern analysis of AGP20, revealed its presence in the female gametophyte cells and pistil tissues. This expression pattern marks the pathway followed by the pollen tube until it reaches the embryo sac inside the ovule, revealing the possible involvement of AGP20 in this process. Several AGPs are related to different aspects of sexual reproduction leading to the formation of seeds. Most of the AGPs are connected to the cell membrane by a glycosylphosphatidylinositol (GPI) anchor that can be cleaved, releasing the AGPs to the extracellular matrix where they can act as signalling molecules. This study focused in one of these proteins – AGP20 – with the aim to obtain two constructs for this protein's function assessment in *Arabidopsis thaliana*: one for tracking AGP20 promoter activity using the reporter gene GUS; and one for the silencing of AGP20 gene by the RNA interference technique and proceed with the phenotypic analysis of the *agp20* knock-down plants.

PS18.15 FASCICLIN-LIKE ARABINOGALACTAN PROTEINS EXPRESSION PATTERN DURING SEED DEVELOPMENT IS HIGHLY CONSERVED ACROSS SPECIES

SUNDAY 1 JULY 2018

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Fasciclin-like Arabinogalactan Proteins (FLAs) are a subclass of Arabinogalactan Proteins (AGPs), which present Fasciclin-like domains in addition to AGP-like glycosylated regions. The Fasciclin domains are putative cell adhesion motifs, first described in Drosophila *melanogaster*. Sequence analysis of the 21 highly divergent AtFLAs, identified two highly conserved regions that define the Fasciclin functional motif, suggesting that the cell adhesion property is conserved. FLAs have been implicated in many developmental roles, yet their function remains largely unclear. Recent studies begin to clarify the role of FLAs in Arabidopsis development. FLAs containing a single FAS domain, like AtFLA11 and AtFLA12, are important for the integrity and elasticity of the plant cell wall matrix and AtFLA3 is involved in microspore development. AtFLA4/SOS5 with two FAS domains and two AGP domains has a role in maintaining proper cell expansion under salt stressed conditions. The role of other FLAs remains to be uncovered. Recently AtFLA9 and ZmFLA7 expression reduction was found to be associated with the abortion of fertilized ovules in *Zea Mays* and *Arabidopsis thaliana*. In Arabidopsis, several AtFLA genes reach their expression maximum during embryo and seed development and the expression pattern of these genes was found to be highly similar in cork oak. Orthologues of these same genes were identified in hemp, poplar and cork oak. This new evidence hints toward an important role for FLAs in processes underling embryogenesis and seed maturation.

PS18.23 FASCICLIN-LIKE ARABINOGALACTAN PROTEINS INVOLVED IN PLANT REPRODUCTION: AN ANALYSIS FROM *QUERCUS* TO *ARABIDOPSIS*

SUNDAY 1 JULY 2018

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Plants have developed elaborate sexual reproductive structures, the flowers, where the male and female sex organs are present. Several fasciclin-like arabinogalactan protein (FLA) genes are known to be involved in different reproductive processes in the model plant *Arabidopsis thaliana*. FLAs are a subclass of highly glycosylated hydroxyproline-rich glycoproteins that have glycomodules together with one or two conserved fasciclin domains, which may mediate cell-cell and cell-extracellular matrix adhesion.

In *Quercus suber*, a dominant tree in the Portuguese Montado, male flowers develop much sooner than the female ones, providing an interesting system for comparative studies of development and sexual reproduction. In an attempt to find FLA genes differentially expressed in male and female *Q. suber* flowers, transcriptome data and bioinformatics tools such as BLAST were used against *Arabidopsis* FLAs data. With this approach 16 QsFLA-like genes that clustered into four major groups were identified. At least five QsFLAs which clustered in the same clade are differentially expressed in the male and female gametophytes.

The characterisation of T-DNA insertion mutant lines of Arabidopsis genes *FLA1, FLA4* and *FLA8*, orthologs of *QsFLA* genes putatively related to the development of reproductive tissues is being performed. At the same time the expression of these genes by promoter-reporter (GFP or GUS) fusions is currently being studied.

PS18.24 EXPRESSION OF ALLERGENS IN *BETULA PENDULA* POLLEN UNDER ATMOSPHERIC POLLUTION INFLUENCE

SATURDAY 30 JUNE 2018

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Previous work showed an increase in allergen reactivity with patient sera in pollen exposed to different pollutants. *Betula pendula* pollen, exposed to atmospheric pollutants, was used to determine changes in intracellular accumulation and in the transcription of two major allergens, Bet v 1, a pathogenesis-related protein member of PR-10 family, and Bet v 2, a major pollen allergen, profilin. Allergens were located in pollen by immunofluorescence microscopy and transmission electron microscopy and labelling was most abundant in the cytoplasm and external wall. Differential gene expression was ascertained by Real-Time Quantitative Reverse Transcription PCR. These changes were observed after exposing the pollen to a controlled atmosphere in an environmental chamber system enriched with various levels of nitrogen dioxide (NO_2) and ozone (O_3), which are two of the most abundant aerosol pollutants in industrialized countries. Preliminary results suggest a possible influence of pollutants, particularly of ozone. The interaction between pollen allergens and gaseous pollutants seem to lead towards an increase in pollen's allergenic potential.

PS18.25 VPS13 IS INVOLVED IN THE miRNA-DEPENDENT TRANSLATIONAL REPRESSION PATHWAY REQUIRED FOR OVULE DEVELOPMENT IN *ARABIDOPSIS THALIANA*

SUNDAY 1 JULY 2018

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Post-transcriptional repression mediated by miRNAs is a key regulator of developmental processes in all Eukaryotes. In plants, miRNAs repression can act in two different ways: by RNA cleavage or through translational repression. While many factors involved in RNA cleavage has been identified, only the ARGONAUTA1 (AGO1)-RISC complex and ALTERED MERISTEM PROGRAM 1 (AMP1) proteins have been related with translational repression. However, it remains unclear how AGO1 and AMP1 factors are interrelated and how they associate to endoplasmic reticulum (ER) to interfere with ribosomes.

To address this question, we investigated the role of VACUOLAR PROTEIN SORTING-ASSOCIATED PROTEIN 13 (VPS13), a membrane-associated protein known to be involved in cytosolic vesicles trafficking in human and yeast, whereas its function in plant has been until studied only in root development. By analysing the ovule phenotype of the *vps13-1* insertional mutant, we observed that most of mature ovules show a clear outgrowth of the inner integuments and an arrest of the outer integuments. This condition was similarly identified in *ago1* and in *amp1* mutant, suggesting that *VPS13* may be involved in the same pathway. Furthermore, we found that the three proteins exhibit the same localization patterns on the ER and that both AGO1 and AMP1 were able to interact with the C-terminal part of VPS13 protein. These results strongly support the idea of VPS13 as a new component of the miRNA-mediated translation inhibition complex. Ongoing experiments are aimed to identify targets of VPS13-AGO1-AMP1 complex whose regulation by miRNA is required proper ovule development.

PS18.26 REGULATION OF SPOROGENESIS THROUGH AUXIN-DEPENDENT PATHWAYS

SATURDAY 30 JUNE 2018

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Unlike animals, plants generate their germlines during post-embryonic development. Starting from a single somatic cell, the germline is established through a differentiation process known as sporogenesis. Sporogenesis requires a finely tuned spatio-temporal orchestration of transcriptional and hormonal mechanisms controlling cell proliferation and differentiation. So far, the only gene known to abolish sporogenesis is NOZZLE/SPOROCYTELESS (NZZ/SPL). The *nzz/spl* mutant displays male and female sterility due to the absence of micro and megasporogenesis, along with other defects on ovule and integument development.

Although NZZ was discovered in 1999, the molecular mechanism of action of NZZ has been reported recently, revealing that NZZ acts as a transcriptional co-repressor by interacting with TOPLESS and TOPLESS-LIKE proteins and TCP (TEOSINTE BRANCHED/CYCLOIDEA/PCF) transcription factors. However, the genes and processes regulating sporogenesis downstream of NZZ remain largely unknown. Our results show that NZZ is regulating auxin pathways and we have revealed several auxin-related genes regulated by NZZ.

PS18.37 BYEPASS – A ROBUST AND VERSATILE HOMOLOGY-(IN)DEPENDENT MULTI-FRAGMENT ASSEMBLY FOR FUNCTIONAL TRANSGENESIS

SUNDAY 1 JULY 2018

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Stream-lined, robust and rapid gene-stacking methods are crucial in molecular biology. We have generatedByepass, a suite of modules that allow for gene stacking by homology-based cloning in yeast and/or bacteria, or by *in vitro* ligase-dependent or independent DNA assembly. Among others, a palette of GFP-derivatives for reporter fusions have been incorporated, and the constructed >100 modules can help cargo genetic constructs to plant systems for functional analyses. We demonstrate the versatile application of *Byepass* to study development in plant and animal systems. The *Byepass* modules will shortly be fully available to all researchers, and will particularly be resourceful for easy and economical transgenesis in model and crop plants.

PS18.38 *BOECHERA* REVISITED: DEVELOPMENTAL HETEROCHRONY AND EPIGENETICALLY COORDINATED TRANSCRIPTIONAL REWIRING UNDERLIE APOMIXIS

SATURDAY 30 JUNE 2018

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Successful apomixis – asexual reproduction through seeds – requires coordinated formation of meiotically unreduced female germline and parthenogenesis. Our recent work demonstrated that Boechera apomicts display aberrant upregulation of specific transcription factors including a stem cell regulator crucial for specification of the female meiotic precursor, and a genomically imprinted MADS-box gene. Interestingly, this upregulation is underlined by deregulation of the genes encoding core DNA methylation machinery. In contrast to the previous reports, we provide evidence that initiation of apomeiosis in the apomictic Boechera accessions occurs asynchronously with the ovule development. This heterochrony is accompanied by the gain of gene expression of the transcription factors and downregulation of a few core meiotic genes. Based on changes in DNA methylation footprints and concomitant shifts in gene expression, we propose that epigenetically regulated gene expression alteration during ovule development might likely be a hallmark of soma-to-asexual germline transition and ensuing parthenogenesis in higher plants.

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