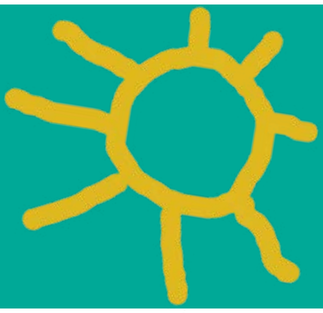


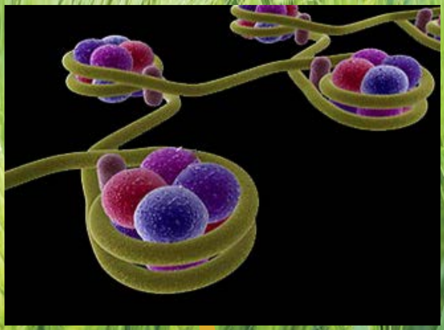
SPS Summer School 2018

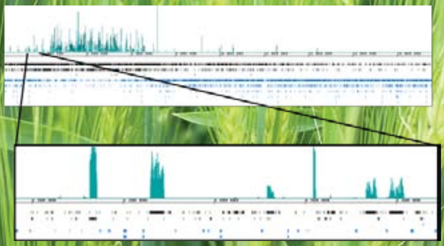
July 8th to 13th 2018

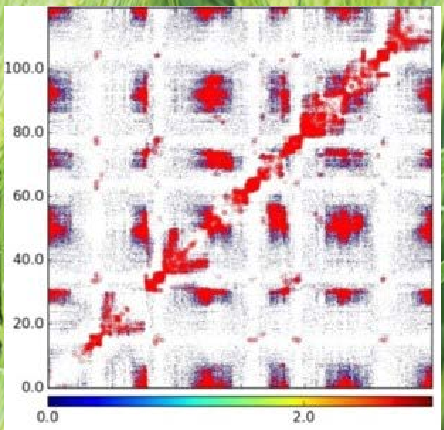
near Paris, France

« PLANT EPIGENETICS AND EPIGENOMICS »

Program







SACLAY PLANT SCIENCES

Planning at a glance

8 AM, 9 AM, 10 AM, 11 AM, 12 PM, 1 PM, 2 PM, 3 PM, 4 PM, 5 PM, 6 PM, 7 PM, 8 PM

Sunday 8th	Monday 9th	Tuesday 10th	Wednesday 11th	Thursday 12th	Friday 13th
	8:30 AM Session 1	9 AM Session 2	9 AM Visit of IPS2	8:30 AM Session 3	9 AM Session 4
	10 :30 AM Coffee break	10:45 AM Coffee break		10:15 AM Coffee break	10:45 AM Coffee break
	11 AM Session 1	11:15 AM Session 2		10:30 AM Session 3	11:15 AM Session 4
	12:45 PM Lunch	12:15 PM Lunch	12 PM Lunch	12:30 PM Lunch	12:15 PM Lunch
	2:30 PM Session 1	2 PM Session 2 (Practical training)	1PM Presentation of SPS Visit of IJPB	2 PM Session 3 (Practical training)	1:30 PM Session 4 (Practical training)
	4 PM Coffee break	4 PM Coffee break		4 PM Coffee break	3:30 PM Coffee break
5 PM Introduction	4:30 PM Session 1	4:30 PM Session 2	4 PM Visit of the Versailles Castle	4:30 PM Session 3	4 PM Session 4
5:30 PM Poster session / Discussion	6 PM Poster session / Discussion	5:30 PM Session 2 (Discussions)		5:30 PM Session 3 (Discussions)	5 PM S4 (Discussions)
					5:30PM Closing discussions
					6 PM End of the Summer School
8 PM Dinner	8 PM Dinner	8 PM Dinner	7:30 PM Dinner in Versailles	8 PM Dinner	

Session 1:
Molecular basis of plant epigenetics / Methodologies

Session 2:
What is the relationship between cell fate and epigenetics?

Session 3:
Role of the epigenetics in the integration of environmental signals

Session 4:
Transgenerational epigenetics & Plant breeding

Program

Sunday July 8th

5 PM - 5:30 PM: Introduction (Martin Crespi)

5:30 PM - 7:30 PM: Poster session / Discussion about the participants' projects (Part 1)

7:30 PM : Dinner

Monday July 9th

Session 1:
Molecular basis of plant epigenetics / Methodologies

8:30 AM - 9:30 AM: History of epigenetics (Jonathan Weitzman)

9:30 AM - 9:45 AM: Discussion

9:45 AM - 10:30 AM: DNA methylation (Nicolas Bouché)

10:30 AM - 11 AM: Coffee break

11 AM - 11:45 PM: Histone modifications and histone variants (Aline Probst)

11:45 AM - 12:45 PM: Spatial organisation of plant chromatin (Chang Liu)

12:45 PM: Lunch

2:30 PM - 3:15 PM: Long non-coding RNAs (Martin Crespi)

3:15 PM - 4 PM: Plant small RNAs (Hervé Vaucheret)

4 PM - 4:30 PM: Coffee break

4:30 PM - 5:15 PM: Epitranscriptomics (Cécile Antonelli)

5:15 PM - 6 PM: Methodologies - IPS2 EPIGENOMIC platform presentation (David Latrasse)

6 PM - 7:30 PM: Poster session / Discussion about the participants' projects (Part 2)

8 PM: Diner

Tuesday July 10th

Session 2:
What is the relationship between cell fate and epigenetics?

9 AM - 10 AM: Plant morphology (Cristel Carles)

10 AM - 10:45 AM: Chromatin and photomorphogenesis (Fredy Barneche)

10:45 AM - 11:15 AM: Coffee break

11:15 AM - 12:15 PM: Epigenetics in the germline (Filipe Borges)

12:15 PM: Lunch

2 PM - 4 PM: Practical session: Bioinformatic analysis of ChIPseq data (Lorenzo Concia and Moussa Benhamed)

4 PM - 4:30 PM: Coffee break

4:30 PM - 5:30 PM: Environmental epigenetics (Ortrun Mittelsten Scheid)

5:30 PM - 6 PM: Discussion with the invited speakers

6 PM - 7:30 PM: Discussion about the practical training session

8 PM: Diner

Wednesday July 11th

8:15 AM - 8:45 AM: Bus trip to Gif-sur-Yvette

9 AM - 11:30 AM: Visit of the Institute of Plant Sciences Paris-Saclay (IPS2, Gif-sur-Yvette)

11:30 AM - 1 PM: Bus trip to Versailles and lunch

1 PM - 3:30 PM: Presentation of the Saclay Plant Sciences network
Visit of the Jean-Pierre Bourgin Institute (IJPB, Versailles)

3:30 AM - 3:45 PM: Bus trip to the Versailles Castle

4 PM - 7 PM: Visit of the Versailles Castle and its gardens

7:30 PM - 10 PM: Dinner in Versailles

10 AM - 10:30 PM: Bus trip to the Centre Port-Royal

Thursday July 12th

Session 3:
Role of the epigenetics in the integration of environmental signals

8:30 AM - 9:30 AM: Abiotic stress (Leandro Quadrana)

9:30 AM - 10:15 AM: Plant-microbe interactions (Christine Lelandais)

10:15 AM - 10:45 AM: Coffee break

10:45 AM - 11:30 PM: DNA damage and epigenetics (Jean Molinier)

11:30 AM - 12:30 PM: Epigenetic stress memory (Jose Gutierrez-Marcos)

12:30 PM: Lunch

2 PM - 4 PM: Practical session: Small RNA analysis (Thomas Blein and Jérémie Bazin)

4 PM - 4:30 PM: Coffee break

4:30 PM - 5:30 PM: Biotic stress (Lionel Navarro)

5:30 PM - 6 PM: Discussion with the invited speakers

6 PM - 7:30 PM: Discussion about the practical training session

8 PM: Diner

Friday July 13th

Session 4:
Transgenerational epigenetics & Plant breeding

9 AM - 10 AM: Arabidopsis transgenerational memory (Pierre Baduel)

10 AM - 10:45 AM: Plant breeding and epigenetics (Abdel Bendahmane)

10:45 AM - 11:15 AM: Coffee break

11:15 AM - 12:15 PM: Plant speciation (German Martinez)

12:15 PM: Lunch

1:30 PM - 3:30 PM: Practical session: DNA methylation analysis (Nicolas Bouché)

3:30 PM - 4 PM: Coffee break

4 PM - 5 PM: Epigenetics and transposable elements (Etienne Bucher)

5 PM - 5:30PM: Discussion with the invited speakers

5:30 PM - 6 PM: Closing discussion (Martin Crespi, Nicolas Bouché, Moussa Benhamed)

6 PM : End of the Summer School

Speakers

Pierre Baduel

Main research interests

Genome Evolution, Transposable Elements, Polyploidy

Selection of 3 major recent publications

Baduel P, Arnold B, Weisman CM, Hunter B, and Bomblies K (2016) Habitat-Associated Life History and Stress-Tolerance Variation in Arabidopsis arenosa. Plant Physiol. vol. 171, no. 1 pp. 437–451.

Baduel P, Hunter B, Yeola S, and Bomblies K (2017) A ticket to ride - Allele delivery by rail in secondary ruderal colonization by Arabidopsis arenosa. bioRxiv.

Wilton PR, Baduel P, Landon MM, and Wakeley J (2017) Population structure and coalescence in pedigrees : Comparisons to the structured coalescent and a framework for inference. Theor. Popul. Biol. vol. 115 pp. 1–12.

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IBENS

Fredy Barnèche

Main research interests

Determining how and when chromatin-based or epigenetically controlled mechanisms influence plant adaptive responses to environmental cues, with a specific emphasis on light conditions

Selection of 3 major recent publications

Nassrallah A, Rougee M, Bourbousse C, Drevensek S, Fonseca S, Iniesto E, Ait-Mohamed O, Deton-Cabanillas AF, Zabulon G, Ahmed I, Stroebel D, Masson V, Lombard B, Eeckhout D, Gevaert K, Loew D, Genovesio A, Breyton C, de Jaeger G, Bowler C, Rubio V and F Barneche. (2018) DET1-mediated degradation of a SAGA-like deubiquitination module controls H2Bub homeostasis. BioRxiv. doi: 10.1101/309732

Bourbousse C, Mestiri I, Zabulon G, Bourge M, Formiggini F, Koini MA, Brown SC, Fransz P, Bowler C, Barneche F. (2015) Light signaling controls nuclear architecture reorganization during seedling establishment. PNAS. 112(21):E2836-44

Bourbousse C., Ahmed I., Roudier F., Zabulon G., Blondet E., Balzergue S., Colot V., Bowler C. and F. Barneche. (2012) Histone H2B monoubiquitination facilitates the rapid modulation of gene expression during Arabidopsis photomorphogenesis. PLoS Genetics. 8: e1002825

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Moussa Benhamed

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IPS2
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Paris - Saclay

Thomas Blein

Main research interests

Quantitative regulation of plant root growth by lncRNAs

Selection of 3 major recent publications

Arabidopsis Heat Shock Transcription FactorA1b regulates multiple developmental genes under growth and stress conditions Waleed S. Albihlal, Igor Chernukhin, Thomas Blein, Ramona Persad, Irabonosi Obomighie, Martin Crespi, Ulrike Bechtold and Philip M. Mullineaux. J Exp Bot. 2018 in press.

A SWI/SNF Chromatin Remodelling Protein Controls Cytokinin Production through the Regulation of Chromatin Architecture. Jégu T, Domenichini S, Blein T, Ariel F, Christ A, Kim SK, Crespi M, Boutet-Mercey S, Mouille G, Bourge M, Hirt H, Bergounioux C, Raynaud C, Benhamed M. PLoS One. 2015;10(10):e0138276. doi: 10.1371/journal.pone.0138276

A miR169 isoform regulates specific NF-YA targets and root architecture in Arabidopsis. Sorin C, Declerck M, Christ A, Blein T, Ma L, Lelandais-Brière C, Njo MF, Beeckman T, Crespi M, Hartmann C. New Phytol. 2014;202(4):1197-211. doi: 10.1111/nph.12735.

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IPS2
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Filipe Borges

Main research interests

- Reprogramming and transgenerational silencing of transposable elements
- Evolution of epigenetic regulation in eukaryotic systems
- Single-cell genomics and epigenomics

Selection of 3 major recent publications

Borges, F., Parent, J.S., van Ex, F., Wolff, P., Martínez, G., Köhler, C., Martienssen, R.A.: Transposon-derived small RNAs triggered by miR845 mediate genome dosage response in Arabidopsis. Nature Genetics (2018)

Borges, F., Martienssen, R.A.: The expanding world of small RNAs in plants. Nature Reviews Molecular Cell Biology (2015)

Calarco, J.P.*, Borges, F.*, Donoghue, M.T.A, Van Ex, F., Jullien, P.E., Lopes, T., Gardner, R., Berger, F., Feijó, J.A., Becker, J.D., Martienssen, R.A.: Reprogramming of DNA methylation in pollen guides epigenetic inheritance via small RNA. Cell (2012) *These authors contributed equally

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http://www-ijpb.versailles.inra.fr/en/sgap/equipes/Epigenetics/index.html

Nicolas Bouché

Main research interests

DNA methylation – Plant epigenetics

Selection of 3 major recent publications

Brousse C, Liu Q, Beauclair L, Deremetz A, Axtell M.J. and Bouché N. A non-canonical plant microRNA target site. Nucleic Acids Research, 2014, 42(8):5270-9

Agorio A, Durand S, Fiume E, Brousse C, Gy I, Simon M, Anava S, Rechavi O, Loudet O, Camilleri C, Bouché N. An Arabidopsis Natural Epiallele Maintained by a Feed-Forward Silencing Loop between Histone and DNA. PLoS Genetics. 2017 Jan 6;13(1):e1006551

Corem S, Doron-Faigenboim A, Jouffroy O, Maumus F, Arazi T, Bouché N. Redistribution of CHH methylation and small interfering RNAs across the genome of tomato ddm1 mutants. The Plant Cell. 2018 in press

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http://www-ijpb.versailles.inra.fr/en/sgap/equipes/stress/index.htm

Cécile Bousquet-Antonelli

Main research interests

Post-transcriptional regulations of gene expression in response to heat stress;
- mRNA decay, storage, translation
- m6A readers, YTH domain proteins
- heat stress
- *Arabidopsis thaliana*

Selection of 3 major recent publications

Merret et al (2017) Plant Physiol 174: 1216

Merret et al. (2015) NAR 43: 4121-4132

Merret et al (2013) Cell Reports, 5: 1279-1293

+ Scutenaire J., Deragon JM., Jean V., Benhamed M., Raynaud C., Favory JJ, Merret R. and Bousquet-Antonelli C. et al. The YTH domain protein ECT2 from Arabidopsis thaliana is an m6A reader required for normal trichome branching (2018) In revision

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LABORATOIRE GENOME et DEVELOPPEMENT des PLANTES

Etienne Bucher

Main research interests

Epigenetics, transposable elements, plant breeding, genome assembly, evolution

Selection of 3 major recent publications

Daccord, N., Celton, J. M., Linsmith, G., Becker, C., Choisne, N., Schijlen, E., … Bucher, E. (2017). High-quality de novo assembly of the apple genome and methylome dynamics of early fruit development. Nature Genetics, 49(7), 1099–1106. https://doi.org/10.1038/ng.3886

Thieme, M., Lanciano, S., Balzergue, S., Daccord, N., Mirouze, M., & Bucher, E. (2017). Inhibition of RNA polymerase II allows controlled mobilisation of retrotransposons for plant breeding. Genome Biology, 18(1), 1–10. https://doi.org/10.1186/s13059-017-1265-4

Ito, H., Gaubert, H., Bucher, E., Mirouze, M., Vaillant, I., & Paszkowski, J. (2011). An siRNA pathway prevents transgenerational retrotransposition in plants subjected to stress. Nature, 472(7341), 115–9. http://www.ncbi.nlm.nih.gov/pubmed/21399627

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IRHS
Institut de Recherche en Horticulture et Semences

Christel Carles

Main research interests

Chromatin Dynamics and Development
Key words : Chromatin, transcriptional activation, plant development, stem cells, differentiation, flower morphogenesis, *Arabidopsis thaliana*

Selection of 3 major recent publications

J. Engelhorn, R. Blanvillain, C. Kröner, H. Parrinello, M. Rohmer, D. Pose, F. Ott, M. Schmid, C.C. Carles* (2017). Dynamics of H3K4me3 chromatin marks prevails over H3K27me3 for gene regulation during flower morphogenesis in Arabidopsis thaliana. Epigenomes, 1(2), 8; doi:10.3390/epigenomes1020008.

F. Moreau, E. Thevenon, R. Blanvillain, I. Lopez-Vidriero, J.M. Franco-Zorrilla, R. Dumas, F. Parcy, P. Morel, C. Trehin and C.C. Carles* (2016). The Myb-domain protein ULTRAPETALA1 INTERACTING FACTOR 1 controls floral meristem activities in Arabidopsis. Development, 143(7):1108-19. IF= 6,60

D.S. Ó'Maoiléidigh, B. Thomson, A. Raganelli, S.E. Wuest, P.T. Ryan, K. Kwaśniewska, C.C. Carles, E. Graciet, F. Wellmer (2015). Gene network analysis in Arabidopsis thaliana flower development through dynamic gene perturbations. Plant J. 83(2):344-58. IF= 6,58

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Lorenzo Concia

Main research interests

Plant epigenetics, replication timing program, chromosome conformation capture

Selection of 3 major recent publications

Concia, L., Brooks A.M., Wheeler E., Zynda G., Wear E.E., LeBlanc C., Song J., Lee T.J., Pascuzzi P.E., Martienssen R., Vaughn M.W., Thompson W., Hanley-Bowdoin L. (2018). Genome-Wide Analysis of the Arabidopsis thaliana Replication Timing Program. Plant Physiol. Advance online publication. doi: 10.1104/pp.17.01537

Wear E.E., Song J., Zynda G.J., LeBlanc C., Lee T.J., Mickelson-Young L., Concia L., Mulvaney P., Szymanski E.S., Allen G.C., Martienssen R.A., Vaughn M.W., Hanley-Bowdoin L., Thompson W.F. (2017) Genomic Analysis of the DNA Replication Timing Program during Mitotic S Phase in Maize (Zea mays) Root Tips. Plant Cell 29: 2126–2149

Zynda G.J., Song J., Concia, L., Wear E.E., Hanley-Bowdoin L., Thompson W.F., Vaughn M.W., (2017) Repliscan: a tool for classifying replication timing regions. BMC Bioinformatics 18: 362

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IPS2
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Martin Crespi

Main research interests

Our laboratory is interested in deciphering the mechanisms of action of regulatory non-coding RNAs in root growth and development. Our results support the notion that a variety of non-coding RNAs through their interaction with specific proteins (such as transcription factors, splicing or chromatin regulators) modulate the developmental adaptation of the root system to the environment

Selection of 3 major recent publications

Non coding transcription by alternative RNA polymerases dynamically regulates an auxin-driven chromatin loop. F. Ariel, T. Jegu, D. Latrasse, N. Romero-Barrios, A. Christ, M. Benhamed and M Crespi (2014) Molecular Cell 55(3):383-96

Long non-coding RNA modulate alternative splicing regulators in Arabidopsis. Bardou F, Ariel F, Simpson C, Romero-Barrios N, Laporte P, Balzergue S, Brown J and Crespi M (2014) Developmental Cell 30(2):166-76.

Splicing regulation by long noncoding RNAs. Romero-Barrios N, Legascue MF, Benhamed M, Ariel F, Crespi M. (2018) Nucleic Acids Res. doi: 10.1093/nar/gky095.

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Jose Gutierrez-Marcos

Main research interests

Research in my group focuses on the study of developmental plasticity in plants using molecular genetics, genomics and epigenomics approaches.

Selection of 3 major recent publications

Papareddy R, Dickinson HG, Boutiller K, VandenBosch KA, Ohki S, Gutierrez-Marcos JF (2014) Central Cell Derived Peptides Regulate Early Embryo Patterning in Flowering Plants. Science 344:168-172.

Wibowo A., Becker B., Marconi G., Durr J., Price J., Hagmann J., Papareddy R., Kageyama J., Becker J., Weigel D., and Gutierrez-Marcos JF. Exposure to environmental stress induces transient epigenetic memory responses (2016). eLife 5:e03457

Wibowo, A., Becker, C., Durr, J., Papareddy, R., Santain, Q., Spaepen, S., Hilton, S., Bending.,G., Schulze-Lefert, P., Weigel., D. and Gutierrez-Marcos, J. (2018) Incomplete reprogramming of cell-specific epigenetic marks during asexual reproduction leads to heritable phenotypic variation in plants. PNAS.

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David Latrasse

Main research interests

Plant epigenomics

Selection of 3 major recent publications

Latrasse D, Jégu T, Li H, de Zelicourt A, Raynaud C, Legras S, Gust A, Samajova O, Veluchamy A, Rayapuram N, Ramirez-Prado J, Kulikova O, Colcombet J, Bigeard J, Genot B, Bisseling T, Benhamed M, Hirt H. MAPK-triggered chromatin reprogramming by histone deacetylase in plant innate immunity. Genome Biology. (2017) Jul 6;18(1):131. doi: 10.1186/s13059-017-1261-8.

Latrasse D, Rodriguez-Granados N, Veluchamy A, Mariappan KG, Bevilacqua C, Crapart N, Camps C, Sommard V, Raynaud C, Dogimont C, Boualem A, Benhamed M, Bendahmane A. The Quest for Epigenetic Regulation Underlying Unisexual Flower in Cucumis Melo. Epigenetics and Chromatin. (2017) Jun 6;10:22. doi: 10.1186/s13072-017-0132-6. eCollection 2017.

Molitor A.*, Latrasse D*, Zytnicki M, Andrey P, Houba-Hérin N, Hachet M, Battail C, Del Prete S, Alberti A, Quesneville H, Gaudin V. The Arabidopsis hnRNP-Q Protein LIF2 and the PRC1 subunit LHP1 function in concert to regulate the transcription of stress-responsive genes. The Plant Cell (2016).

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Christine Lelandais-Brière

Main research interests

Root and nodule development, small RNA and epigenetics

Selection of 3 major recent publications

The sunflower genome provides insights into oil metabolism, flowering and Asterid evolution. H Badouin1, J. Gouzy1, CJ Grassa1, F Murat, SE Staton, L Cottret, C Lelandais-Brière, et al. (2018) Nature online, doi:10.1038/nature22380

Noncoding RNAs, emerging regulators in root endosymbioses. Lelandais Briere C., Moreau J., Hartmann C., Crespi M. (2016). Mol Plant Microbe Interact. 29(3):170-180

The small RNA diversity from Medicago truncatula roots under biotic interactions evidences the environmental plasticity of the miRNAome. Formey D, Sallet E, Lelandais-Brière C, Ben C, Bustos-Sanmamed P, Niebel A, Frugier F, Combier J, Debellé F, Hartmann C, Poulain J, Gavory F, Wincker P, Roux C, Gentzbittel L, Gouzy J, Crespi M. (2014) Genome Biol. 15(9):457.

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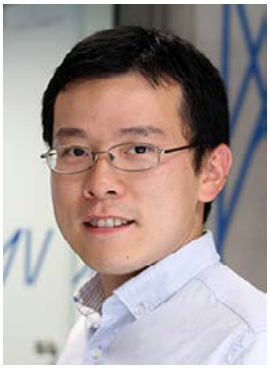
Chang Liu



Main research interests

Plant chromatin structure and dynamics

Selection of 3 major recent publications

Wangsheng Zhu, Bo Hu, Claude Becker, Ezgi Süheyla Doğan, Kenneth Wayne Berendzen, Detlef Weigel and Chang Liu. (2017) Altered chromatin compaction and histone methylation drive non-additive gene expression in an interspecific Arabidopsis hybrid. Genome Biology 18:157.

Chang Liu, Ying-Juan Cheng, Jia-Wei Wang, and Detlef Weigel. (2017) Prominent topologically associated domains differentiate global chromatin packing in rice from Arabidopsis. Nature Plants 3, 742–748.

Xiuli Bi, Ying-Juan Cheng§, Bo Hu, Xiaoli Ma, Rui Wu, Jia-Wei Wang and Chang Liu. (2017) Non-random domain organization of the Arabidopsis genome at the nuclear periphery. Genome Research 27, 1162-1173.

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EBERHARD KARLS
UNIVERSITÄT
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Germán Martinez

Main research interests

Epigenetics, RNA silencing, stress, development

Selection of 3 major recent publications

Martinez et al. Paternal easiRNAs regulate parental genome dosage in Arabidopsis. Nature Genetics (2018)

Martinez et al. tRNA-derived small RNAs target transposable element transcripts. Nucleic Acids Research (2017)

Martinez et al. Silencing in sperm cells is directed by RNA movement from the surrounding nurse cell. Nature Plants (2016).

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Ortrun Mittelsten Scheid

Main research interests

Plant genetics and epigenetics, chromatin dynamics in connection with stress, development and DNA repair

Selection of 3 major recent publications

Dubin M, Mittelsten Scheid O, Becker C (2018) Transposons: a blessing curse. Current Opinions in Plant Biology 42: 23-29

Probst AV, Mittelsten Scheid O (2015) Stress-induced structural changes in plant chromatin. Current Opinions in Plant Biology 27: 8-16

Pikaard CS, Mittelsten Scheid O (2014) Epigenetic regulation in plants. Cold Spring Harbor Perspectives in Biology 6: pii: a019315

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Jean Molinier

Main research interests

DNA repair and epigenomics

Selection of 3 major recent publications

D. Córdoba-Cañero, V. Cognat, RR. Ariza, T. Roldán Arjona, J. Molinier (2017). Dual control of ROS1-mediated active DNA demethylation by the DNA DAMAGE BINDING protein 2 (DDB2). Plant J. 6 :1170-1181.

C. Schalk, V. Cognat, S. Graindorge, T. Vincent, O. Voinnet, J. Molinier (2017). Small RNA-mediated repair of UV-induced DNA lesions by the DNA DAMAGE BINDING protein 2 and ARGONAUTE 1. PNAS. 14 : E2965-E2974.

C. Schalk, S. Drevensek, A. Kramdi, M. Kassam, I. Ahmed, V. Cognat, S. Graindorge, M. Bergdoll, N. Baumberger, D. Heintz, C. Bowler, P. Genschik, F. Barneche, V. Colot, J. Molinier (2016). DNA DAMAGE BINDING PROTEIN 2 (DDB2) Shapes the DNA Methylation Landscape. Plant Cell. 9 : 2043-2059.

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Aline V. Probst

Main research interests

Role of histone variants in chromatin organization and function

Selection of 3 major recent publications

Simon L, Rabanal FA, Dubos T, Oliver C, Lauber D, Poulet A, Vogt A, Mandlbauer A, Le Goff S, Sommer A, Duborjal H, Tatout C, Probst AV. (2018) Genetic and epigenetic variation in 5S ribosomal RNA genes reveals genome dynamics in Arabidopsis thaliana. Nucleic Acids Research. doi.org/10.1093/nar/gky163

Duc C, Benoit M, Détourné G, Simon L, Poulet A, Jung M, Veluchamy A, Latrasse D, Le Goff S, Cotterell S, Tatout C, Benhamed M, Probst AV. (2017), Arabidopsis ATRX Modulates H3.3 Occupancy and Fine-Tunes Gene Expression. Plant Cell. 29(7):1773-1793.

Duc C, Benoit M, Le Goff S, Simon L, Poulet A, Cotterell S, Tatout C and Probst AV (2015) The histone chaperone complex HIR maintains nucleosome occupancy and counterbalances impaired histone deposition in CAF-1 complex mutants. Plant J, 81(5): 707-22

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GReD
genetics
reproduction
& development

Leandro Quadrana

Main research interests

Plant epigenetics and epigenomics
Transposable elements

Selection of 3 major recent publications

Quadrana, L., and Colot, V. (2016). Plant Transgenerational Epigenetics. Annu Rev Genet 50, 467-491.

Quadrana, L., Bortolini Silveira, A., Mayhew, G.F., LeBlanc, C., Martienssen, R.A., Jeddeloh, J.A., and Colot, V. (2016). The Arabidopsis thaliana mobilome and its impact at the species level. Elife 5.

Quadrana L., Almeida J., Asís R., Duffy T., Dominguez P. G., Bermúdez L., Conti G., Silva J. V. C. da, Peralta I. E., Colot V., Ası R., Peralta I. E., Colot V., Conti G., Corre J. V, Asurmendi S., Fernie A. R., Rossi M., Carrari F. (2014 Natural occurring epialleles determine vitamin E accumulation in tomato fruits. Nat. Commun. 5: 4027.

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Hervé Vaucheret

Main research interests

Epigenetics - RNA silencing

Selection of 3 major recent publications

Elvira-Matelot, Hachet, Shamandi, Comella, Saez-Vasquez, Zytnicki, Vaucheret, (2016a). Arabidopsis RNASE THREE LIKE2 Modulates the Expression of Protein-Coding Genes via 24-Nucleotide Small Interfering RNA-Directed DNA Methylation. Plant Cell 28, 406-425.

Elvira-Matelot, Bardou, Ariel, Jauvion, Bouteiller, Le Masson, Cao, Crespi, Vaucheret (2016b). The Nuclear Ribonucleoprotein SmD1 Interplays with Splicing, RNA Quality Control, and Posttranscriptional Gene Silencing in Arabidopsis. Plant Cell 28, 426-438.

Shamandi, N., Zytnicki, M., Charbonnel, C., Elvira-Matelot, E., Bochnakian, A., Comella, P., Mallory, A.C., Lepere, G., Saez-Vasquez, J., and Vaucheret, H. (2015). Plants Encode a General siRNA Suppressor That Is Induced and Suppressed by Viruses. PLoS Biol 13, e1002326.

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Jonathan Weitzman

Main research interests

We study how infectious agents develop intricate mechanisms to hijack the genetic and epigenetic machinery of their host cells to change phenotypic states. We investigate how the intracellular parasite *Theileria* hijacks host signaling pathways to maintain cell transformation. We recently identified epigenetic events in the host cell nucleus that are induced by the intracellular parasite and we also study epigenetic regulators of the parasite genome. The *Theileria*-infected leukocytes serve as a model to explore the plasticity of cellular phenotypes, the determinants of cell identities and the evolutionary strategies of interacting cellular systems.

Selection of 3 major recent publications

Marsolier J*, Pineau S*, Medjkane S, Perichon M, Yin Q, Flemington E, Weitzman MD, Weitzman JB. OncomiR addiction is generated by a miR-155 feedback loop in Theileria-transformed leukocytes. (2013) PLoS Pathogens 9(4):e1003222. doi: 10.1371/journal.ppat.1003222

Cheeseman K, Weitzman JB. Host-parasite interactions: an intimate epigenetic relationship. (2015) Cell Microbiol. 2015 17:1121-32. doi: 10.1111/cmi.12471

Marsolier J, Perichon M, DeBarry JD, Villoutreix BO, Chluba J, Lopez T, Garrido C, Zhou XZ, Lu KP, Fritsch L, Ait-Si-Ali S, Mhadhbi M, Medjkane S, Weitzman JB. Theileria parasites secrete a prolyl isomerase to maintain host leukocyte transformation. (2015) Nature 520:378-82

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