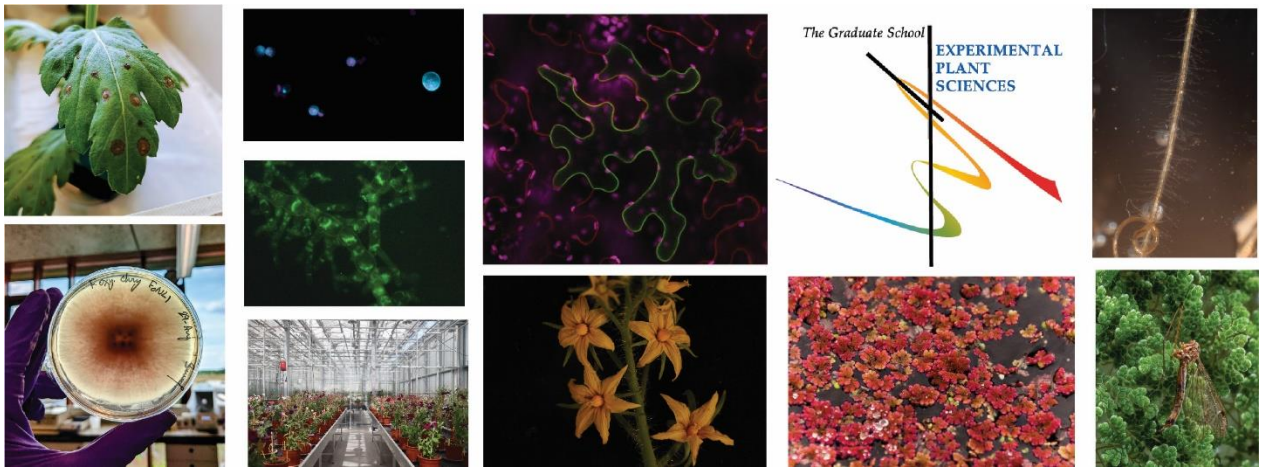
Annual Meeting
Experimental Plant Sciences



17 & 18 April 2023

Hotel De Werelt, Lunteren

Welcome

Dear participant,

We are very happy to welcome you this year to the Dutch Annual Meeting Experimental Plant Sciences. Also this year we have an excellent program with three well known keynote speakers and plenty of opportunities to network. The poster session is back in the program. The EPS PhD council is organizing the poster awards and will reward the three best posters with a prize. This year we also introduce the EPS Awards for the first time. Members of the EPS community could nominate their colleagues for the three following awards: EPS Spotlight, EPS Mentor and EPS Young researcher. The EPS Award committee is really excited to announce the winners.

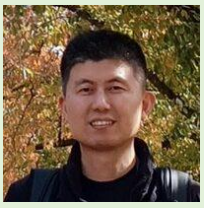
Once more welcome in Lunteren and enjoy the meeting!!!

Organizing Committee

Prof. Guido van den Ackerveken (Chair)

Prof. Christa van Testerink

Prof. Jian Xu



Prof. Gerco Angenent

Dr. Ingrid Vleghels

EPS Office

Dr. Susan Urbanus

Dr. Juliane Teapal

Anja Mosselman

Sponsors

The Annual Meeting Experimental Plant Sciences 2023 would not be possible without the financial support by NWO.

We greatly appreciate the sponsor of this year's meeting:

Gold Sponsor

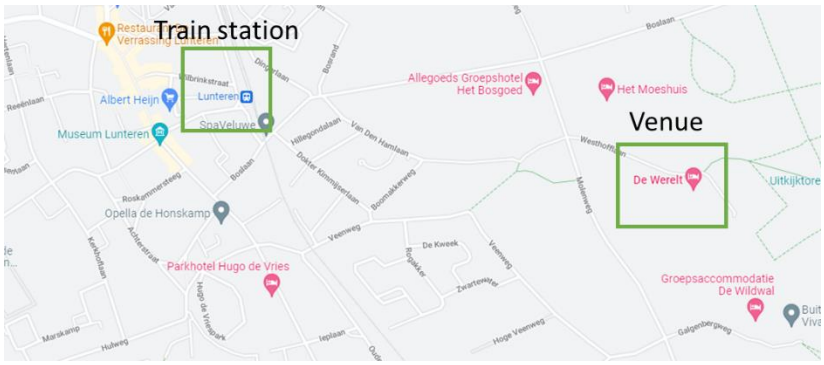
Silver Sponsor

Bronze Sponsor

Venue

Address

Hotel De Werelt
Westhofflaan 2
6741 KH Lunteren



Travel information

You can reach the hotel by car or bike (45 mins from Wageningen). There is free parking next to the hotel. The train station is in walking distance to the Venue (see map). It will take approximately 15- 20 min to walk. For Monday morning we arranged a taxi bus to bring you to the venue. The bus will stand outside of the train station from 8:30 until 09:45. On Tuesday, after the meeting is finished, a taxi bus will bring you back to the train station. If you plan to use the train please check the NS side for any updates before your travel.

Hotel Rooms

If you reserved a room (single, double with twin beds or double with double bed), you can check in from **Monday 15:00** onwards. Please pick up the key at the reception of the hotel. Breakfast will be served between 8:00 and 9:00. Please check out before the meeting starts on **Tuesday** morning (not later than **10:00**).

The hotel has arranged a room where you can store your luggage during the meeting.

Lactation room

There is a lactation room including fridge located in the D wing of the hotel. Please always check with the reception if it is free to use.

Pray and Calming room

We reserved a pray and calming room for both days. Please contact Juliane Teapal if you want to make use of it.

Extra Information

Registration

The registration opens 08:30 on Monday morning. When you enter the hotel you will find the registration area on the right side. Please pick up your badge before the meeting starts.

Catering

Coffee/ Tea and water will be available all day long throughout the whole venue. For lunch and dinner all diet wishes are taken into account, but if something is missing please contact: Juliane Teapal.

Each participant receives two consumption vouchers (at the back of your badge). You can use them on both days for soft drinks, beer and wine. Further drinks can be purchased on your own costs. Please be aware that you can only pay with card, no cash possible.

PhD/postdoc/PI-hour

The PhD, postdoc hour and PI hour will take place on Monday from 17:30 until 19:00.

PhD hour location : Air (parallel session)

Postdoc hour location: Room 21

PI meeting location: Water (parallel session), only on invitation

Poster Presentation

With this program you receive the number of your poster board. Please hand in your poster during the registration. We will make sure your poster ends up at the correct board. The posters can be visited from the first coffee break after the lunch on Monday until the last coffee break before the lunch on Tuesday. The **poster session** takes place on Monday from 20:30 until 22:00.

Social activities

Party

This year we arranged a venue for a small party. On Monday evening the room **FIRE** will turn into a party room including a dancefloor and a small bar, starting at 21:30. We are also very happy to announce that Nanne Taks (UvA) will be our DJ for this evening. At midnight the sound and lights will be turned off. Enjoy!

Running activity

Ready to get up early ? Join the morning run under the guidance of Jason Gardiner (PI at UU Translational Plant Biology). Meet up in front of the conference center for the warming up at 07:00.

Programme

Monday 17 April 2023

08:30-09:25	Registration and Coffee		
09:25 - 09:30	Welcome		
Plenary Session 1	Chair: Guido v.d. Ackerveken		
09:30-10:15	**Jonathan Jones**		
10:15-10:45	Petra Bleeker (UvA)		
10:45-11:15	Coffee break		
11:15-11:45	Rashmi Sasidharan (UU)		
11:45-12:15	Joris Sprakel (WUR)		
12:15-12:45	Daan Weits (UU)		
12:45-12:55	EPS Awards		
12:55-14:15	Lunch		
Parallel Session 1	**Biotic Interactions I (Air)**	**Genomics I (Water)**	**Cell Biology (Fire)**
14:15-14:35	Miguel Ramirez Gaona (WUR)	Jillis Grubben (WUR)	Yosapol Harnvanichvech (WUR)
14:35-14:55	Ava Verhoeven (UU)	Meixin Yang (WUR)	Enric Martínez-Calvó (UvA)
14:55-15:15	Thomas Aalders (UvA)	Jorge Aleman Baez (WUR)	Bas Jacobs (WUR)
15:15-15:45	Coffee break	Coffee break	Coffee break
Parallel Session 2	**Biotic Interactions II (Air)**	**Genomics II (Water)**	**Physiology (Fire)**
15:45-16:05	Arezoo Rahimi (LEI)	Iqbal Maulana (WUR)	Ludovico Caracciolo (WUR)
16:05-16:25	Gijs Selten (UU)	Dong Zhang (WUR)	Lisa Oskam (UU)
16:25-16:45	Valerie Buijs (KNAW)	Mandy Ravensbergen (WUR)	Phuong Nguyen (WUR)
16:45-17:05	Pedro Beschoren da Costa (WUR)	Nam Hoang (WUR)	Kees Ketting (WUR)
17:05-17:20	Flash Talks	Flash Talks	Flash Talks
17:30-19:00	PI/postdoc/PhD hour		
19:00-20:30	Dinner		
20:30-22:00	Poster Session		
21:30-00:00	Party		

Tuesday 18 April 2023

07:00-08:00	Running activity		
Parallel Session 3	**Development I (Air)**	**Stress (Water)**	**Novel Methods (Fire)**
09:00 - 09:20	Judit Nadal-Bigas (WUR)	Jasper Lamers (WUR)	Mitja M. Zdouc (WUR)
09:20 - 09:40	Thalia Luden (LEI)	Linge Li (UU)	Sebastian Tonn (UU)
09:40 - 10:00	Honglei Wang (WUR)	Martijn Jansen (RU)	Peter Bos (WUR)
10:00 - 10:20	Flash Talks	Flash Talks	Flash Talks
10:20 - 10:50	Coffee break	Coffee break	Coffee break
Parallel Session 4	**Development II (Air)**	**Biotic Interaction III (Water)**	**Non-Model Species (Fire)**
11:00 - 11:20	Iris Zahn (WUR)	Dario Ramirez (NIOO/UU)	Manuel Aguirre Bolaños (UU)
11:20 - 11:40	Merijn Kerstens (WUR)	Sietske van Bentum (UU)	Francesco Garassino (WUR)
11:40 - 12:00	Nina Guarneri (WUR)	Nanne Taks (UvA)	Erbil Güngör (UU)
12:00 - 13:45	Lunch		
Plenary Session 2	Chair: Christa Testerink		
13:45-14:30	**Peter Kuipers Munneke**		
14:30 - 15:00	Charlotte Gommers (WUR)		
15:00-15:30	Coffee break		
Plenary Session 3	Chair: Jian Xu		
15:30-16:00	Sandra Irmisch (LEI)		
16:00 - 16:45	**Caroline Dean**		
16:45 - 17:00	Poster Award		
17:00 - 17:10	Closing remarks		

Monday, 17 April 2023

08:30 - 09:25 Registration and Coffee/Tea

09:25 - 09:30 Welcome

Plenary Session 1 Chair Guido van den Ackerveken (Room Earth)

09:30-10:15 **Keynote speaker Jonathan Jones**, The Sainsbury Laboratory, UK

10:15-10:45 **Petra Bleeker** , University of Amsterdam,
"Well-being in the face of adversity; harnessing how specialised metabolites help a plant protect itself"

10:45-11:15 Break

11:15-11:45 **Rashmi Sasidharan**, Utrecht University,
"Plant abiotic stress research at UU: honoring a legacy""

11:45-12:15 **Joris Sprakel,** Wageningen University and Research,
"Feel the Force: New perspectives in Green Mechanobiology"

12:15-12:45 **Daan Weits**, Utrecht University,
"Low oxygen, key ingredient of the plant stem cell niche?"

12:45-12:55 **EPS Award**

12:50-14:15 Lunch

14:15-15:15 **Parallel Session 01**

15:15-15:45 Break

15:45-17:05 **Parallel Session 02**

17:05-17:20 **Flash Talk Session 01**

17:30-19:00 **PhD hour** (room Air) /**PI hour** (room Water)/ **Postdoc hour** (room 21)

19:00-20:30 Dinner

20:30-22:00 **Poster Session**

22:00-24:00 **Party** (room Fire)

Tuesday, 18 April 2023

09:00-10:00 **Parallel Session 03**

10:00-10:20 **Flash Talks 02**

10:20-11:00 Break

11:00-12:00 **Parallel Session 04**

12:00-13:45 Lunch

Plenary Session 2 Chair: Christa Testerink (Room Earth)

13:45-14:30 **Keynote Peter Kuipers Munneke**, Utrecht University
"Plants and water in a warming world"

14:30 - 15:00 **Charlotte Gommers,** Wageningen University and Research
"Chloroplast development and signalling in a changing environment"

15:00-15:30 Break

Plenary Session 3 Chair: Jian Xu (Room Earth)

15:30-16:00 **Sandra Irmisch** , Leiden University,
"Plant Natural Products - From Metabolite Biosynthesis to Engineering Production Systems"

16:00 - 16:45 **Keynote Speaker Caroline Dean**, John Innes Centre, UK
"Mechanism of a cold-induced epigenetic switch"

16:45 - 17:00 **Poster Award**

17:00 - 17:10 **Closing remarks**

Parallel Sessions

Parallel Session 01

Date: 17 April 2023
Time: 14:15 – 15:15

Session: Biotic Interactions I (Room: Air)

Chair: Wen Huang , Wageningen University and Research

14:15-14:35 **Miguel Ramirez Gaona**, Wageningen University and Research
"A novel tomato susceptibility gene for necrotrophic fungi"

14:35-14:55 **Ava Verhoeven**, Utrecht University
"A hidden pandemic: Healthy-looking Arabidopsis plants can secretly host the latent comovirus ArLV1"

14:55-15:15 **Thomas Aalders**, University of Amsterdam
"Specific members of the TOPLESS family are susceptibility genes for Fusarium wilt"

Session: Genomics I (Room: Water)

Chair: Jason Gardiner, Utrecht University

14:15-14:35 **Jillis Grubben**, Wageningen University and Research
"Creation of inversions in chromosomes, using CRIPSR-Cas, has led to striking new insights"

14:35-14:55 **Meixin Yang**, Wageningen University and Research
"Evolutionary history of Fusarium asiaticum dissected through pangenomic population analyses"

14:55-15:15 **Jorge Aleman Baez**, Wageningen University and Research
"Pursuit of the genomic elements involved in cabbage (B. oleracea) leafy head formation"

Session: Cell Biology (Room Fire)

Chair: Pamela Strazzer, University of Amsterdam

14:15-14:35 **Yosapol Harnvanichvech**, Wageningen University and Research
"Identification of a novel structure surrounding the Arabidopsis embryo"

14:35-14:55 **Enric Martínez-Calvó,** University of Amsterdam
"Keep it purple: Stabilization of anthocyanin pigments in food crops"

14:55-15:15 **Bas Jacobs**, Wageningen University and Research
"Microtubule nucleation complex behaviour is critical for cortical array homogeneity and xylem wall patterning"

Parallel Session 02

Date: 17 April 2023
Time: 15:45 – 17:20

Session: Biotic Interactions II (Room: Air)

Chair: Daniel Zendler, University of Amsterdam

15:45-16:05 **Arezoo Rahimi**, Leiden University
"A flavobacterium-induced ERF transcription factor promotes root hair formation and alleviates drought stress in Arabidopsis "

16:05-16:25 **Gijs Selten,** Utrecht University
"Dissecting bacterial root colonization strategies using complex synthetic communities on diverse hosts"

16:25-16:45 **Valerie Buijs,** KNAW
"A glimpse into mycology research at the NVWA"

16:45-17:05 **Pedro Beschoren da Costa** , Wageningen University and Research
"Family Comamonadaceae and Order Rhizobiales respond to Jasmonic Acid induction in Arabidopsis thaliana and Brassica oleracea"

17:05-17:20 **Flash Talks**

Session: Genomics II (Room: Water)

Chair: Mariana Silva Artur, Wageningen University and Research

15:45-16:05 **Iqbal Maulana**, Wageningen University and Research
"Co-expression transcriptomics analysis reveals genotype-dependent gene expression regulation in M. hapla - tomato interaction"

16:05-16:25 **Dong Zhang,** Wageningen University and Research
"Effectoromics-Based identification of Synchytrium endobioticum resistance: A Breakthrough in mining for resistance against obligate biotrphic pathogens."

16:25-16:45 **Mandy Ravensbergen,** Wageningen University and Research
"RNA-dependent RNA polymerases and an epigenetic RNAi defense strategy against geminiviruses"

16:45-17:05 **Nam Hoang**, Wageningen University and Research
"The Gynandropsis gynandra genome provides insights into whole-genome duplications and the evolution of C4 photosynthesis in Cleomaceae"

17:05-17:25 **Flash Talks**

Session: Physiology (Room: Fire)

Chair: Melissa Leeggangers, Utrecht University

15:45-16:05 **Ludovico Caracciolo**, Wageningen University and Research
"3D analysis of chloroplasts in folio"

16:05-16:25 **Lisa Oskam,** Utrecht University
"Leaf movement dynamics in response to light and auxin"

16:25-16:45 **Phuong Nguyen,** Wageningen University and Research
"Bridging phenomics, genomics and bioengineering: Genetic research of photosynthesis efficiency"

16:45-17:05 **Kees Ketting**, Wageningen University and Research
"Uncovering mRNA storage and translation in seeds"

17:05-17:25 **Flash Talks**

Parallel Session 03

Date: 18 April 2023

Time: 09:00 – 12:20

Session: Development I (Room: Air)

Chair: Maritza van Dop, Radboud University Nijmegen

09:00 - 09:20 **Judit Nadal-Bigas**, Wageningen University and Research
"The art of multitasking: PEBPs and their role in seed quality determination"

09:20 - 09:40 **Thalia Luden**, Leiden University
"Rejuvenator: the potential of regulating plant longevity"

09:40 - 10:00 **Honglei Wang,** Wageningen University and Research
"Identifiation and genetic charactiziation of a polyembryonic mutant"

10:00- 10:20 **Flash Talks**

Session: Stress (Room: Water)

Chair: Steven Arisz, University of Amsterdam

09:00 - 09:20 **Jasper Lamers,** Wageningen University and Research
"Sodium-specific Responses of the Root Are Tightly Regulated in a Spatio-temporal Manner"

09:20 - 09:40 **Linge Li**, Utrecht University
"Shedding Light on Shade Avoidance: a cellular investigation of stem elongation of tomato cultivars"

09:40 - 10:00 **Martijn Jansen**, Radboud University Nijmegen
"Flower-bud cooling as a mechanism underlying a QTL for pollen thermotolerance in the field"

10:00- 10:20 **Flash Talks**

Session: Novel Methods (Room: Fire)

Chair: Emilie Wientjes, Wageningen University and Research

09:00 - 09:20 **Mitja M. Zdouc,** Wageningen University and Research
"FERMO: a New Graphical User Interface Dashboard for Metabolomics Data Analysis"

09:20 - 09:40 **Sebastian Tonn**, Utrecht University
"Exposing lettuce downy mildew: UV light reveals hidden symptoms"

09:40 - 10:00 **Peter Bos** , Wageningen University and Research
"Expanding the thylakoid membrane"

10:00- 10:20 **Flash Talks**

Parallel Session 04

Date: 18 April 2023

Time: 11:00 – 12:00

Session: Development II (Room: Air)

Chair: Kiki Spaninks, Leiden University

11:00 - 11:20 **Iris Zahn,** Wageningen University and Research
"SOC1 and FUL homologs together promote the floral transition in tomato."

11:00 - 11:20 **Merijn Kerstens,** Wageningen University and Research
"Spiraling out of Control: Regulation of Phyllotactic Stability in Arabidopsis and cucumber"

11:40 - 12:00 **Nina Guarneri ,** Wageningen University and Research
"Mediators of non-canonical root branching are involved in nematode-induced cellular hypertrophy"

Session: Biotic Interaction III (Room: Water)

Chair: Bart Schimmel, Utrecht University

11:00 - 11:20 **Dario Ramirez,** NIOO/ Utrecht University
"The potato microbiome: the missing piece from the potato domestication puzzle"

11:00 - 11:20 **Sietske van Bentum**, Utrecht University
"Plant-mediated selection of microbes in the field: mycorrhiza depletion in naturally-infected soybean plants"

11:40 - 12:00 **Nanne Taks**, University of Amsterdam
"An Arabidopsis CC-NLR acts in hydathodes against infection by the vascular pathogen Xanthomonas campestris pv. Campestris"

Session: Non-Model Species (Room: Fire)

Chair: Cloé Villard, Wageningen University and Research

11:00 - 11:20 **Manuel Aguirre Bolaños,** Utrecht University
"Tulip Life Cycle Shortening: The ups and downs of tulip's dropper formation"

11:00 - 11:20 **Francesco Garassino**, Wageningen University and Research
"Comparative transcriptomics/genomics of the extreme photosynthesis species Hirschfeldia incana with close relatives"

11:40 - 12:00 **Erbil Güngör**, Utrecht University
"Role of secondary metabolites in the Azolla-Nostoc symbiosis"

Flash Talks

The Flash Talks are part of the parallel sessions.

Session 01

Date: 17 April 2023
Time: 17:05 – 17:20

Session: Biotic Interactions I (Room: Air)

Chair: Daniel Zendler, University of Amsterdam

17:05 -17:10 **Margarita Simkovicova**, University of Amsterdam
"Combating Vascular Diseases: Identifying the “Guardians” of the Xylem Sap"

17:10 -17:15 **Juan Sanches**, Utrecht University
"Identification of the conserved iol gene cluster involved in rhizosphere competence in Pseudomonas"

17:15-17:20 **Misha Pauw**, University of Amsterdam
"The Battle in the Hydathodes"

Session: Genomics (Room: Water)

Mariana Silva Artur, Wageningen University and Research

17:05 -17:10 **Tom Theeuwen**, Wageningen University and Research
"A novel cytoplasmic male sterility system discovered in Arabidopsis thaliana"

17:10 -17:15 **Pamela Afopke**, Wageningen University and Research
"Broad mites resistance in African jute mallow"

17:15 - 17:20 **Dirk-Jan van Workum,** Wageningen University and Research
“Lactuca super-pangenome reveals importance of presence/absence variation for lettuce breeding”

Session: Physiology (Room: Fire)

Chair: Melissa Leeggangers, Utrecht University

17:05 -17:10 **Elmar van der Wijk,** Radboud University Nijmegen
"Unravelling the cis-regulatory mechanisms of the stress-responsive Phytoglobin 1 gene at a single-cell resolution by integrating 'omics in Arabidopsis thaliana"

17:10 -17:15 **Priyanka Chopra,** Leiden University
"Remember or die: when plants face recurring heat stress events"

17:15 - 17:20 **Tom Rankenberg,** Utrecht University
"Flooding resilience is determined by leaf age"

Session 02

Date: 18 April 2023
Time: 10:00 – 10:20

Session: Development (Room: Air)

Chair: Maritza van Dop, Radboud University Nijmegen

10:00 - 10:05 **Nora Gigle Bisceglia,** Utrecht University
"Inhibition of pectin modification alleviates salinity stress responses in Arabidopsis thaliana"

10:05 - 10:10 **Mohamad Abbas**, Utrecht University
"From O2 with LOV; shedding new 'light' on altitude adaption"

10:10 - 10:15 **Gyongyi Macias Honti**, Utrecht University
Mapping ethylene effect in hypoxia

10:15 - 10:20 **Melissa Leeggangers,** Utrecht University
"Preparing for the storm: Ethylene as an early warning signal"

Session: Stress (Room: Water)

Chair: Steven Arisz, University of Amsterdam

10:00 - 10:05 **Virendrasinh Khandare**, Wageningen University and Research
"The role of cysteine oxidative modifications of Cysteine Rich Receptor Kinases in extracellular ROS perception"

10:05 - 10:10 **Judith Lanooij**, Wageningen University and Research
"Assigning peptide ligands to Cysteine-Rich Receptor Kinases using a high-density peptide microarray"

10:10 - 10:15 **Vera Putker**, Wageningen University and Research
"Gpa2-induced selection pressure affects the prevalence of 1 the virulence effector RBP-1 of Globodera pallida"

10:15 - 10:20 **Scott Hayes,** Wageningen University and Research
"Warm temperature and mild water deficit interdependently control root elongation"

Session: Novel Methods (Room: Fire)

Chair: Emilie Wientjes, Wageningen University and Research

10:00 - 10:05 **Micha Gracianna Devi,** Wageningen University and Research
"Accelerating plant breeding programs using rapid phenotyping tools for insect resistance and behavioural trait analysis"

10:05 - 10:10 **Yang Song**, Utrecht University
"Microbiome-based prediction of potato growth in the field"

10:10 - 10:15 **Maarten Jongsma,** Wageningen University and Research
"TRACK//GENE: a novel method of identifying induced and constitutive, insect resistance and susceptibility genes by means of video tracking with EntoLab"

10:15 - 10:20 **Jason Gardiner,** Utrecht University
"Understanding and engineering the logic behind plant decisions"

Poster Abstracts

The posters will be located in Earth (plenary room) from the first coffee break after lunch on Monday the 17th until the last coffee break before lunch on Tuesday the 18th. The poster session will take place after the dinner, from 20:30 until 22:00. All posters are in the run for the EPS Poster award, which is organized from the EPS PhD council. The prize will be awarded on Tuesday the 18th at 16:45, after the end of the 3rd plenary session.

1. *"Understanding the genetics of common scab resistance in potato crop"*
   Fatima Latif Azam, Laboratory of Plant Breeding ,Wageningen University and Research

   Common scab, caused by Streptomyces spp., is worldwide one of the most important skin blemish diseases in potato, leading to a significant reduction in economic value. Resistant varieties are the most effective way of dealing with this disease, because control by irrigation is expensive and unsustainable in the long term, if not contributing to yield.
   The aim of this project is to identify the hereditary factors involved in resistance to common scab. Several sources of resistance are known, such as the old potato varieties Jubel and Hindenburg, as well as modern tetraploid and diploid varieties. These are being used to create mapping populations for field trials. Specifically, we are trying to understand whether resistance is controlled by a single locus or by multiple small-effect QTL with additive effect. Because a vast body of historical data on scab resistance is available, for ~ 500 varieties with SNP array genotypic data, a GWAS-analysis is being carried out. Pot assays and in vitro assays will be developed to test for resistance gene by isolate interactions with reference strains of Streptomyces spp.. Knowledge on the spectrum of resistance is essential to breed for broad-spectrum scab resistant varieties.
   Identification of molecular markers associated with alleles contributing to common scab resistance will simplify the long-term objective of breeding resistant varieties with greater efficiency and less expense than in conventional field screening.

2. "Development of new low sporing cultivars of Pleurotus ostreatus"
   Karin Scholtmeijer, Laboratory of Plant Breeding ,Wageningen University and Research

   People working in mushroom farms can become seriously ill (severe allergic reactions and lung problems) when frequently exposed to high concentrations of spores. Especially P. ostreatus is known to produce huge amounts of spores that are released from early stages in mushroom development, Therefore, access to spore-less or low sporulating strains of P. ostreatus is of great importance for commercial cultivation of these mushrooms. A

sporeless strain (SPOPPO), developed via a natural occurring sporeless mutant is already on the market. However, cultivars with properties important for e.g., the Asian market are not yet available. To obtain sporeless cultivars, germplasm with disrupted pathways towards sporulation are needed.

For food, non-GMO strains are strongly preferred, requiring random mutagenesis. Two methods to mutagenize P. ostreatus protoplasts were tested, EMS and UV. SNP analysis of resequenced mutants showed that EMS only resulted in a low mutation rate (average 20 mutations), while UV irradiation resulted in much higher mutation rates (average 278 mutations). Currently, mutants are being analysed by 2-D pooled sequencing to screen for mutations in genes that are known to be involved in sporelessness (e.g., the MSH4 gene).

3. *"Lactuca super-pangenome reveals importance of presence/absence variation for lettuce breeding"*

Dirk-Jan van Workum, Laboratory of Bioinformatics, Wageningen University and Research

Plant breeding heavily relies on genetic diversity in (wild) plant accessions that can be crossed with a crop of interest. The integration of genomes from cultivated species and their wild relatives in a super-pangenome allows for the discovery of genetic mechanisms underlying traits of interest, such as pest resistance. For lettuce (Lactuca sativa L.) and its wild relatives, a growing number of genetic resources enables the analysis of hitherto unknown genetic mechanisms.

We constructed a super-pangenome for Lactuca covering 474 accessions spanning 4 species (including primary, secondary and tertiary gene pools). Using this resource, we show that presence/absence variations (PAVs) of both reference and non-reference genes are important targets for lettuce breeding. Functional enrichment analyses of core and dispensable genes show that transcription regulators are conserved whereas plant resilience genes are variable in the Lactuca super-pangenome. Illustrating the usability of PAVs for breeding, we demonstrate how a deletion in a lipid-transfer protein is specific to Oilseed lettuce. Finally, we show that PAV-GWAS and copy-number variation (CNV)-GWAS are not only in congruence with SNP-GWAS but also provide novel leads for Bremia resistance among other phenotypes. The provided methodology and data provide a strong basis for research into PAVs, CNVs and other variation underlying important biological traits of lettuce and other crops.

4. "Specific members of the TOPLESS family are susceptibility genes for Fusarium wilt in tomato and Arabidopsis"

Thomas Aalders, Molecular Plant Pathology, University of Amsterdam

Vascular wilt disease, caused by the fungal pathogen Fusarium oxysporum (Fo), is a major threat for many important crops. Dominant genetic resistance to Fo is rare and typically overcome by the constantly evolving fungus. As an alternative Susceptibility (S) genes of the host can be inactivated to potentially confer broad and durable resistance. Here, we identify tomato S gene candidates required for susceptibility to Fo. The Fo effector SIX8, which is present in many pathogenic isolates but absent in non-pathogenic ones, was found to specifically interact with two members of the TOPLESS family from tomato: TPL1 and TPL2. SlTPL1 knockouts exert strongly reduced susceptibility to Fusarium wilt. An even stronger resistance was observed in tpl1;tpl2 mutants, albeit with a mild pleiotropic phenotype. The undesired phenotype can be alleviated by grafting, as tpl1:tpl2 mediated resistance was found to be root-mediated. Single and double knockouts of Arabidopsis TPL and/or TPR1 showed a similar reduction in Fo susceptibility. Therefore, we conclude that TPLs are genuine S genes whose inactivation can confer resistance to F. oxysporum.

5. *"Together or Apart? Unique and redundant functions of MADS-box transcription factors in tomato fruit"*

Xiaowei Wang, Plant Developmental Systems**,** Wageningen University and Research

Fruit development and ripening in tomato involves coordination and tight regulation of gene expression. MADS-domain transcription factors are important in many biological processes of plants and interactions between MADS-domain proteins are essential for their functions. In tomato (Solanum lycopersicum), several MIKC-type MADS-domain proteins, such as FUL1, FUL2, MADS-RIN, playing a role in fruit development and ripening have been identified, but an in-depth characterization of their unique and (partially) redundant functions is lacking. In this project, we aim to elucidate further the tomato fruit development and ripening regulation exerted by MADS-box TFs and their interactions among each other and with other genes, particularly for FUL1, FUL2. We will use CRISPR/Cas and RNAi to generate single mutants and combinations thereof to reveal any redundant functions or cooperativity among these TFs during fruit development and ripening. Altogether, this study will unveil the molecular regulatory network of MADS-BOX together with other TFs and of FUL1/2 in fruit development and ripening.

6. *"The role of chloroplast-derived signals in intercellular communication"*

Eline D. C. Eggermont[12], Zico X. Verhoeff[3], Charlotte M. M. Gommers[2], Jeroen de Keijzer[1]

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Chloroplasts are organelles with an endosymbiotic origin and possess their own genome and protein synthesis machinery. Retrograde signals (RS) inform the nucleus about chloroplast development and operational status under changing environmental conditions. The developmental state of the chloroplast has an impact on whole plant development via RS, including the development in distal organs. Moreover, a number of recent discoveries have established that signals originating in the chloroplasts control plasmodesmata, the direct cell-to-cell conduits for many physiologically and developmentally relevant signals. Therefore, RS might be directly linked to developmental signalling across cells and tissues through plasmodesmata. We aim to determine how RS regulate local and distal plant cell development. In order to do so, we will use the bryophyte Physcomitrium patens as a model. This moss grows long, filamentous chains of cells called protonema. Despite its simple structure, this tissue exhibits cell-differentiation accompanied by distinct chloroplast development. Thus, this model gives the opportunity to study the interplay between overall plant development and chloroplast development as well as conveniently track the intercellular communication during this process. By investigating RS pathways in P. patens, we will also better understand the evolution of this process in land plants. A better understanding of the maintenance of chloroplast function during suboptimal conditions might prove essential when improving photosynthesis in crops for yield-improvement in the future.

7. *"Allelic variation in the autotetraploid potato: genes involved in starch metabolism as a case study"*

Hongbo Li, Department of Plant Breeding, Wageningen University and Research

The allelic variation pattern in the autotetraploid potato is less explored. Here, we identified 81 genes involved in starch metabolism and detected 65,245 allelic variants in six haplotype-resolved autotetraploid potato genomes. Comparative analyses revealed uneven distribution of allelic variants among gene haplotypes and that the vast majority of deleterious mutations in these genes were retained in heterozygous state in

autotetraploid potato. Population genetic analyses identified starch biosynthetic genes that have been possibly diverged between potato varieties with high or low starch content. These results increase our understanding of haplotype diversity in autotetraploids and will also facilitate functional characterization of genes contributing to starch-related traits in potato.

8. *"Build the wall! Characterization of root barriers in the legume family."*
Leonardo Jo, Plant Environment Signaling. Utrecht University

The root exodermis is characterized by the deposition of two secondary cell wall polymers, suberin and lignin in the outermost cortex layer. Many plant species can dynamically develop the exodermis in response to abiotic stresses. The phytohormone abscisic acid (ABA) is a core bridge between the abiotic stress perception and the exodermis differentiation program. Yet very little is known on how the ABA signal is integrated into the exodermis regulatory network. Our work aims to investigate the ABA regulatory network involved in exodermis differentiation of roots in different plant species. We focus on the legume family (Fabaceae) as it contains a diversity of exodermis forms with a wide range of developmental responses to ABA.
We developed Cell Layer Adjusted Pixel Intensity (CLAPI) method to characterize the cell type specific accumulation of suberin and lignin in roots. Using this method, we identified a wide range of exodermis type in the legume family. We found a few species with constitutively suberized and lignified exodermis, while others showed the unique ability to promote the exodermal differentiation only in the presence of ABA. Interestingly, we observed that the pattern of suberin and lignin deposition in the cortex differs across distinct legume species in response to ABA. While a few species showed a more diffuse deposition of suberin and lignin in the cortex, other species promoted the accumulation of these polymers specifically in the outermost layer of the cortex. Our next steps are building gene regulatory network models of the exodermis development across the legume family.

9. *"Dissecting the regulatory regions of the pleiotropic transcription factor FUL2 in tomato"*
Kai Thoris, Plant Developmental Systems, Wageningen University and Research

Pleiotropic genes are genes that influence more than one trait and can therefore be problematic for plant breeding. Unintended effects can occur when breeding for a single trait, as one mutation in the coding sequence can disturb all traits at once. Molecular breeding tools and phylogenetic analysis can be used to have a more modular look at pleiotropic genes and subsequently dissect their functions, so that more specific breeding

can be achieved. An example of a pleiotropic gene is the transcription factor FUL2 in tomato. FUL2 is one of the two co-orthologs of the Arabidopsis FRUITFULL (FUL) gene and regulates fruit development, fruit ripening, flowering time and inflorescence architecture. To understand how FUL2 is regulated and performs these different functions, we aim to identify and characterize the cis-regulatory elements that are required for tissue-specific activity. Phylogenetic footprinting was performed to identify conserved regulatory motifs, which were then screened against transcription factor binding site (TFBS) databases to reveal potential binding sites. The identified conserved motifs were then characterized with various methods such as CRISPR/Cas12a mutagenesis, yeast one-hybrid and GUS reporter lines.

10. *"Tulip reproduction and the role of PEBPs"*

Francesca Bellinazzo, Laboratory of Molecular Biology, Wageningen University and Research

The ornamental crop Tulipa gesneriana (tulip) is widely known for its beautiful flowers, which are at the basis of its long history of cultural and economical value. Tulip can reproduce through flowers and storage organs, the bulbs. It derives that two reproductive ways are utilized, sexual and vegetative. Current knowkedge on the regulation of both reproduction strategies (and, possibly, their cross-talk) is limited. Recent studies on other plants that produce storage organs (such as potato and onion), have highlighted the role of PHOSPHATIDYLETHANOLAMINE-BINDING PROTEINS (PEBPs) as key molecular switches of both flowering and storage organ formation, through complex formation with transcriptiona factors. Plant PEBPs constitute a very conserved gene family, which in Angiosperms can be divided in three main clades: FLOWERING LOCUS T-like (FT-like), TERMINAL FLOWER-like (TFL1-like) and MOTHER OF FT AND TFL1-like (MFT-like). In Monocots, expansion of the FT-like clade resulted in numerous paralogs which sometimes evolved into antagonistic pairs, competing for binding to the same transcription factors, and therefore determining the timing of a developmental event. Our research is aimed at characterizing the PEBP family in tulip, and ultimately understand their involvement in orchestrating tulip's dual reproduction.

Transcriptome mining resulted in the identification of eight full-length PEBPs in tulip. Sequence comparisons show amino acid substitutions at key positions, pointing towards functional diversification. Additional analyses such as RT-qPCR, yeast-two hybrid and heterologous overexpression contributed to shape the hypothetical role of TgFT1 and TgFT3 as antagonistic regulators of bulb formation, while the flowering regulators seem to be the meristem-expressed TgFT4 and TgTFL1. Moreover, the leaf-born TgFT2 signal

could in principle affect both reproductive modesm opening the possibility of a PEBP-mediated crosstalk between the two types of reproduction.

11. *"Genome control of superior thermomemory in plants"*
Tobias Staacke and Salma Balazadeh, Institute of Biology Leiden (IBL), Leiden University

Heat waves are becoming more frequent and intense, causing a great threat to agriculture. Due to the sessile lifestyle of plants and their necessity to endure such unfavorable conditions, they have developed a remarkable capacity to establish a memory of heat stress. With this so-called thermomemory, plants retain the experience of previous moderate (non-lethal) heat stress exposure (priming) and survive a subsequent, otherwise lethal heat stress. A previous study from our lab has demonstrated the existence of natural variation between Arabidopsis thaliana accessions for the strength and duration of thermomemory and identified a plastidial regulatory module (FtsH6-HSP21) to be involved in superior thermomemory of accession N13. We now identified another accession (ACC1) with a much higher thermomemory capacity than N13, Col-0, and its reported mutants. Expression patterns of known thermomemory genes are virtually identical in ACC1 and Col-0, suggesting that ACC1 employs memory mechanisms that are conserved across accessions but also other, entirely unknown regulators that provide superior thermomemory. We are applying genetic and systems biology approaches to unravel the genes and mechanisms underlying ACC1's high thermomemory capacity. The progress and recent results will be presented.

Sedaghatmehr, M., Mueller-Roeber, B. and Balazadeh, S. (2016) The plastid metalloprotease FtsH6 and small heat shock protein HSP21 jointly regulate thermomemory in Arabidopsis. Nature Communications, 7:12439.

12. *"Concentration is key: unravelling mechanisms controlling Auxin Response Factor stability"*
Martijn de Roij, Laboratory of Biochemistry, Wageningen University and Research

The signalling molecule auxin controls nearly all developmental processes in land plants through a the nuclear auxin signalling pathway (NAP). The NAP consists of an auxin receptor TIR1/AFB, its Aux/IAA degradation substrate, and the DNA-binding ARF transcription factors. While an extensive qualitative understanding of the pathway and its interactions has been obtained by studying the flowering plant Arabidopsis thaliana, it is so far unknown how these translate to quantitative system behaviour in vivo, a problem that is confounded by large NAP gene families in this species. Here, we used the minimal NAP of the liverwort Marchantia polymorpha to quantitatively map NAP protein

accumulation and dynamics in vivo through the use ofusing knock-in fluorescent fusion proteins. Beyond revealing the native accumulation profile of the entire NAP protein network, we discovered that the two central ARFs, MpARF1 and MpARF2, are proteasomally degraded. We mapped the degrons of both MpARFs to specific domains and show that MpARF2 dimerization is an important factor for degron accessibility and thus protein stability. In future work we aim to fully uncover the molecular mechanisms which define MpARF stability through a variety of approaches which will allow us to study functional implications of targeted MpARF proteolysis for plant development.

13. *"Fine tuning desiccation tolerance in developing seeds of Arabidopsis thaliana using controlled drying."*
Asif Ahmed Sami, Laboratory of Plant Physiology, Wageningen University and Research

Desiccation tolerance (DT) is the capacity of cells to withstand extreme losses of water without incurring irreversible damage. DT played a decisive role in facilitating the successful transition of plants from an aquatic to a terrestrial lifestyle. However, following terrestrialization, DT was gradually lost from the vegetative tissues of most angiosperms and became restricted to only seeds, spores, and pollens. Interestingly, in most seeds, DT is acquired during the maturation phase of development, before the seeds experience a gradual decrease in their total water content leading to an osmotic stress. Previous studies have mostly focused on the role of ABA in DT acquisition, however, the role of controlled drying or osmostress alone or in conjunction with ABA, on the regulation of seed DT has not yet been deciphered. In this project, we aim at understanding how DT acquisition is regulated and what is the effect of drying on seed survival. For that we optimized drying treatments to seeds of Arabidopsis thaliana during several maturation stages by - (i) fast drying the seeds outside the silique, and (ii) slow drying inside the silique. We found that drying seeds at early and mid-maturation inside the siliques improves their DT acquisition. From here on the plan is to perform RNA-seq and degradome-seq in these seeds to investigate what transcriptome and the translatome changes, respectively, accompany acquisition of DT during seed development.

14. *"Exploring proteome interaction with immune receptors by using proximity labeling"*
Tatiana Marti Ferrando, Laboratory of Plant Breeding, Wageningen University and Research

The plant immune system comprises a complex network of mechanisms and it needs a more complete understanding. In this context, pattern recognition receptors (PRRs) play a key role in defense against pathogens. However, little is known about PRR-interacting

proteins and their regulation upon pathogen perception. We applied a TurboID-based approach to study the interactors of the PRR ELicitin Receptor (ELR) in Nicotiana benthamiana in presence or absence of the INF1, an elicitin from Phytophthora infestans. We found that ELR-TurboID is able to biotinylate other PRRs at the plasma membrane including the well-known co-receptor SUPRESSOR OF BIR1 (SOBIR1), as well as proteins involved in vesicular trafficking. When INF1 is present, we reported less interaction with these PRRs and more specific interaction with PAMP-triggered immune (PTI) related proteins, such as the BRI1 ASSOCIATED RECEPTOR KINASE 1 (BAK1) and the RESPIRATORY BURST OXIDASE HOLOMOG D (RBOHD). We further evaluated the application of this approach using SOBIR1-TurboID in a wild potato Solanum microdontum. Enriched proteins from SOBIR1-TurboID treatment showed interaction with proteins related to defence and growth such as BOTYRIS-INDUCED KINASE1 (BIK1) homologs and BRASSINOSTEROID-SIGNALLING KINASE (BSK) homologs. Interestingly, we indentified common interactors of ELR in N. benthamiana and SOBIR1 in S. microdontum as REMORIN, RPM1-INTERACTING PROTEIN 4 (RIN4) and PROTEIN PHOSPHATASE 2C (PP2C). These findings illustrate the dynamics of the plant cell and reveal potential interactors to be exploited in plant breeding. In conclusion, we successfully applied TurboID proximity labeling in a non-model crop plant and created a roadmap for future research in protein-protein interactions with PRRs among plant species.

15. *"Achieving Durable Resistance Against Tomato Leaf Mold: Past, Current, and Future Perspectives"*

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Tomato leaf mold is caused by the fungus Fulvia fulva (syn. Cladosporium fulvum). Resistant tomato recognizes F. fulva avirulence (Avr) effectors by means of Cf receptor proteins, resulting in hypersensitive response-based resistance. So far, several Cf genes have been characterized and deployed, however the durability of these genes has proven to be limited. Durable resistance remains elusive since F. fulva readily overcomes Cf resistance by loss or mutation of the corresponding Avr effector, after which the deployed Cf gene becomes ineffective. To achieve a more durable form of genetic resistance, we are introgressing, mapping and characterizing a significant number of novel Cf genes from wild Solanum germplasm. In parallel, we are using CRISPR-Cas9 technology to generate

knockouts of the corresponding effectors in F. fulva to determine their contribution to fungal virulence on susceptible tomato. We hypothesize that (combinations of) Cf genes corresponding to effectors that strongly contribute to virulence will result in more durable resistance. So far, we have taken steps towards mapping of the novel Cf genes, and we have generated knockouts of the corresponding effectors in F. fulva. Additionally, we have identified Avr9B matching the Cf-9 homolog, Cf-9B, explaining the sequential breakdown of the widely used Cf-9 resistance locus, and currently we are working on identifying Avr6, which matches the most recently deployed Cf protein, Cf-6.

16. *"Lettuce Big Vein associated Virus ORF3 encodes a 30K-like protein that facilitates cell-to-cell movement"*

Wijnand Schravesande, Laboratory of Molecular Plant Pathology, University of Amsterdam

Viral movement proteins (MPs) are critical for the local spread of viruses in plants by modulating plasmodesmata, membrane-lined pores connecting plant cells through cell walls. Lettuce Big-Vein associated Virus, a member of the Rhabdoviridae, has been linked to the Lettuce Big Vein Disease complex. This viral disease is characterized by vein clearing, banding, and retarded growth of lettuce plants. Despite that this virus is known for decades, its viral proteins have not been studied in detail yet. Using structural predictions, we found that ORF3 of Lettuce Big-Vein associated Virus (LBVaV) appears to adopt the structural topology of the 30K-like movement protein family. This is remarkable, since classical protein multiple sequence alignment was unable to show such relationship. We next showed that ORF3 locates at the plasmodesmata by expressing it in concert with the marker protein PDCB1. To show that ORF3 from LBVaV facilitates cell-to-cell movement of plant viruses, movement-impaired infectious clones of Potato Virus X (PVX) and Tomato Mosaic Virus (ToMV) were co-expressed with LBVaV ORF3. LBVaV ORF3 indeed facilitated movement of both plant viruses. The combined observations revealed that LBVaV ORF3 encodes a 30K-like movement protein that facilitates viral cell-to-cell movement.

17. *"Combating Vascular Diseases: Identifying the "Guardians" of the Xylem Sap"*

Margarita Simkovicova, Laboratory of Molecular Plant Pathology, University of Amsterdam

The fungus Fusarium oxysporum (Fo) is a destructive pathogen of a wide variety of crop species. Four different resistance (R) genes (I, I2, I3 and I7) are employed in cultivated tomatoes to protect against Fo f.sp. lycopersici (Fol). These R-genes encode structurally

diverse immune receptors that recognize Fol effectors in different root tissue layers. Even though R-protein activation prevents disease, Fol still colonizes the vessels of resistant tomato varieties, the extent of colonization depending on the R-gene present. The mechanisms by which the different R-genes control vascular Fol abundance are currently unknown. Since Fo resides mostly in xylem tissues during infection, we hypothesize that specific compounds in the xylem sap restrict Fol proliferation. In this study, the xylem sap proteomes of Fol-inoculated resistant plants were compared to that of mock-treated plants using label-free quantitative LC-MS/MS. The quantity of various Fol effector proteins varied between R-gene lines corresponding to the observed differences in fungal proliferation. Besides several unique proteins, all four R-receptors induced the accumulation of the same set of five proteins (e.g. pathogenesis-related proteins, glucosidases, endochitinases). To assess their involvement in Fol resistance, these candidates are currently being knocked out or overexpressed. Preliminary data indicate that these proteins are key players in resistance against Fol.

18. *"Seed stored mRNAs: Dynamics during seed priming"*

Patricija Gran, Laboratory of Plant Physiology, Wageningen University and Research

Seed priming is a pre-sowing treatment that enables a more efficient and uniform germination. However, it negatively affects seed longevity. In this work, the mRNA dynamics underlying a hydropriming treatment has been investigated. Polysome profiling was performed on seeds during different stages of hydropriming. Ribosome nascent chain complex sequencing (RNC-seq) elucidated transcriptomic and translatomic changes during the treatment. In contrast to mature dry seeds, hydroprimed seeds contain polysome complexes indicating that the mRNAs that need to be translated during germination are already associated to ribosomes, leading to a quicker germination upon re-imbibition. During priming, seeds lose part of their stress-related transcriptome. This work highlights the genes that might play a central role in faster germination and/or reduced longevity following the priming treatment.

19. *"The eXodermis files: uncovering gene regulatory networks behind (dynamic) exodermis development and evolution"*

Rianne Kluck, Laboratory of Plant-Environment Signaling, Utrecht University

Since the transition out of the water, plants have had to evolve and adapt to the dry and ever-changing environmental conditions on land. One of the adaptations angiosperms evolved is the root barrier cell types: the endodermis and the exodermis. The endodermis

evolved earlier, its physical barriers being suberin and/or lignin depositions in the cell walls. The exodermis evolved later and likely co-opted parts of the endodermis network for deposition of lignin and/or suberin to the first sub-epidermal cortex layer(s) in order to control water and solute uptake in stressed soil conditions. Despite the physiological relevance of this adaptation, a consistent angiosperm-wide characterization of exodermis that takes into account stress conditions, screening methods, developmental age, and growth media is currently lacking. Therefore we are screening several phylogenetically distinct angiosperms in control and stress conditions using abscisic acid (ABA) as a stress signal. We have selected three major angiosperm families, Poaceae, Brassicaceae, and Fabaceae, to investigate exodermis diversity, dynamics, regulation, and networks. To eXpose whether a species has hidden characteristics in the exodermis cell file, we use sectioning, histology, and confocal imaging. Moreover, we will study the spatiotemporal aspects of transcription during ABA-induced exodermis development in various species. Combining the morphological and physiological exodermis diversity with underlying transcriptional responses on a multi-species level, we will infer which gene networks regulate distinct exodermis cell file types in a phylogenetic context.

20. *“GRAS38 transcription factor function in tomato shelf-life”*

Victor Aprilyanto, Bioscience, Wageningen University and Research

"GRAS38 is a transcription factor that was discovered to be actively expressed during tomato ripening and it is positively regulated by MADS-RIN. An RNAi knockdown of GRAS38 can prolong fruit shelf life via its regulation of several cell wall metabolism genes (such as PL, PG, XYL1, TBG4, and MAN1), although the direct effect on fruit shelf life is not unambiguously established. In this study, we would like to study the role of GRAS38 function by creating null mutants and observing the effect on fruit phenotypes as well as the expression of downstream target genes. Tomato plants bearing gras38-KO were created using CRISPR/Cas12a. Two out of five mutants (cr1 and cr4) were selected for further phenotyping as they contain frameshift mutations. Current phenotyping results showed that both gras38-cr1 and -cr4 have similar day-to-breaker and whole fruit firmness to that of the wild-type. Further tests will be conducted on these two mutants, including a fruit shelf life test and gene expression on several cell wall metabolism genes.

Keywords: GRAS38, shelf life, cell wall"

21. *"A leap into the unknown: understanding host-jumping by Fusarium oxysporum in cucurbits"*
Babette Vlieger, Laboratory of Molecular Plant Pathology, University of Amsterdam

Fusarium wilt disease, caused by the fungus Fusarium oxysporum (Fo), affects over one hundred plant species, resulting in significant crop losses globally. Pathogenic Fo strains are often host specific, only able to infect one or a few related plant species. Fo. f. sp melonis (Fom) and Fo f. sp. cucumerinum (Foc) are host-specific Fusarium strains that cause disease in melon and in cucumber, respectively. In contrast, Fo f. sp. radicis-cucumerinum (Forc) can infect three different hosts within the cucurbits: cucumber, melon and watermelon. In previous research, the first 'non-host' avirulence gene was found in Fom, Effector Candidate for Cucurbits (ECC1aFom). Transferring this gene, which encodes a small secreted protein, into a Forc strain compromised its ability to infect cucumber. Based on these findings, we aim to determine plant responses that control compatibility with cucurbit-infecting Fo isolates and to uncover how Fo evolved compatibility towards different cucurbit species. To identify the role of ECC1a and its homologs in host compatibility, knock-out mutant strains of Fom and Forc were generated using a CRISPR/Cas9-mediated genome editing approach. The mutants were tested for altered virulence on cucurbits. Preliminary results indicate that ECC genes are promising effector candidates to be involved in Fo virulence on different cucurbit species.

22. "*Hijacking the plant DNA replication machinery - towards the structure of the viral replication initiator protein and its interaction partners"*
Sandra Eltschkner, Laboratory of Molecular Plant Pathology, University of Amsterdam

Problems with begomoviruses have been heavily aggravated in recent years; particularly Tomato Yellow Leaf Curl Virus (TYLCV) causes severe damage on tomato and cucurbits impacting growers worldwide. Climate change has allowed the spread of the main vector for viral transmission, the whitefly Bemisia tabaci, which is now present in massive populations in more moderate climate zones including the Mediterranean. With the ban of pesticides and a lack of strong resistance genes in our crops, we urgently need alternative strategies to halt viral spread.
Due to their small genome, these viruses rely on host factors for DNA replication. The viral proteins need to reprogram the host cell cycle to stimulate entry of the S phase, and to recruit the plant DNA-replication machinery to the viral DNA. Only one viral protein, the Replication initiator protein (Rep), is essential and sufficient to promote viral DNA

replication inside plant cells. Rep interacts with a multitude of plant proteins including PCNA, a central processivity factor for DNA polymerases. Our goal is to elucidate the structure of Rep from TYLCV in complex with tomato PCNA. To this end, it will be critical to trap Rep in a fixed conformation and stoichiometry with PCNA to obtain a complex suitable for structural studies. Elucidating the Rep-PCNA interaction interface will provide invaluable insight in how Rep orchestrates rolling-circle DNA replication – a likely conserved mechanism among Circular Rep-encoding single-stranded DNA (CRESS-DNA) viruses – and help to identify their weak spot.

23. *"Dissecting salt-dependent regulation of the floral transition in Arabidopsis using promoter editing"*

Joram Dongus, Laboratory of Plant Physiology, Wageningen University and Research

Salt delays plant growth and development in Arabidopsis, including flowering & bolting time. Using a Genome-wide association study (GWAS) we set out to identify regulators that delay the floral transition exclusively during salt stress. This analysis revealed that the absence of a highly variable region in the promoter of a UDP-GLYCOSYLTRANSFERASE (UGT) correlates with reduced UGT expression and delayed bolting during salt stress. To assess whether the absence of this variable region is causal for the reduced UGT expression and delayed bolting time, we employed CRISPR/Cas9 editing to delete the variable region from the Arabidopsis Col-0 reference genome. In line with our observations in naturally occurring Arabidopsis accessions, UGT variable region deletion mutants bolt and flower later in salt stress, but behave like Col-0 wild type in mock conditions. This indicates that this region contains key cis-elements that regulate the floral transition during salt stress. Currently, we are aiming to use Cas9-nickase (D10A) to make more specific mutations inside the variable region to dissect which cis-elements are responsible for the salt-dependent flowering & bolting time phenotype. Furthermore, we aim to identify upstream and downstream regulators of UGT in the salt-dependent floral transition.

24. *"Can green be seen? Identifying a green light photoreceptor."*

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Plants use light as their primary energy source. That light, converted to chemical energy via photosynthesis, is essential for the survival of life on earth. To finetune the use of light, plants continuously monitor their environment to optimize their growth and

development. In dense plant stands, there is a relative enrichment of green and far-red light compared to the photosynthetically active blue and red light that is used in photosynthesis. These spectral changes are followed by dedicated wavelength-specific photoreceptors that cover most of the visible light spectrum. However, to date, no dedicated green light receptor has been identified, although plants do respond to green light perception by changing their growth and development. In this project, we aim to find a green light photoreceptor that sheds new light on how plants perceive their environment.

25. *"Friend or Foe: Colonization of alternative hosts by the banana pathogen Fusarium odoratissimum TR4"*
Lisanne Kottenhagen, Laboratory of Phytopathology, Wageningen University and Research

Global banana production is severely affected by Fusarium Wilt of Banana (FWB), a devastating fungal vascular wilt disease. The responsible pathogen is Fusarium odoratissimum, also known as Tropical Race 4 (TR4). Current control measures are inadequate to stop the fast spread of the disease. Although FWB drastically impacts banana production by aggressively destroying banana plants, the causal agent TR4 can also be a harmless endophytic colonizer of other plants. How alternative hosts aid into the spread of TR4 is currently unknown. To test how and if alternative hosts could play a role in disseminating TR4, the plant model species S. viridis was inoculated with TR4 and observed for colonization. It was observed that TR4 could successfully colonize the plant, without causing any disease symptoms. Even more so, TR4 was found back in the whole plant e.g. roots, stem and seeds. The virulence of the re-isolated TR4 was tested by introducing the re-isolated TR4 back to banana. Residing in an alternative host did not affect the virulence of TR4. Together, these findings show that TR4 is a successful endophytic colonizer of alternative hosts. Current disease control measures do not take alternative hosts into consideration to control the spread of TR4. Further research is needed to uncover how seeds play a role in transmitting and spreading TR4.

26. *"Reducing Saccharina latissima detachment by adaptations in culture management"*
Harald Holm, Laboratory of Cell Biology, Wageningen University and Research

Seaweeds are currently an underused source of food, feed and for medicine, bioplastics and bio stimulants. Cultivation in the North Sea consists mostly of kelp species seeded onto ropes. Kelp has a biphasic life cycle with alternating gametophyte and sporophyte

life stages. To seed the commercially interesting sporophyte, a mix of gametophytes and young sporophytes that are attached to the female gametophytes is used. Currently, the seeding process is highly inefficient: up to 99% of the material is lost. We aim to improve attachment of seeding material by identifying and understanding the factors that play a role in attachment. We have developed a novel method to quantitatively assess kelp attachment and have investigated the roles of the age of the seeding material and the substrate. We show that after gametophyte seeding, they gradually increase their attachment strength to a substrate over a period of two weeks. Attachment of young sporophytes doesn't increase of attachment over two weeks. Our results suggest that the majority of losses occur during the first days after seeding. The method that we developed allows for high throughput screening of different substrates, strains, and treatments for their performance in attachment to identify optimal seeding conditions to minimize losses.

27. *"Plant defense strategies to attack by multiple herbivores"*

Erik Poelman, Laboratory of Entomology, Wageningen University and Research

Plants may effectively tailor defenses by recognizing their attackers and reprogramming their physiology. Although most plants are under attack by a large diversity of herbivores, surprisingly little is known about the physiological capabilities of plants to deal with attack by multiple herbivores. Studies on dual herbivore attack identified that defense against one attacker may cause energetic and physiological constraints to deal with a second attacker. How these constraints shape plant plasticity in defense to their full community of attackers is a major knowledge gap in plant science. Our recent work identifies that species richness of herbivores as well as their trait composition affect how plants deal with simultaneous attack by multiple herbivores. Attack by a more species rich aphid community result in stronger compromises of resistance to attack by a caterpillar. Leaf chewing herbivores enhanced induced resistance to subsequent attack by a leaf chewer, regardless of the number of species that were attacking the plant. When multiple herbivores attack in sequence, the identity of earliest as well as most recent herbivore attacking the plant determine how plants deal with current herbivore attack. Moreover, by linking attacker patterns in the field and resistance to dual attack, we identified that plant defense strategies may be adaptive to deal with more common patterns of herbivore attack than to rare. This identifies that some of the physiological concepts developed by studies on single and dual herbivore attack mismatch with the adaptive nature of plant responses in community context. Identifying plant plasticity to deal with their full community of attackers is key in understanding plant defense strategies and requires

unified terminology to illustrate the repertoire of plant plasticity matching ecological patterns of attack.

28. *"TRACK//GENE: a novel method of identifying induced and constitutive, insect resistance and susceptibility genes by means of video tracking with EntoLab"*
Maarten Jongsma, Business Unit Bioscience, Wageningen University and Research

We have developed EntoLabTM, consisting of hardware and software to identify genes affecting over 30 different insect behaviour traits on detached leaves in plant populations. The platform was tested on a maize MAGIC population (16 founders, 300 genotypes, 50K SNPs), and we could validate that the method identifies both known and novel resistance QTLs. The system recorded for 16 hrs and could clearly distinguish constitutive and induced traits. Furthermore, it also distinguished them from potential susceptibility loci as those were associated with distinctly different behaviours such as prolonged feeding time. Throughput was 30 genotypes per day, and each genotype was tested twice, each time with 9 aphids. The video recordings were analyzed automatically to extract the track data. Tracks were transformed into >30 statistical behaviour traits and associated genetic loci/SNPs. A new TKI project could cross validate resistance with e.g. metabolites to obtain a deeper understanding of underlying principles.

29. *"Decoding ARF DNA-binding: MpARF1-His146's potential role in DNA-binding"*
Juriaan Rienstra, Laboratory of Biochemistry, Wageningen University and Research

Auxin Response Factors (ARFs) are the ultimate arbiters of the nuclear auxin signalling pathway (NAP), since ARFs decide which genes are auxin response by virtue of their DNA-binding. ARFs have a preference for TGTCNN motifs, consisting of a core, unchangeable TGTC and two final, variable nucleotides. The ARF crystal structure revealed how a single histidine residue, H146 in MpARF1, is the key for either high affinity motifs (TGTCGG) or medium affinity motifs (TGTCTC). In this project, we aim to investigate how natural variation for this histidine residue could affect DNA-binding and ultimately, the phenotype of the plant. To that end, we use a complementation assay in Marchantia polymorpha, a liverwort with a minimalistic NAP. We find that the mutations H146N and H146Y result in partial complementation of the Mparf1-4 null mutant, that this is likely due to altered DNA-binding affinity, and that lower DNA-binding affinity of MpARF1-H146N can be compensated for by higher in vivo expression.

30. *"Photosynthetic response to fluctuating light"*

Anna Calabritto, Laboratory of Physics and Astronomy, Vrije University Amserdam

Photosynthesis allows plants to convert the energy of the sun into biomass. Crop yields are subjected to fluctuations in irradiance that reduce photosynthetic light-use efficiency. Our aim is to obtain an overview of short- and long-term physiological and developmental responses of tomato and Arabidopsis to fluctuating light conditions.

31. *"A novel cytoplasmic male sterility system discovered in Arabidopsis thaliana"*

Tom Theeuwen, Laboratory of Genetics, Wageningen University and Research

Proteins encoded by the nuclear and organellar genomes interact to perform essential biochemical processes such as respiration and photosynthesis. Genetic variation in this so-called cyto-nuclear interactions can result in profound phenotypic differences. A well-known phenotype associated with variation for cyto-nuclear interactions is cytoplasmic male sterility (CMS). Most CMS systems are the result of transcription of a putative mitochondrial gene (orf). Often the gene interferes with expression of genes encoding ATP synthase subunits. Fertility can be restored via RNA editing, mediated by nuclear encoded pentatricopeptide repeat proteins. CMS systems in different plant species are caused by orfs that have a high degree of homology, but how such homologous orfs appear remains largely unexplored. Recently, an Arabidopsis thaliana cybrid panel was constructed that combined 60 species-representative organellar genomes with four divergent nuclear genomes. Screening of this cybrid panel for sterility revealed a new CMS system induced by the Staro-2 organellar genomes. Plants with the Staro-2 organellar genomes produce viable pollen, but the pollen numbers are substantially reduced, likely due to a failure of anther dehiscence. De novo assembly of the organellar genomes reveals a highly rearranged mitochondrial genome, in which an insertion compared to Col-0 is found. The insertion carries an orf predicted to encode a 225 amino acid sequence, referred to as orf225Staro-2. Furthermore, we reveal a minimum of four Restorer of Fertility loci, that only allow full restoration of fertility when homozygous alleles from both Col-0 and Staro-2 are combined. The orf225Staro-2 shows a high degree of similarity with mitochondrial orfs in B. napus and some other related Brassicaceae species, which suggests a common ancestor. However, as a part of the chimeric orf225Staro-2 has a 100% similarity with the Atp8 gene in A. thaliana, but seven SNPs compared to the orf in B. napus, we conclude that orf225Staro-2 arose independently within A. thaliana. This suggests that CMS systems can evolve independently, but result in orfs with high sequence homology.

32. *"Understanding the role of insect herbivory on the balance between cross- and self-pollination in Brassica rapa"*

Hanneke Suijkerbuijk, Laboratory of Entomology, Wageningen University and Research

Individual plants can be associated with a very broad insect community; from antagonists such as specialist and generalist herbivores, to mutualists such as natural enemies of pests and pollinators. Apart from direct damage to flowers and seeds, herbivores affect plant reproduction indirectly by changing plant-pollinator interactions or pollen acceptance mechanisms. The aim of my research is to understand how herbivory affects the Brassica rapa mating system through its effect on cross-pollination and self-incompatibility in Brassica rapa.

To truly understand how herbivory affects plant reproduction, we need more insights in the entire reproductive pathway: from pollen production, to pollen transfer by pollinators, (self) pollen acceptance by the stigma and ultimately seed set. How herbivory affects the full sum of female (seed formation) and male (pollen transfer) components of reproduction is poorly understood.

So far, we have collected a large set of data on the pollination and fitness of herbivore-treated and control plants of different genetic lines of Brassica rapa in common garden field studies. For pollination, we looked at pollinator community composition, the number of pollinators, the number of flowers visited per plant and the time spend by pollinators on flowers and plants. The first look at the data indicates that for the attraction of pollinators, the different genetic lines may respond differently to herbivory by chewing herbivores (Pieris brassicae and Mamestra brassicae).
In a greenhouse pilot study we found an indication that herbivory may decrease the level of self-incompatibility in a self-incompatible Brassicaceae (Sinapis arvensis). Plants were individually enclosed in nets to ensure self-pollination and treated with larvae of the mustard beetle (Phaedon cochleariae). On average, control plants produced fewer seeds than herbivore treated plants (103 seeds and 172 seeds respectively). We are currently investigating this further in a large greenhouse study on Brassica rapa, as well as with microscopy and qPCR experiments.

33. *"Remember or die: when plants face recurring heat stress events"*

Priyanka Chopra, Department of Plant Sciences, Leiden University

Plants have an inherent ability to survive certain levels of heat stress (HS) called basal thermotolerance. In nature, stresses are recurrent, and their intensity increases

occasionally. In addition to coping with a single event of HS, plants have also evolved the ability to establish 'thermomemory' by retaining the experience from previous exposure to HS. Establishing thermomemory helps plants to cope with recurrent and possibly more escalated HS conditions. Thermomemory is an important molecular mechanism to ensure optimal plant growth and survival after repetitive severe HS events. However, the molecular mechanisms controlling plant thermomemory are still largely unknown. We aim to unravel regulatory mechanisms and molecular components in establishing thermomemory in different cellular compartments in Arabidopsis thaliana and crops such as Solanum lycopersicum (tomato). Previous studies in our lab showed that sustained thermomemory requires higher levels of HSP21 (a small plastidial heat shock protein). We found that the plastid-localized metalloprotease FtsH6 regulates HSP21 abundance. Other targets of FtsH6 (that might be potential novel memory components) are not yet known. In addition to FtsH6, we found that autophagy (a conserved intracellular process involved in protein degradation in eukaryotes) complements FtsH6 in degrading HSP21, thus resetting the memory of heat stress (HS) in Arabidopsis. We are investigating 1) the functional link between autophagy and FtsH6, 2) the proteins that are targeted and degraded by them, and 3) their transcriptional regulators. Recent findings will be presented.

34. *"Effect of bacterial volatiles on A. thaliana and B. oleracea drought stress resilience"*

Zulema Carracedo Lorenzo[1,2], Marcel Dicke[2], Karen Kloth[2], Christa Testerink[1], Rumyana Karlova[1]

[1] Wageningen University, Laboratory of Plant Physiology

[2] Wageningen University, Laboratory of Entomology

Plant roots are in a close relationship with soil microorganisms, some of which can promote plant growth and resilience to different (a)biotic stresses. Microbial volatile organic compounds (VOCs) have been proven to play an important role in the interaction between soil microorganisms and the host plant. In this project, we aim to understand how three different Pseudomonas strains can increase the resilience to drought in Arabidopsis thaliana and Brassica oleracea var. Rivera through their VOCs. Our results show that in vitro, the Pseudomonas VOCs increased the resilience of Arabidopsis thaliana to osmotic stress. RNA-seq analysis, revealed that the bacterial VOCs induced important transcriptional changes in the plant root, that were more pronounced under drought conditions compare to well-watered conditions. Additionally, an in vivo experiment in the crop Brassica oleracea, shown that the Pseudomonas VOCs were also increasing plant

resilience to drought stress in non-sterile conditions. Altogether, our study contributes to understand the mechanisms by which microbial VOCs increase plant resilience to drought stress and suggests their potential to improve drought stress tolerance of crops

35. *"Revive broken NLR-genes"*

Daniel Zendler, Laboratory of Molecular Plant Pathology, University of Amsterdam

Plant pathogens are next to changing environmental and climatic conditions one of the major threats to food security worldwide. A major aspect of plant breeding involves the introgression of natural genetic resistances that have arisen from co-evolution of plants with their respective pathogens. The process of identifying novel resistances and then subsequently introgress them into elite cultivars is a time consuming and labor-intensive process which in case of dominant resistance traits like NOD-like receptor genes (NLRs) has only a limited durability in the field. Fast evolving pathogens like viruses can overcome such resistances sometimes by a single amino-acid change in their effector proteins. One example for this would be the interaction of the non-structural movement (NSm) protein of the tomato spotted wilt virus (TSWV) with the coiled-coil NLR (CNL) Sw5b protein where the amino-acid change Y118A causes breaking of the NLR mediated resistance. To counteract the evolutionary adaption of pathogens we propose a pipeline on molecular evolution via error prone PCR coupled with a high-throughput screening method for fast discovery of gain of function mutations in domain regions corresponding to effector recognition.

36. *"How Plant Leaves Navigate the Canopy: Signals and Mechanisms*"

Sanne Matton, Laboratory of Plant-Environment Signaling, Utrecht University

Plants are able to detect several different wavelengths of light, for example blue, red and far-red . This enables them to adequately adjust their growth for optimal light capture and thereby photosynthesis. Via their phytochrome photoreceptors plants are able to detect a difference in red (R) and far-red light (FR) abundance. A low red to far-red light ratio (low R:FR) is an indication of shade from a neighboring plants. Upon low R:FR perception A. thaliana responds by, among other shade avoidance responses, shifting growth investment towards increased petiole elongation and more upwards growth (hyponasty). As shade within a canopy is almost never homogeneously distributed over the whole plant, understanding responses towards local FR-enrichment is relevant to better understand how plant leaves navigate the canopy.

Previous research has shown that the location of R:FR perception determines the

response. Local FR-enrichment on the leaf tip leads to hyponasty, and local FR-enrichment on the petiole leads to petiole elongation. In this poster we describe the mechanisms behind horizontal movement upon local FR-enrichment on one side of the leaf lamina (FRside). The transcription factors PIF4, PIF5 and PIF7 and the auxin efflux carriers PIN3, PIN4 and PIN7 have an important role in both FR induced vertical and horizontal leaf movement. Horizontal petiole movement upon FRside can be inhibited by applying N-1-naphthylphthalamic acid (NPA), a direct inhibitor of PIN activity, on the petiole-lamina junction. Increase in auxin signaling visualized with the pDR5::GUS construct on one side of the petiole upon FRside is absent in plants treated with NPA on the petiole-lamina junction.

37. *"Molecular and chemical cues in the endophytic microbiome"*

Brandon Ford, NIOO-KNAW

We recently discovered that plants under attack by fungal root pathogens can actively recruit endophytic microbes inside their root tissues (endosphere) for protection. We showed that Cupriavidus and Stenotrophomonas species were significantly enriched in the root endosphere of sugar beet upon Rhizoctonia solani infection. In addition, metagenomic analyses of the endosphere showed a high abundance of genes encoding for phenazines, non-ribosomal peptide synthetases (NRPSs) and lanthipeptides associated with these taxa, but their functional roles in plant colonisation and protection are yet unknown. To characterise the taxonomic, genomic and functional traits of Cupriavidus and Stenotrophomonas, we established a collection of 45 Cupriavidus and 310 Stenotrophomonas isolates from sugar beet root endosphere and selected five unique isolates after dereplication based on BOX-PCR and 16S amplicon sequences. Genome sequencing, in vitro and in vivo antagonistic activity and metabolomics experiments are ongoing to investigate their functional potential and to resolve the role of the identified BGCs in endophytic colonization and plant protection. We also analysed the genomic sequences in MicroLIFE, a new bioinformatic pipeline to identify specific genomic features associated with the endophytic lifestyle of bacteria. Our initial results from MicroLIFE showed a large degree of genomic variation among the endophytic Cupriavidus isolates and those isolated from other environments. In conclusion, our results and ongoing experiments will shed light on microbiome assembly in the endosphere and which genes and metabolites are expressed in plants under siege.

38. *"Root flooding prepares the shoot for future low oxygen stress through systemic signaling."*

Melissa Leeggangers, Laboratory of Plant Stress Resilience, Utrecht University

Flooding can negatively impact plant performance and development, and reduces crop production in agricultural fields. Improving flood tolerance in plants is important for limiting yield losses. Plants are impacted by flooding due to the slow diffusion of gases in water which causes a reduction of oxygen availability. Limited gas diffusion also leads to entrapment of the volatile hormone ethylene in flooded tissues. In nature, flooding events start with water saturation of the soil (waterlogging). Thus, plant roots are the first to experience low oxygen stress. When the rainfall persists, water levels rise and eventually, the shoot is also submerged. It is unknown whether a root-derived signal can trigger a survival mechanism in the shoot to protect the shoot meristem. Plants often use long-distance signaling to survive suboptimal conditions. However, the underlying mechanisms of a root-derived signal during a flooding event are uncharacterized. Our results demonstrate that a period of waterlogging prior to hypoxia enhances shoot hypoxia tolerance. Ethylene signaling and 1-aminocyclopropane-1-carboxylic acid (ACC) transport are important components of the survival mechanism leading to this enhanced tolerance of the shoot.

39. *"A population derived from Solanum chacoense segregates for soft-rot resistance in a detached petiole assay"*

Elizabeth Yanez, Laboratory of Plant Breeding, Wageningen University and Research

Many efforts have been dedicated to potato to introgress resistance against soft rot bacteria but success has been limited. One of the main obstacles has been the low reproducibility of plant assays to identify resistant reliable phenotypes that can be associated to genetic markers. In this study, we used a petiole test to characterize the resistance to Pectobacterium parmenteri using a segregating population derived from a Solanum chacoense accession showing resistance to petiole maceration. Due to the population size and other constrains the experiment was conducted in two sub experiments. Petiole tests were reproduced in assays independently performed. Disease scores were integrated in one AUDPC value (area under the disease progress curve) for each of the genotypes in each assay. To assess the agreement between result assays, AUDPC values were adjusted to remove additional interference exerted by differences of the disease pressure in the independent assays and a Lin's concordance coefficient

correlation was calculated. To determine phenotype reproducibility the same susceptible individual was used as common reference inside each of the assays to be compared to allocate genotypes into a susceptibility scale. Result reproducibility using a petiole test fluctuated between 7 to 49% and phenotype reproducibility between 54 to 78 %.

40. *"Proximity labelling proteomics to find cell polarity regulators"*

Evgeniya Pukhovaya, Laboratory of Biochemistry, Wageningen University and Research

Cell polarity is the asymmetrical distribution of intracellular structures and proteins. It is an essential trait of multicellular organisms which is thought to have emerged early in land plant evolution. Mechanisms and regulators of polarity establishment in plants are largely unknown. To identify evolutionarily conserved regulators of polarity establishment, we study two plant models – A.thaliana and M.polymorpha. There are several polar protein families present in both species, including the recently identified SOSEKI proteins. To identify potential regulators in polar domain establishment, we performed TurboID-based proximity labelling interactomics – a proteomics technique that allows to identify proteins in the vicinity of the protein of interest through mass spectrometry. We established a library of 13 known polar proteins as ''baits'' overexpressed in Arabidopsis root meristems and Marchantia gemmae/thalli. Almost without exception, these proteins retained their polarity in various tissues, even when misexpressed in the cells where they are normally absent. We identified sets of proteins associated with polar baits. Interestingly, for 46% of the Arabidopsis polar protein interactors, orthologs were also identified in Marchantia in at least one polar domain. We also discovered several conserved interactors that were specific to the lateral polar domain in roots, including protein S-acyltransferases that can possibly regulate membrane localization of polar proteins. This preliminary result shows that proximity labelling polar proteins atlas can be used to identify potential components of polar domains, but genetic and biochemical verification of the interactions between this components is still on the way.

41. *"Uncovering the genetic mechanisms of leaf senescence within a population of Lactuca sativa"*

Jelmer van Lieshout, Department of Plant Sciences, Leiden University

To ensure high-quality leafy crops, it is important to better understand the mechanisms of leaf senescence. Although the regulation of leaf senescence has been thoroughly researched in plant model species, the genetic mechanisms in lettuce remain largely

unknown. Our aim is to gain a better understanding of the genetic mechanisms by examining the variation of leaf senescence in 200 Lactuca sativa accessions. During a field trial, we scored leaf senescence characteristics using a combination of manual measurements, RGB and hyperspectral imaging. Additionally, we induced senescence in a controlled setup by placing leaf disks from young plants in the dark and combining chlorophyll extraction methods with imaging methods. This allowed us to map the variation of leaf senescence within our selected lettuce population. By performing GWAS, we have identified associated SNPs which will be used in the future to identify key regulatory genes, enabling the breeding of more senescence-resistant crops.

42. *"The role of the C-terminal cytoplasmic tail of Cf proteins in determining the intensity of the hypersensitive response"*

Esranur Budak, Laboratory of Phytopathology, Wageningen University and Research

Plants only have an innate immune system to protect themselves against microbial infection. The first layer of this immune system is mediated by extracellular plasma membrane-associated receptors. These cell surface receptors perceive extracellular immunogenic patterns and trigger the initiation of downstream defense signaling, which finally leads to extracellularly-triggered immunity. Cf resistance proteins of tomato that act against the fully extracellular pathogenic fungus Cladosporium fulvum are so-called trans-membrane receptor-like proteins (RLPs) that localize at the cell surface. Cf proteins require two co-receptors for the activation of downstream cellular responses, because of the lack of a cytoplasmic kinase domain. In the resting state, Cf proteins constitutively interact with the receptor-like kinase (RLK) SUPPRESSOR OF BIR1 (SOBIR1), whereas upon recognition of the matching effector of C. fulvum by the Cf protein, the RLK BRI1-ASSOCIATED KINASE (BAK1) is recruited. The overall structure of Cf proteins is typical for LRR-RLPs and consists of an LRR ectodomain, an extracellular juxtamembrane domain (eJM), a TM domain and a intracellular juxtamembrane (iJM) domain. This iJM domain, or C-terminal tail, of Cf proteins is rich in basic amino acid residues, while the corresponding juxtamembrane part of SOBIR1 has opposite charges. Possibly, these opposite charges stabilize the interaction between the Cf protein and SOBIR1. Cf-4 and Cf-9 have identical iJM domains, and Cf-5 and Cf-2 are also identical for this C-terminal tail. Interestingly, the Cf-5/Avr5- and Cf-2/Avr2-triggered responses are slow and activate a less strong hypersensitive response (HR) than the Cf-4/Avr4- and Cf-9/Avr9-triggered response. To understand the role of the C-terminal tail of the Cf proteins in the intensity of the HR, various domains of Cf-5 and Cf-9 were swapped and the chimeric proteins were checked for the intensity of the HR that they trigger upon their activation. The results suggest that

the C-terminal tail of the Cf-proteins, and possibly all RLPs, has a specific role in determining the intensity of the immune response.

43. *"Thrips species and populations differ in virulence on Chrysanthemum accessions"*
Marcella Bovio, Laboratory of Plant Breeding, Wageningen University and Research

Abstract- confidential

44. "Light quality regulates shoot and root architecture in Lettuce"
Siddhant S. Shetty, Laboratory of Plant Environment Signaling, Utrecht University

Increased demand and shortage of arable land necessitates growing crops such as Lettuce in high density planting systems. Shaded plants in these high density planting systems receive highly reflected light enriched in the far red (FR) part of the spectrum1,2. Shade avoidance syndrome is a combination of responses to FR enriched light conditions under shade, that include elongated hypocotyl, increased angle of leaves (hyponasty), lateral root inhibition and primary root growth inhibition3. These light conditions can be mimicked in the lab environment by treating plants with FR light in addition to white light. As a part of the LettuceKnow consortium, this project will focus on understanding the effect of WL + FR light conditions on domesticated Lettuce (L. sativa) shoot and root architecture through both top-down (orthologs) and bottom-up (GWAS and Time series RNA-Seq) approaches.

45. "Investigating a Plant-Based Production System for the Antidiabetic Plant-Derived Metabolite Montbretin A"
Charlotte Hijmans and Sandra Irmisch, Plant Sciences and Natural Products, Institute of Biology, Leiden University

Plants produce a plethora of specialized metabolites (i.e. natural products), many of which have great potential for human health applications. Montbretin A (MbA), found in the ornamental plant montbretia (Crocosmia x crocosmiiflora), is such a promising metabolite, as it can serve as an improved therapeutic for the treatment of type 2 diabetes. To date, MbA, a complex acylated flavonol glycoside, has only been found in small quantities in the underground storage and reproductive organs (the corms) of montbretia. The chemical complexity of the metabolite and the low quantities found within the plant make scalable production through chemical synthesis or conventional agriculture, respectively, not

feasible and unsustainable. Hence, we are exploring ways to enable large-scale MbA production for drug development and application.

Plant tissue culture technologies offer a promising strategy to obtain specialized metabolites in greater quantities from their native sources. However, little attention has been given to the development of a tissue culture system for montbretia thus far, and it remains unclear whether in vitro-grown tissues would produce MbA. Furthermore, the cellular and subcellular localization of MbA production and storage within the corm is unknown but might provide valuable insights for the establishment of a successful tissue culture production system.

As part of my thesis work, I am setting up an in vitro montbretia tissue culture system, using state-of-the-art plant tissue culture techniques. By tailoring available knowledge of tissue culture to montbretia, I have successfully grown plants from seeds using optimized sterilization protocols. Additionally, the induction of callogenesis and/or organogenesis in various explant types was achieved by supplementing the culture medium with growth-promoting phytohormones. In my future research, I plan to explore the effects of stress-related phytohormones and study MbA production in vitro. To elucidate the storage location of MbA within the corm or MbA-producing tissues, my objective is to utilize and adapt state-of-the-art imaging technologies, such as confocal microscopy and desorption electrospray ionization mass spectrometry (DESI-MS). My work aims to advance our understanding of specialized metabolite biosynthesis in specialized plant organs, to contribute to the establishment of a scalable plant-based MbA production system.

46. *"Ratiometric Biosensor TOOLBOX"*

Viktoriia Voloboeva and Gabriele Panicucci, Laboratory of Plant-Environment Signaling, Utrecht University

Oxygen levels in plants vary depending on environment conditions, tissue morphology and metabolic activity. Indeed, meristems experience hypoxia as a chronic condition while normally well oxygenated tissues may experience acute hypoxia as a consequence of either abiotic or biotic stress. The signaling cascade initiated by the impoverished supply of oxygen was shown to be implicated in development, stress response, defense activation and gall formation. Current tools to monitor changes in oxygen levels and its 3D-distribution in tissue have clear limitations. Invasive electrode-based oxygen sensors are unsuitable for microscopic and hard tissues, and oxygen-sensitive dyes are not well absorbed by plant tissue. To bridge this gap we engineered a set of biosensors that detect oxygen levels without wounding or altering the plant. Here we present a state-of-the-art

toolbox of ratiometric, genetically encoded oxygen biosensors that may be employed to investigate oxygen dynamics and signaling at cellular resolution.

47. *"Integrated omics approaches to decipher salt stress responses in tomato."*

Parvinderdeep S. Kahlon[$1], Andrea Schrader[$2], Giuseppe Mannino[$3], Cristina Campobenedetto[3], Nora Gigli Bisceglia[1], Jasper Engel[4], Francesco Cristofano[1], Jeroen Busscher[1], Jules Beekwilder[5], Ric de Vos[5], Robert Hall[1], Valeria Contartese[6], Björn Usadel[7], Christa Testerink[1], Cinzia M. Bertea[3] and Rumyana Karlova[*1]

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Fast and unpredictable climate changes, low rainfall and high land evapotranspiration rates are leading to high soil salinization. Plants respond to salt stress very fast, starting at the molecular/gene expression, to metabolome change and post-transcriptional regulation, ultimately leading to undesirable reduced growth and yield losses. Current crop varieties are not adapted to the high soil salinity and the demand to develop salt-tolerant varieties is high. To discover new potential solutions aimed at reducing the negative impact of soil salinization on plants and their fruits, it is first necessary to understand the biomolecular mechanisms involved in the plant responses to salt stress. In this study, we focused on an economically important crop tomato. We combined transcriptomic and metabolomic approaches to pinpoint potential markers in molecular pathways regulated by salt stress. Clear metabolome and transcriptome-wide effects of salt stress in tomato roots were observed. We identified metabolite- guanosine as one of the molecules involved in salt responses and verified its role in root architecture changes upon exogenous application only under salt stress. Upon correlation of the omics datasets, we identified a potential marker, WRKY80 to regulate salt stress responses. Finally, we confirmed the role of WRKY80 in salt stress resilience using an ectopic expression system in two different species, tomato and Arabidopsis.

48. *"Biological control in a circular agriculture: Improving crop growth and resistance using a residual stream from insect production"*

Els van de Zande, Laboratory of Entomology, Wageningen University and Research

The production of insects as food and feed is increasing rapidly. Therefore, also the resulting residual streams, exuviae and faeces, are increasing. To create a more circular food production system, these residual streams can be used as soil amendment for agricultural crops. Besides adding extra nutrients, the side-streams may also induce defences in the crops and thereby help in crop protection against pest insects. In this study we tested whether soil amendment with mealworm exuviae affects the rhizosphere bacterial community, plant growth, herbivore performance and parasitoid recruitment in the field.

49. *"Thrips tabaci: the cryptic and dominant thrips species in Allium hosts"*

Bettina Porta, Laboratory of Plant Breeding, Wageningen University and Research

Thrips are small insects that encompass around 6000 species, some of which are serious pests. Thrips tabaci is reported as the most harmful in onion cultivation, but other species are found as well. Thrips tabaci is a cryptic species with two different phylogenetic groups and reproductive modes; arrhenotokous (sexual and parthenogenetic) and thelytokous (only parthenogenetic). This research investigated; 1) which thrips species affect onion and related Allium species, 2) the genetic variation present within and between 14 locations worldwide and over time, and 3) the reproductive modes present in the Thrips tabaci populations. Thrips samples, consisting of 33 individuals, were obtained from 14 locations of which three locations were sampled two or three times during the season. Species and haplotypes were determined through DNA barcoding of the COI gene. The reproductive mode of T. tabaci haplotypes was detected using COI specific primers. A Neighbour Joining tree was built using Nei's genetic distance. As expected, T. tabaci was the main species (93%). In addition, we also found Scirtothrips dorsalis, Thrips palmi, Frankliniella intonsa, F. occidentalis and F. tenuicornis on specific locations. Sites sampled multiple times showed that at the end of the season only T. tabaci was present, while other species were present early in the crop season. The haplotypes of T. tabaci grouped into two phylogenetic groups each of which linked to the arrhenotokous and telytokous mode of reproduction respectively. Arrhenotokous T. tabaci were present at certain locations while thelytokous T. tabaci are globally distributed. Genetic diversity was observed between and within T. tabaci populations, except in Mexico where only one haplotype was found. That haplotype was found in 10 of the 14 locations. Some other

haplotypes also showed worldwide distribution. Gene flow by global trading of onions or garlic may be the cause of the worldwide distribution of some T. tabaci haplotypes.

50. *"Insect-associated microbiota repress host plant defenses"*

Silvia Coolen, Magda Rogowska-van der Molen, Ineke Kwakernaak, J. A. van Pelt and Cornelia U. Welte

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The southern green shield bug Nezara viridula is an invasive piercing and sucking pest insect, feeding on important crop plants and posing a threat to worldwide food production. Since insects are known to harbor unique support by microorganisms, our study aims at providing insights into N. viridula-associated microbiota and their effect on host plant defenses. We determined the core bacterial microbiota with 16S rRNA gene amplicon sequencing throughout different development stages and distinguishing gut systems from salivary glands in adult animals. Our results confirms that part of N. viridula microbiota is vertically transmitted, changes throughout insect development and includes a core set of five abundant microbial genera, including Sodalis and Pantoea symbionts. In contrast to prior studies, we confirmed that N. vriridula transmits microbiota during feeding, suggesting that microbes may play a role in interactions between N. viridula and its host plant. We tested the effect of isolated N. viridula microbiota (including yeast) on Arabidopsis thaliana plant defense gene expression via qPCR and found that Sodalis and Pantoea were able to repress plant defenses directed towards insects. Our findings demonstrate that insect-associated microbiota play an important role in interactions between insects and plants, and could therefore be considered a valuable target for the development of sustainable pest control strategies in the future.

51. *"Mapping out the effect of ethylene on the root tip during hypoxic conditions"*

Gyöngyi Macias Honti, Laboratory of Plant Stress Resilience, Utrecht University

The mechanisms behind meristem tolerance to stress conditions have yet remained underexplored. Previous experiments have shown that, in Arabidopsis, an ethylene pre-treatment following subsequent hypoxic stress can enhance root survival. While it is clear that the activating mechanism caused by ethylene accumulation boosts the regrowth

capacity of roots after hypoxia, it is yet unknown how meristem protection is conferred. Is ethylene mediated by specific cell layers in the root? Do specific cell layers communicate signals in order to coordinate meristem protection? In order to address these questions different lines expressing EBF2 in a cell-type specific manner are used to disrupt ethylene and elucidate on what cells are more important for root survival after a hypoxia treatment.

52. *"BABY BOOM regulates IAOx metabolic pathway genes"*

Mengran Li, Laboratory of Molecular Biology, Wageningen University and Research

Somatic embryogenesis (SE) is a form of induced plant cell totipotency where embryos develop from vegetative cells without fertilization. SE can be induced in vitro by ectopic expression of embryo identity transcription factors like the BABY BOOM (BBM) AINTEGUMENTA-LIKE AP2/ERF domain protein. We found that genes in the indole-3-acetaldoxime (IAOx) metabolic pathway (PAD3, FOX1, CYP82C2) are transcriptionally down-regulated by BBM at a very early timepoint during 35S:BBM-mediated somatic embryogenesis. IAOx is an intermediate in tryptophan-dependent auxin (IAA) and defense compound biosynthesis.

Given the role of auxin in promoting BBM-induced cell proliferation, we hypothesized that, similar to superroot mutants, down regulation of IAOx pathway gene expression by BBM would enhance IAA biosynthesis to promote somatic embryogenesis. However, the pad3, fox1 and cyp82c2 mutants reduced 35S:BBM somatic embryo formation in favor of increased ectopic shoot formation. Moreover, exogenous IAOx application to 35S:BBM pad3 and 35S:BBM fox1 lines partly complemented the reduced somatic embryo formation phenotype. Assuming that down-regulation of IAOx pathway genes is positively related to BBM-induced SE, our results suggest that 1) BBM-mediated down-regulation of IAOx-pathway genes does not increase the flux of IAOx to IAA and 2) that down-regulation of IAOx-pathway gene expression is tightly controlled temporally and/or spatially.

53. *"Maroon rice diversity preserves a genomic record of 350 years of colonial history"*

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The Maroons in Suriname and French Guiana descend from enslaved Africans that escaped the plantations during colonial times. In Maroon farming, women have continued the maintenance of a large diversity of rice landraces, their oldest staple crop. Landraces are cultivated crops that have been locally adapted by farmers. Genomic analyses of the Maroon rice landraces may hence clarify from where certain rice varieties were introduced, and as such be a powerful tool in reconstructing historical events in the Maroon past.
Here, we sequenced the genomes of 144 Maroon rice landraces to investigate their geographical origins and the historical contexts associated with their introduction to the Guianas. Using various population genomic methods based on genome-wide SNPs, we show that a subset of the Maroon rice diversity is closely related to some landraces in West Africa and hence may trace back to the trans-Atlantic slave trade (1660-1825). Other subsets of rice diversity can be linked to interactions with diverse ethnic-cultural groups that post-date the era of slavery. These include landraces with long stiff awns brought by indentured laborers from Java (1890-1930), the USA early cultivar Rexoro from rice breeders in Louisiana (1932 onwards), and a more recent cultivar from Hmong refugees from Laos who fled the Vietnamese War (1977 onwards). All in all, our results underline that the Maroon's past is dynamically related to a global history of slavery and colonization. Moreover, the inclusive selection methods of Maroon farmers make their rice variety collections unique cultural heritage. Maroon farmers have been preserving their community's past, and today are important custodians of global rice diversity.

54. *RhizoSMASH: a computational tool to detect rhizocompetence-related bacterial catabolic gene clusters*

Yuze Li, Laboratory of Bioinformatics, Wageningen University and Research

The application of plant growth-promoting rhizobacteria (PGPR) as biofertilizer and biocontrol agents is at the cutting edge of sustainable crop production, making the further understanding and fast identification of rhizobacteria an urgent mission for agricultural green development (AGD). Plants actively distribute nearly 20% of their total photosynthetically fixed carbon through root exudation in forms of both primary and secondary metabolites. The capability to utilize these metabolites is an important determinant to whether a soil bacterium can reside on the rhizosphere. However, the field of study is still looking forward to a designated computational tool to study the catabolism

profile of rhizobacteria. Here, we introduce rhizoSMASH, a computational tool to detect catabolic gene clusters related to the degradation of root exudate metabolites in bacterial genome sequences. As an extension of the well-known biosynthetic gene cluster detection software antiSMASH, our tool finds genes encoding catabolic enzymes with profile hidden Markov models and identifies gene clusters with detection rules composed of the combination of genes. At the present stage, our preliminary version consists of more than 30 detection rules for a variety of degradation pathways. We benchmarked our development-stage tool with 37 published genomes from soil bacterium isolates labeled with rhizosphere colonization capacity. Rhizosphere-colonizers and non-colonizers could be separated based on the presence of catabolic gene clusters in their genomes. In conclusion, our results indicate that catabolic gene clusters for the degradation of root exudates are informative measures for rhizosphere colonization capability of soil bacteria, suggesting rhizoSMASH will become a useful tool to study rhizobacterial metabolism and root-rhizobacteria interaction.

55. *“Phloem Fight: exploring wild tomato phloem to identify whitefly resistance”*

Lissy Denkers, Laboratory of Plant Physiology, University of Amsterdam

The mandatory reduction in systemic pesticide usage drives the development of alternative methods for crop protection against herbivorous insects. Specialised metabolites are known to play a pivotal role in plant-herbivore interactions and there is an incredible natural diversity of compounds present in plants. Such compounds vary from small volatile terpenes to complex decorated molecules. In many plant species these compounds are produced, stored and secreted in specialised tissues, in order to defend themselves against attacking pathogens and insects. In tomato such metabolites are produced and stored “on the outside” in specialised hairs called trichomes. However, trichome-based resistance can have off-target effects on beneficial insects such pollinators and natural enemies of pest insects. In addition to “outside” produced specialised compounds, it is known that the phloem sap, besides photosynthates, also contains a plethora of specialised metabolites “on the inside". Here we explored the phloem as a site of defence against insects that feed specifically from the phloem, focussing on phloem-associated defence metabolites that affect insect proliferation. Whitefly (Bemisia tabaci) has adapted a feeding style to reach the phloem sap whilst avoiding puncturing other cells. We explored the natural variation in the tomato germplasm in resistance against whiteflies and identified a wild tomato on which whitefly nymphal development is hampered. We were able to link this resistance phenotype to the

presence of a specific phloem-based metabolite, a finding that opens up new possibilities for the development of resistant cultivars.

56. *"Role of secondary metabolites in the Azolla-Nostoc symbiosis"*

Erbil Güngör, Laboratory of Plant Stress Resilience, Utrecht University

Azolla is an aquatic fern able to triple its biomass every week while relying solely on atmospheric dinitrogen gas thanks to its cyanobacterial endosymbiont Nostoc azollae. Combined with its high protein content of ∼20% it has potential to serve as a novel plant based protein crop in delta regions by harvesting excess nutrients of flooded agricultural lands. The limiting step for protein extraction is the accumulation of polyphenolic secondary metabolites, such as proanthocyanidins, binding to proteins and interfering with digestion. Severe stress also triggers 3-deoxyanthocyanin accumulation resulting in the characteristic red Azolla mats. Whilst these molecules mainly have been ascribed defensive roles, they also seem to be involved in symbiotic crosstalk.

Nostoc fixes dinitrogen gas inside the leaf pocket: a specialized organ present in each leaf. A permanent Nostoc colony, however, resides at the shoot apex, serving as inoculum for each new leaf developing. If the fern undergoes sexual reproduction, Nostoc also colonizes the developing spores for transfer to the next generation. A structure reoccurring at locations where Nostoc is present are trichomes. We therefore think these trichomes are crucial to regulate the synchronized development of both organisms by secreting signaling molecules.

Cornicinine, a glycosylated triketide delta lactone isolated from the crane fly Nephrotoma cornicina, distorts the Azolla-Nostoc symbiosis. Already at nanomolar concentrations, it turns all Nostoc cells into resting stages called akinetes resulting in chlorotic ferns, most probably because of nitrogen starvation. An apparent effect on sterile Arabidopsis thaliana or free-living filamentous cyanobacteria could not be seen. Why the crane fly accumulates cornicinine, and if it is directly related to Azolla, remains a mystery. Weakening plants by switching off symbioses could, however, be a powerful tool to have for grazers.

57. *"HeatGenes: towards a generic genetic framework for reproductive heat tolerance in plants"*

Max Frencken, Laboratory of Plant Systems Physiology, Radboud University Nijmegen

The increasing occurrence of heatwaves as a consequence of climate change leads to catastrophic yield loss in many food crops. These yield losses are highly correlated to disturbances in pollen development and heat-induced style changes. Which genetic elements are involved in plant reproductive heat tolerance? How conserved are these elements among species? These are some of the questions that we are trying to answer within the HeatGenes project. Using genome-wide association studies and QTL analyses, we set out to discover novel genetic determinants of reproductive heat tolerance in Arabidopsis, tomato and common bean. in the process, we developed reliable and efficient pollen phenotyping assays for Arabidopsis and common bean. Furthermore, we have acquired diversity panels for each of these species which show high variation for pollen viability under heat conditions. At the moment, these assays are being used in the screening of many genotypes in our regulated climate chambers. Ultimately, we expect our results to provide valuable genomic resources in unraveling the genetic framework of reproductive heat tolerance.

58. *"The role of AGC kinases in pollen development"*

Tong Zhao, Institute of Biology, Leiden University

AGC kinases are very conserved kinases in eukaryotes. PDK1 is one of the AGC kinases and considered as a master regulator of other AGC kinases. There are 39 AGC kinases in Arabidopsis thaliana, including two PDK1 genes, we named them PDK1 and PDK2. The pdk1 pdk2 double mutant shows short and twisted pollen tubes and precocious pollen germination in anther. We found another AGC kinase, AGC1.5, can rescue these pollen phenotypes of pdk1 pdk2.

59. *"Shedding Light on Shade Avoidance: a cell-level investigation of stem elongation of tomato cultivars"*

Linge Li, Laboratory of Plant-Environment Signaling, Utrecht University

The global issue of food shortages, exacerbated by population growth, has stimulated scientific efforts to increase crop production. In pursuit of higher crop yields, farmers often sow more crops in a limited area, leading to inevitable competition for limited resources, including light. Many plants respond to this competition by growing taller to access sufficient light and avoid shading, a phenomenon known as the shade avoidance response.

Our research focuses on commercial tomato cultivars M82 and Moneymaker, aiming to investigate similarities and differences in their mechanisms-shade avoidance responses.
To explore this phenomenon, we began by measuring tomato growth under control white light normal and far-red supplemented conditions. Using microscopy and statistical analyses, we observed a significant elongation of the first internode, where pith cells had generated additional layers and increased in length. Subsequently, we harvested internode and pith cell samples from both treatments and conducted tissue-specific RNA-seq experiments.
Our RNA sequencing results revealed a role for the auxin signaling in the internode response to far-red. We proceeded to perform a range of detailed physiological experiments, including, IAA application, and IAA inhibitor application. We also analyzed DR5:GUS expression pattern. These experiments suggested a complex model of shade avoidance response signaling in internode elongation, highlighting the intricate involvement of the auxin signaling pathway.

60. *Using genomic selection to increase photosynthetic protection rates in Arabidopsis thaliana*
Louise Logie, Laboratory of Genetics, Wageningen University and Research

Using genomic selection I aim to show that targeting selection on rapid photosynthetic protection mechanism (non-photochemical quenching(NPQ)) rates, will increase photosynthesis in a magic population of Arabidopsis thaliana. The poster shows how I intend to do this and why this is important to do. Come by to have a chat!

61. *"PHYC mutations decelerated the circadian clock in cultivated lettuce while breeding for delayed flowering time."*
Cèlia Anton Sales, Laboratory of Plant Breeding, Wageningen University and Research

The circadian clock is an endogenous timekeeping mechanism that enables plants to synchronize their metabolic and physiological processes with the daily cycle of the Earth. It influences many agronomic traits, and it has recurrently been targeted through artificial selection during the domestication and improvement of crops. In this study, we performed a species-wide screening of the circadian clock in lettuce, by tracking the circadian leaf movements of 184 different lettuce accessions, including 126 varieties of the cultivated species Lactuca sativa, 35 accessions of its wild ancestor Lactuca serriola, and 23 accessions of the more distantly related wild lettuce species Lactuca saligna. Our findings revealed that during the domestication of lettuce (Lactuca sativa), the circadian clock

period was altered, resulting in a shift from a 24-hour cycle in wild lettuce to a 27-hour cycle in cultivated lettuce. Through genome wide association studies (GWAS) we have identified mutations in the PHYTOCHROME C (PHYC) loci responsible for this change. PHYC is a protein that plays a key role in the plant's circadian clock and flowering processes. We propose that a slower clock in lettuce is a result of breeding efforts aimed at delaying bolting, a process that precedes flowering and is generally considered undesirable in lettuce. By selecting for PHYC allelic variation, it was possible to modify the timing of bolting and delay flowering, while indirectly slowing the plant's circadian clock and increasing its yield under long days. These findings suggest that PHYC likely promotes photoperiodic flowering in lettuce and provides another example of the importance of the circadian clock in plant biology and the development of crops.

62. *"Essential Oils as Green Pesticides for Sustainable Agriculture"*

Julia Mars, Laboratory of Plant Systems Physiology, Radboud University Nijmegen

Although the use of synthetic pesticides helps to maintain crop yields, their use has detrimental effects on ecosystems and human health and led to pathogen resistance. Natural products are an excellent alternative to such pesticides, provided they are environmentally friendly, economical, targeted and biodegradable and their use does not significantly affect crop yields compared to conventional pesticides. Several studies have reported that essential oils (EOs) have a broad spectrum of activity against plant pathogens, including oomycetes and fungi. But before EOs can be used as pesticides, many fundamental and practical questions need to be answered. Our interdisciplinary research team, that consists of biologists and chemists, focusses mainly on two questions: I) is the effect of EOs direct, meaning the effect is either fungistatic/fungicidal, or is it indirect, meaning EOs have an effect on the plant immune system, thus "priming" the plant for future microbial attack, and II) can we overcome the disadvantages of using EOs in the field, like low rain fastness, volatility and degradation, through nanoencapsulation of the substance. With the expectation that the results can be extrapolated to other crops, a case study in viticulture (Grapevine-downy mildew) was chosen for this short-term project.

63. *"Morphological and Cytological Analyses for Leaf Curving in Cabbage Development"*

Zihan Liu, Laboratory of Plant Breeding, Wageningen University and Research

Leafy heads are representing the harvested organs of cabbage (Brassica oleracea), formed by the wrapping and overlapping of leaves. Cabbage vegetative growth goes through

seedling, rosette, folding and heading stages. The expanded leaves of each of these stages are characterized by morphological differences. The leaf blade of seedling and rosette leaves are flat while the leaf blade of folding and heading leaves are in/upward curving. We are interested in the genetics of this typical domestication trait and set out to analyse leaf development. Besides leaf curvature, essential to form a leafy head, leaf shape is also associated with leafy head shape (pointed, flat, round). In this study, we assess leaf tissue growth between flat rosette and curved heading leaves both at whole leaf and cytological levels. We compared cellular organization focusing on adaxial palisade cells and abaxial spongy parenchyma cells at different positions of the leaf. The results demonstrated two trends: a) a higher growth rate of the leaf centre compared to the marginal leaf tissues leads to a bowl-like leaf and b) a higher growth rate of the leaf abaxial compared to the leaf adaxial side leads to an inward curving leaf of heading leaves. Besides, we noticed that leaf shape contributes to leafy head shape in addition to the specific leaf curvature. Overall, differential growth between the leaf ad/abaxial and central/marginal parts shape the heading leaves resulting in leafy head formation.

64. *"The potential of volatile organic compounds (VOCs) from bacterial seed endophytes on Arabidopsis thaliana seed germination and seedling growth under abiotic stresses"*

Sasiwimon Siricharoen, Laboratory of Plant Physiology, Wageningen University and Research

Seeds harbor various microorganisms within their tissues without causing any harm, the so-called seed endophytes. The seed endophytes have been shown to influence plant performance at the early developmental stage, including seed germination and seedling establishment, by producing volatile organic compounds (VOCs). We investigated the effect of potential VOCs from a bacterial seed endophyte isolated from wild cabbage seeds (E44) on seed germination and seedling growth of Arabidopsis thaliana under salinity and osmotic stresses We found that seeds sown under salinity (125mM) or osmotic stress (300mM mannitol) showed higher and faster germination when sown in the presence of E44. Similarly, we observed that Arabidopsis seedlings showed a higher growth (fresh weight and root length) under 75mM NaCl or 150mM sorbitol in the presence of E44. In our setup the E44 endophytic bacteria is cultivated in a separate plate than the seed and seedling, indicating that their VOCs are potentially stimulating germination and growth. We are now investigating if different Arabidopsis ecotypes respond differently to E44, and in the future we will identify what specific VOCs emitted by E44 are stimulating Arabidopsis seed germination and seedling growth under abiotic stresses.

65. *"R gene-induced selection pressure affects the prevalence of the virulence effector RBP-1 of Globodera pallid"*

Vera Putker, Laboratory of Nematology, Wageningen University and Research

The potato cyst nematode (PCN) is considered a dominant threat to yield for major food crops such as potato and tomato. Current control strategies mainly depend on crop rotation and the use of resistant cultivars. In potato the single dominant resistance (R) gene Gpa2 activates effective host-specific resistance to the PCN Globodera pallida population D383. More specifically, the matching effector gene eliciting Gpa2-mediated immune responses is the effector gene RBP-1. However, resistance breaking populations in the field such as Rookmaker harbour specific RBP-1 alleles evading resistance. It is however unknown how these alleles behave in natural populations under selection. Here we aim to understand the genetic dynamics of RBP-1 during infection under selection pressure of an R gene.

We monitored nematode development during 21 days in avirulent (D383) and virulent (Rookmaker) G. pallida populations in potato plants with or without the R gene Gpa2. In these in vitro infection assays, after 21 days, Rookmaker juveniles developed into females in both potato lines. D383 juveniles however were not able to develop into females in the resistant potato line, and a strong plant immune response was visible, while in the susceptible potato line D383 was able to develop into females. In parallel, we conducted the same experiment but harvested infected root segments at 6 dpi for RNA isolation and transcriptomics. In total, we revealed 326 differentially expressed genes (DEGs) upon nematode infection, of which 13 DEGs were specifically regulated in Rookmaker infection on the resistant potato line. Amongst them, we found that in D383 RBP-1 is upregulated compared to Rookmaker, irrespective of the presence of the R gene Gpa2.

Our data show the strong selection pressure exerted by Gpa2, as well as differences in expression between avirulent and virulent populations. We are currently using two long-read reference genomes of both D383 and Rookmaker to investigate the genomic organisation of RBP-1. We will also map the allelic variation of RBP-1 before infection and in young females during infection to reveal the effect of the Gpa2 selection pressure on RBP-1.