



Epigenetics of Temperature & Light Responses in Plants

COST EPICATCH CA19125
Workshop

March 15th-16th, 2023
Volcani Center, Israel

Abstract Book



COST EPICATCH CA19125 Workshop

Volcani center - Israel

“Epigenetics of temperature & light responses in plants”

DAY 1 - Wednesday, March 15th, 2023

09:00-09:30	Registration
09:30-09:45	Welcome and introduction
	Session 1 Temperature and light responses in plants Chair: David Honys
9:45-10:30	Keynote lecture: Pierre Goloubinoff , University of Lausanne, Switzerland How do plants feel the heat and survive? Detection of plant epimutants reversibly defective in the heat-shock response (HSR)
10:30-11:00	Khalil Kashkush , Ben-Gurion University, Israel Structure and extent of DNA methylation- based epigenetic variation in wild emmer wheat (<i>T. turgidum ssp. dicoccoides</i>) populations
11:00-11:30	Eyal Fridman , Volcani Center, Israel Barley thermal plasticity under warming environment - tango of two genomes
11:30-12:00	Coffee break
12:00-12:30	Giora Ben-Ari , Volcani Center, Israel Elevated temperatures negatively affect olive oil production and quality
12:30-13:00	David Honys , Czech Academy of Sciences, Czech Republic Multi-omics approach to describe gene expression dynamics in developing pollen of <i>Arabidopsis thaliana</i>
13:00-13:30	Yogev Burko , Volcani Center, Israel Regulation of plant growth in response to environmental changes
13:30-14:00	Eirini Kaiserli , Glasgow University, United Kingdom TANDEM ZINC-FINGER/PLUS3 integrates light and warm temperature signalling in plant nuclear hubs
14:00-15:30	Free time
	Session 2 Plant epigenetic mechanisms Chair: Sotirios Fragkostefanakis
15:30-16:15	Keynote lecture: Nir Ohad , Tel-Aviv University, Israel The role of epigenetic regulation in autonomous embryo development
16:15-16:45	Ofir Hakim , Bar-Ilan University, Israel 1D and 3D modes of gene regulation
16:45-17:15	Naama Segal , IOLR, The National Center for Mariculture, Israel Epigenetic mechanisms involved in foreign gene expression silencing in different microalgae
17:15-17:30	Closing remarks

DAY 2 - Thursday, March 16th, 2023

09:00-09:15	Opening
	Session 3 Epigenetic aspects of temperature and light responses in plants Chair: Eirini Kaiserli
09:15-10:00	Keynote lecture: Martijn Van Zanten , Utrecht University, The Netherlands Optimal plant performance under suboptimal high temperature conditions; HDA9 promotes auxin biosynthesis to trigger thermomorphogenesis
10:00-10:30	Sophie Brunel-Muguet , INRAE, France Towards a better characterization of heat stress recurrence: A case study in oilseed rape
10:30-11:00	Rea Laila Antoniou Kourounioti , Glasgow University, United Kingdom Epigenetic and cold-dependent control of flowering time in Arabidopsis
11:00-11:30	Coffee break
11:30-11:50	Puglia Giuseppe Diego , Institute for Agricultural and Forestry Systems in the Mediterranean, National Research Council, Italy Alternating temperatures trigger dormancy release through epigenetic regulation in Cynara cardunculus
11:50-12:10	Michal Lieberman-Lazarovich , Volcani Center, Israel The role of DNA methylation in heat stress response in tomato
12:10-12:40	Sotirios Fragkostefanakis , Goethe University Frankfurt am Main, Germany Regulation of heat stress response and thermotolerance: how plants survive, recover and remember the hot days
12:40-13:10	Moussa Benhamed , University of Paris-Saclay, France Exploring the chromatin-based regulation of enhancer promoter contact and its impact on gene expression in tomato
13:10-13:20	Closing remarks



Epigenetics of Temperature & Light Responses in Plants
COST EPICATCH CA19125
Workshop

March 15th-16th, 2023
Volcani Center, Israel

Oral Presentation Abstracts

epicatch

Epigenetics of Temperature & Light Responses in Plants

Oral Presentation Abstracts

How do plants feel the heat and survive? Detection of plant epimutants reversibly defective in the heat-shock response (HSR).

Anthony Guihur, Baptiste Bourguine and **Pierre Goloubinoff**

Department of Plant Molecular Biology, Faculty of Biology and Medicine, University of Lausanne, CH-1015 Lausanne, Switzerland, Pierre.Goloubinoff@unil.ch

Global warming urges for a better understanding of the molecular mechanisms by which higher plants sense and respond to sharp increments of the ambient temperature and appropriately accumulate protective heat-shock proteins (HSPs) and metabolites (Guihur et al., TIBS doi:10.1016/j.tibs.2022.05.004). We designed a transgenic *Arabidopsis thaliana* reporter line expressing from a conditional heat-inducible promoter, a fusion gene encoding for nano-luciferase and D-amino acid oxidase, whose expression in the presence of D-valine was toxic to the plant. Whereas at 22°C, seedlings grew unaffected by D-valine and did not emit light and without D-valine, most seedlings survived iterative heat shocks and strongly emitted light, on D-valine, only 2% survived heat shocks and did not emit light. Remarkably, 20 times less seedlings (0.01%) survived the heat-shocks in the presence of both D-valine and a DNA-methylation inhibitor. RNAseq analysis showed that most heat-shock survivors on D-valine failed to carry out the entire HSR, corresponding to the heat-induced expression of hundreds of different HSP genes from different chromosomes. Some epimutants repressed their HSR only during youth, others during their entire life and moreover transmitted their HSR inhibition phenotype to up to 50% of first-generation descendants. Our results suggest that higher plants can activate a general epigenetic program, whereby in 1 out of 25 wild type plants, a master regulator can block the entire HSR during youth, or the entire lifetime, and moreover transmit an HSR inhibition phenotype to up to half of next generation plants. The results suggest that the excessive accumulation of thermo-protective HSPs and metabolites during iterative heat stresses has strong tradeoff on plant fitness.

Structure and extent of DNA methylation- based epigenetic variation in wild emmer wheat (*T. turgidum ssp. dicoccoides*) populations.

Khalil Kashkush

Department of Life Sciences, Ben-Gurion University, Beer-Sheva 84105, Israel

The genetic structure and differentiation of wild emmer wheat suggests that genetic diversity is eco-geographically structured. However, very little is known about the structure and extent of the heritable epigenetic variation and its influence on local adaptation in natural populations. Here, the structure and extent of the heritable methylation-based epigenetic variation were assessed within and among natural populations of *Triticum turgidum ssp. dicoccoides*. We used methylation sensitive amplified polymorphism and transposon methylation display techniques, to assess the methylation status of random genomic CCGG sites and CCGG sites flanking transposable elements, respectively. Both techniques were applied to the DNA of 50 emmer accessions which were collected from five different geographically isolated regions. In order to ensure the assessment of heritable epigenetic variation, all accessions were grown under common garden conditions for two generations. The most significant conclusion of this work is the observation of population-unique heritable methylation patterns in emmer wheat accessions originating from five geographically isolated regions. Our data indicate that methylation-based epigenetic diversity might be eco-geographically structured and might be partly determined by climatic and edaphic factors.

epicatch

Barley Thermal Plasticity Under Warming Environment - Tango of Two Genomes

Eyal Fridman¹, Lalit D. Tiwari¹, Schewach Bodenheimer^{1,2}, Adi Doron-Feigenbaum¹, Khalil Kashkush³, and Eyal Bdolach^{1,3}

1 Institute of Plant Sciences, Agricultural Research Organization (ARO), The Volcani Center;

2 The RH Smith Institute for Plant Sciences in Agriculture, Faculty of Agriculture, The Hebrew University of Jerusalem, Rehovot;

3 Department of Life Sciences, Ben-Gurion University

In plants, the role of chloroplasts and mitochondria (plasmotype) in controlling circadian clock plasticity and overall plant robustness has not been elucidated. We investigate the fitness and circadian clock variation in the wild barley (*Hordeum vulgare* ssp. *spontaneum*) collection (Hubner et al., 2009) and in derived interspecific populations. Our goal is to better understand a major crop's genetic and phenotypic evolution and to utilize naturally-occurring variations for breeding and biotechnology. Our studies identified drivers of the clock (DOC) loci that control the loss of clock plasticity between wild and cultivated populations; these loci also show the signature of selection in the genome and some show heat-dependent effects on yield robustness (Prusty et al., 2021). In the wild populations, we identified and experimentally validated key DOCs, including the chloroplast in which alleles of the *rpoC1*, a member of the RNA polymerase complex, are modulating the clock plasticity in barley (Bdolach et al., 2019). Furthermore, heterologous over-expression of two barley *RpoC1* alleles in *Arabidopsis* showed significant differential plasticity under elevated temperatures (Tiwari et al., 2022). The pleiotropic effects of the DOC on plant fitness in the field, including that of the plasmotype, prompt us to develop advanced mapping populations for further research and pre-breeding. I will present the utilization of this first built cytonuclear multiparent population (CMPP) for modelling genetic basis of plasticity and for developing better adapted barley to different climatic scenarios.

Relevant references: doi: 10.1111/pce.13606, doi: 10.22541/au.166987850.00982018/v1, *Molecular Ecology* 18: 1523–1536, doi: 10.1111/nph.17284.

Multi-omics approach to describe gene expression dynamics in developing pollen of *Arabidopsis thaliana*

Božena Klodová¹, David Potěšil², Lenka Steinbachová¹, Christos Michailidis¹, Dieter Hackenberg¹, Zbyněk Zdráhal², Jörg D. Becker⁴, David Twell³, **David Honys**¹

1 Institute of Experimental Botany of the Czech Academy of Sciences, Laboratory of Pollen Biology, Praha, Czech Republic

2 Mendel Centre for Plant Genomics and Proteomics, Central European Institute of Technology, Masaryk University, Brno, Czech Republic.

3 Department of Genetics and Genome Biology, University of Leicester, United Kingdom.

4 Instituto de Tecnologia Química e Biológica António Xavier, Universidade Nova de Lisboa. Oeiras, Portugal

Angiosperm sexual reproduction depends on successful delivery of the two male gametes to female ovules. During the male gametophyte development, gene expression is strictly regulated and undergo dynamics changes to ensure correct developmental progression, pollen tube germination and rapid growth through the pistil and eventual double fertilisation. Transcriptomic analyses of developing pollen have been addressed in several species. In this study, by integrating various -omics approaches, we addressed the gene expression dynamics in four stages of microgametogenesis in two *Arabidopsis* accessions (Col-0 and Ler-0) to provide complex regulatory map on protein, transcripts and isoform level. We compared original published pollen microarray-based platform data to demonstrate superiority of RNA-seq approach but also high reproducibility of the two methods. The analysis identified additional regulatory mechanisms including several thousands of long non-coding RNAs with potential role in pollen development previously undocumented. Also stood out where differential isoforms events and translation dynamics throughout the developmental stages and across accessions. In summary this work summarises the dynamics in gene expression and main regulatory trends in two accessions of *Arabidopsis thaliana*.

Funding: Czech Ministry of Education, Youth and Sports (LTC20028), Czech Science Foundation (21-15856S, 23-07000S), and European Regional Development Fund-Project “Centre for Experimental Plant Biology” (No. CZ.02.1.01/0.0/0.0/16_019/0000738.)

Regulation of plant growth in response to environmental changes

Joanne Chory¹ and Yogev Burko²

1 Plant Sciences, Salk Institute, HHMI, 10010 N. Torrey Pines Rd., La Jolla, 92037, USA

2 The Institute of Plant Sciences, ARO, Volcani Center, 68 Hamakabim Road, 7505101, Rishon LeZion, Israel

The size of plant organs is highly responsive to environmental conditions and displays phenotypic plasticity in response to light and temperature. The stem of shade-avoiding species elongates to outcompete neighboring plants and secure access to sunlight. Similar elongation occurs at high temperatures. We found that shade combined with warm temperature produces a synergistic stem elongation response in Arabidopsis and tomato, greater than either stimulus alone. In Arabidopsis, the synergistic elongation depends on the transcription factor PHYTOCHROME-INTERACTING FACTOR 7 (PIF7) and auxin. In addition, the warm temperature is sufficient to promote PIF7 DNA binding but not transcriptional activation. We suggest that additional, unknown factor/s must work downstream of the phyB-PIF-auxin module. These results and the role of tomato SIPIFs in mediating these responses will be discussed.

epicatch

TANDEM ZINC-FINGER/PLUS3 integrates light and warm temperature signalling in plant nuclear hubs.

Eirini Kaiserli, Anna Zioutopoulou, Tianyuan Xu, Jack Bunyan and Micaela Milani

School of Molecular Biosciences, College of Medical, Veterinary and Life Sciences, University of Glasgow, UK, eirini.kaiserli@glasgow.ac.uk

Photomorphogenesis and flowering initiation are two of the most dramatic developmental transitions during the life-cycle of a plant that are triggered by an ensemble of environmental and endogenous stimuli and signalling networks. The talk will focus on the molecular function of TZP (TANDEM ZINC-FINGER PLUS3) as an integrator of light and temperature signalling at the level of transcription. TZP interacts with the photoreceptor and thermosensor phyB and controls hypocotyl elongation and flowering by modulating the expression of chromatin regulators and growth promoting factors. Recent studies uncovering the novel role of TZP in thermomorphogenesis will be presented.

epicatch

The role of epigenetic regulation in autonomous embryo development

Nir Ohad

School of Plant Sciences and Food Security, Faculty of Life Sciences, Tel Aviv University, Tel Aviv 69978. Israel, NirO@tauex.tau.ac.il

The life cycle of land plants alternates between gametophytic and sporophytic generations. We have found that a key component regulating this cycle in flowering plants is the Polycomb group complex (PcG) which catalyzes histone H3K27 methylation, facilitating epigenetic control of gene expression profiles. Using the evolutionary early-diverged land plant model species *Physcomitrella patens* we further show, that abolishment of FIE and CLF PcG proteins, leads to fertilization-independent sporophyte development. PpFIE accumulates in haploid meristematic cells and cells undergoing fate transition during dedifferentiation programs. In the absence of PpFIE, apical stem cells are unable to develop leafy gametophytes. Moreover, they also develop sporophytic-like structures. The PpFIE aberrant mutant phenotype can be partially rescued by the *Arabidopsis thaliana* FIE gene, representative of angiosperms, thus illustrating the functional conservation of the protein throughout plant evolution. The expression profile in PpFIE and PpCLF mutants allowed identifying key players whose expression is induced in a PpFIE mutant while silenced in the wild-type gametophyte. Among these genes, we have identified BELL1 homeobox gene which is expressed exclusively in the egg cell. Lines constitutively expressing BELL1, give rise to functional sporophytes. These apogamous sporophytes fully differentiate and produce spores as in WT. The mechanisms and development of BELL1-induced apogamous sporophytes provide insights into the evolution of multicellular sporophytes from an ancestor with a haplontic life cycle, and may serve as an entry point to understand apomixis in other plants.

1D and 3D Modes of Gene Regulation

Ofir Hakim

Bar Ilan University

Gene expression networks that determine tissue-specific identity and responses are highly organized within the three dimensional (3D) nuclear space. Yet, the molecular basis of genome organization and the causal link between its structure and function are poorly understood. I will show how monitoring the coordinated dynamics of transcription networks, chromatin structure, transcription factor binding, and genome architecture led to uncovering key players and novel layers of transcriptional reprogramming during cancer development, rapid response to hormones in animal cells and organ identity in *Arabidopsis thaliana*.

epicatch

Epigenetic mechanisms involved in foreign gene expression silencing in different microalgae

Na'ama Segal

Israel Oceanographic and Limnological Research, The National Center for Mariculture.

Microalgae are a diverse group of single-cell photosynthetic organisms with the ability to adapt to extreme habitats and produce various essential biological products. Throughout the years, much effort has been made to generate improved microalga product quality and yield. One way is by inserting transgenes into the microalgae. However, the full potential of using algae as heterologous systems for transgene expression has yet to be achieved. The epigenetic mechanism regulates gene expression and acts as a defense line. By using special modification, the epigenetic mechanism affects the DNA, regulates gene expression, and leads to difficulties in transgene expression. The Sirtuin protein family are Histone Deacetylases proteins that act as repressors via the deacetylation of Acetyl groups in the histone tails, which changes to a positive charge of the histone and causes the DNA to coil around the histone. The gene homologous to SIRT6 in *C. reinhardtii* was shown to be associated with transgene silencing. One mutation in this gene interrupts the removal of the acetyl group leading to high transgene expression levels. This discovery opens a hatch to using a novel new method to study the effect of the epigenetics mechanism on transgene expression in different microalgae and the understanding of the mechanisms that regulate it.

epicatch

Optimal plant performance under suboptimal high temperature conditions; HDA9 promotes auxin biosynthesis to trigger thermomorphogenesis

Martijn van Zanten

Plant Stress Resilience, Institute of Environmental Biology, Utrecht University, The Netherlands;
m.vanzanten@uu.nl

Several plant species can adjust their architecture in response to mild increases in temperature below the heat stress threshold. This process is known as thermomorphogenesis and is characterized by elongation of e.g. hypocotyls and petioles and upward leaf movement. The resulting open plant structure promotes leaf cooling and thereby allows for optimal performance under suboptimal high temperature conditions. Thermomorphogenesis phenotypically resembles the shade avoidance response, that is triggered by a low red-to-far red ratio and low blue light, and is tightly controlled by epigenetic processes, most notably eviction of the repressive histone H2A.Z variant followed by H3.3 positioning.

We found that the chromatin modifying enzyme HISTONE DEACETYLASE 9 (HDA9) is required for thermomorphogenesis but not the shade avoidance response. At warm temperatures, HDA9 protein is stabilized and allows for the expression of YUCCA8, a rate-limiting enzyme in auxin biosynthesis. Our work thus assigns a role to histone deacetylation in activating gene expression, which is atypical for this class of enzymes. Specifically, we demonstrate that HISTONE DEACETYLASE 9 mediates histone deacetylation at the TSS of YUCCA8, which stimulates eviction of H2A.Z variant from nucleosomes of the YUCCA8 promoter. This allows binding of the transcription factor PHYTOCHROME FACTOR 4 (PIF4) that is required for YUCCA8 induction and auxin accumulation. In follow-up work we recently showed that both HDA9 and PIF4 recruitment to the YUCCA8 locus requires MEDIATOR25 and that PIF4 and HDA9 compete for binding to the same MEDIATOR25 protein domain. We propose a working model wherein MEDIATOR25 docks HDA9 to the YUCCA8 locus in young seedlings, which triggers HDA9-mediated local chromatin remodeling events to a permissive environment, followed by competitive PIF4 binding to MED25, replacing HDA9, and activation of YUCCA8 transcription.

Towards a better characterization of heat stress recurrence: A case study in oilseed rape.

Sophie Brunel-Muguet¹, Lethicia Magno¹, Jérémy Delamare¹, Lorane Lefranc¹, Benoît Bernay², Jessica Soyer³

1 Normandie Univ, UNICAEN, INRAE, UMR 950 Ecophysiologie Végétale, Agronomie et nutriments N, C, S, SFR Normandie Végétale (FED 4277), Esplanade de la Paix, 14032 Caen, France

2 Plateforme Proteogen, US EMerode, Université de Caen Normandie, 14000 Caen, France.

3 Université Paris-Saclay, INRAE, AgroParisTech, UMR BIOGER, 91123 Palaiseau, France.

The expected increased frequency of heat waves is a major threat to field crops that complete their reproductive phase over spring and summer in temperate regions. Although many studies investigated the effects of high temperatures during the crop reproductive stage on yield and seed quality, the responses of plants to repeated stressing events are much less documented. However, these new climatic features raise the following questions (i) how plants face stress recurrence during their life cycle, (ii) can stress recurrence induce stress memory and even acclimation, and (iii) are specific mechanisms implemented. Over the last few years, our group performed several heat stress experiments to characterize the effects of different temperature profiles that differed in terms of intensity, duration, timing and frequency of the stressing events, in oilseed rape. The leading objectives were to identify thermoprimering protocols and the associated molecular regulations, mainly at the epigenetic level. Our results indicated that most yield components and quality criteria (e.g. fatty acids concentration and composition) were negatively impacted by heat whether intense or moderate but to different extents according to the pods cohort, thus meaning that the timing of stress application is determining. No alleviating effect (i.e. primering) of an early stress followed by a 5 day-recovery phase prior to heat peaks was observed whereas a gradual increase prior to the heat peaks helped reduce their negative effects. These last effects were associated to several histone post translational modifications, and at the proteomic level, to sulfur-metabolic processes and oxidative stress. Our analyses led to conclude that (i) the effect of a succession of heat stress events does not match the sum of the individual effects, which reflects stress memory, (ii) a gradual increase prior to an intense stress helps the plants acclimating while primering-induced processes can be reset after a too long duration of recovery. Overall, these datasets acquired at different scales of analysis will provide useful information to improve crop performances predictions by either implementing process-based crop models or developing data-mining approaches.

Epigenetic and cold-dependent control of flowering time in Arabidopsis

Rea L Antoniou-Kourounioti¹, Jo Hepworth², Yusheng Zhao³, Julia Qüesta⁴, Caroline Dean⁵, Martin Howard⁵

1 School of Molecular Biosciences, University of Glasgow, G12 8QQ, Glasgow, UK

2 Department of Biosciences, Durham University, DH1 3LE, Durham, UK

3 Institute of Genetics and Developmental Biology, Chinese Academy of Sciences, Beijing, China

4 Centre for Research in Agricultural Genomics, Barcelona, Spain

5 Department of Cell and Developmental Biology, John Innes Centre, NR4 7UH, Norwich, UK

6 Department of Computational and Systems Biology, John Innes Centre, NR4 7UH, Norwich, UK

Some plants must experience a prolonged period of cold before they can flower, thus ensuring that winter has passed. This process, called “vernalization”, is controlled by the gene FLOWERING LOCUS C (FLC) and its regulators in *Arabidopsis thaliana*. In this talk I will discuss work which has combined mathematical modelling with experiments to understand how plants set up and how they satisfy this cold requirement. The epigenetic regulation of FLC is the crucial step in this process, including whether it occurs by default (without an environmental signal needed), which is controlled through genetic variation, or if it requires this prolonged cold period. In the second case, the epigenetic silencing of this gene occurs quantitatively, correlated with the duration of cold, and its stability depends on the FLC sequence. Mathematical models have been developed in this work for the temperature sensing and epigenetic regulation of this gene which can predict its expression in field conditions and have given us a deeper understanding into the mechanisms of these processes.

Alternating temperatures trigger dormancy release through epigenetic regulation in *Cynara cardunculus*

Puglia Giuseppe Diego¹, Frazzetto Paola², Huarte Hector Roberto³

1 Institute for Agricultural and Forestry Systems in the Mediterranean (ISAFoM), National Research Council (CNR), Catania, Italy

2 Department of Biological, Geological and Environmental Sciences, University of Catania, Catania, Italy

3 CONICET/Universidad Nacional de Lomas de Zamora, Facultad de Ciencias Agrarias,, Llavallol, Argentina

Light and alternating temperatures are considered the principal signals for seed dormancy termination in many plant families since they can provide important information about soil burial depth. Epigenetic regulation has recently been shown to play an important role in dormancy release through the regulation of chromatin accessibility and silencing of dormancy-associated genes. *Cynara cardunculus* L. is a Mediterranean species with a wide genetic pool consisting of artichoke, the wild and leafy cardoon. Their propagation by germination is hampered by the presence of residual seed dormancy. In the present study, we carried out a transcriptomic analysis of seed imbibed at constant and alternating temperatures to identify principal drivers in seed dormancy release. We observed that incubation at alternating temperatures was associated with an upregulation of argonaute 1 and 4 (AGO1 4) *C. cardunculus* homologs, which are components of the RNA-induced silencing complex (RISC) involved in the silencing of genes associated with dormancy maintaining. In addition, similar expression patterns were found for Histone Deacetylase 2B homologs in seeds exposed to alternating temperatures. These preliminary findings support the hypothesis that epigenetics regulation through gene silencing and histone deacetylation acts as a negative regulator of seed dormancy and is triggered by alternating temperatures in *Cynara cardunculus*.

The tomato *ddm1b* mutant links heat stress tolerance with DNA methylation-mediated transcriptional regulation

G. Miller¹, P. Kumar¹, A. Faigenboim¹, N. Bouche², S. Fragkostefanakis³, **M. Lieberman-Lazarovich**

1 Institute of Plant Sciences, Agricultural Research Organization, Volcani Center, Rishon LeZion, Israel

2 Institut Jean-Pierre Bourgin, INRA, AgroParisTech, CNRS, Université Paris-Saclay, France

3 Department of Biosciences, Molecular Cell Biology of Plants, Goethe University Frankfurt am Main, Frankfurt am Main, Germany

Heat stress is a major environmental factor limiting crop productivity, thus presenting a food security challenge. Various approaches are taken in an effort to develop crop species with enhanced tolerance to heat stress conditions. Since epigenetic mechanisms were shown to play a regulatory role in mediating plants' responses to their environment, we investigate the role of DNA methylation in response to heat stress in tomato (*Solanum lycopersicum*), a major vegetable crop. We recently found that the tomato *ddm1b* mutant, deficient in DNA methylation, shows very little phenotypic effect under normal growth conditions, however, under controlled heat stress conditions, we observed higher fruit set and seed set rates, as well as a higher survival rate at the seedling stage, compared with the background genotype. In search for genes underlying the heat stress tolerance of the mutant, we carried out a transcriptomic analysis, which highlighted a unique transcriptional response of the mutant. Coupled with DNA methylation analyses, we identified a Differentially Methylated Region (DMR) in the promoter of a specific heat stress transcription factor (HSF), which was transcriptionally upregulated in the mutant. Since this DMR overlaps a predicted promoter heat stress responsive element, our current model suggests that a specific loss of DNA methylation in the promoter of this HSF led to the activation of this gene therefore promoting heat stress tolerance of the *ddm1b* mutant.

Regulation of heat stress response and thermolerance: how plants survive, recover and remember the hot days

Sotirios Fragkostefanakis, Sarah Ullrich, Ayat Bakery

Department of Molecular and Cell Biology of Plants, Goethe University Frankfurt, Max-von-Laue Str9, 60438, Frankfurt am Main, Germany

Plants experience heat stress (HS) at temperatures where growth and development are negatively affected. Survival from HS is dependent on the upregulation of hundreds of genes with protective functions for protein and cellular homeostasis such as heat shock proteins (HSPs). The majority of these genes are regulated by the family of HS transcription factors (HSF). In tomato, HsfA1a is the master regulator of HS response. Additional HSFs, such as HsfA2 and HsfA7 are important for HS acclimation and memory, the ability of a plant to store the information of a past HS incident and optimize the response in case of a new one. Class B HSFs act as co-repressors and are important for the attenuation of the response during recovery from stress. The interplay between activators and repressors adjusts stress response intensity to optimize survival and minimize interference with growth and development. The functional relevance of these networks will be discussed on the example of tomato.

epicatch

Exploring the chromatin-based regulation of enhancer promoter contact and its impact on gene expression in tomato

Moussa Benhamed

Université de Paris, Institute of Plant Sciences Paris-Saclay (IPS2), F-75006 Paris, France.

Epigenetic regulations have become a major focus of research activity in the current post-genomics era, a period in which the complete genome sequence of multiple model organisms is known. Yet the linear conception of the genome has been replaced by a highly complex and dynamic 3-dimensional organization of chromatin within the nucleus (Rodriguez-Granados et al., 2016; Concia et al., 2020 ; Huang et al., 2021) creating new challenges for the understanding of the control of gene expression but also possibilities to modulate these pathways. Major advances have been made regarding the chromatin regulation of biological processes in model species such as *Arabidopsis thaliana*. However, the extrapolation of these findings to crop species, such as tomato, remains a challenge. Indeed, the role of the 3D chromatin reorganizations in gene regulation, and how promoter-enhancer contacts are established in response to stress as well as the role of TFs in promoter-enhancer contacts remain largely unknown. In this context, my lab explores the chromatin-based regulation of 3D enhancer promoter contacts and how these nuclear reorganizations impact gene expression in tomato.

epicatch