Societat Catalana de BIOLOGIA

V JORNADA DE CROMATINA I EPIGENÈTICA

Organitzada per la Secció de Biologia Molecular de la Societat Catalana de Biologia (SCB)

amb el Barcelona Chromatin Club (BCC)

INSTITUT D´ESTUDIS CATALANS

Carrer del Carme, 47

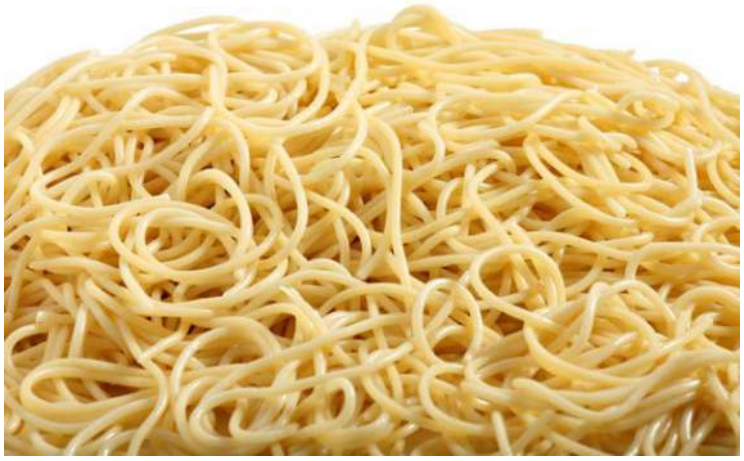
Barcelona

10 de març de 2015

V ANNUAL CHROMATIN AND EPIGENETICS SYMPOSIUM

Organized by the Molecular Biology section of the Catalan Society of Biology (SCB)
—Albert Jordan—

and the Barcelona Chromatin Club (BCC)
—Sonia Forcales & Marcus Buschbeck—



March 10, 2015

IEC: carrer del Carme, 47, Barcelona

Prat de La Riba hall

Sponsored by:

Institut d'Estudis Catalans

Covalab

Active Motif

IMPPC

PROGRAM

8.20-8.50 ***Registration and documentation pickup***

8:50 ***Opening***

Session I. *Chair: Marian Martínez Balbás (IBMB-CSIC)*

9.00-9.20 **15min+5**
Lorenzo Pasquali (IGTP-IJC)
3D chromatin structure and cis regulatory networks in human pancreatic islets

9.20-9.40 **15min +5**
Lourdes Campos (Eng.Quim.-UPC)
Underwinding and kinking DNA with HMG proteins

9.40-10.00 **15min +5**
Francesc Piferrer (ICM-CSIC)
Environmental effects during early development mediated by epigenetic mechanisms in fish

10.00-10:20 **15min +5**
Bernhard Payer (CRG-PRBB)
X-chromosome reactivation during mouse development and stem cell reprogramming

10.20-10:40 **15min +5**
Albert Jordan (IBMB-CSIC-PCB)
Specificities on the genomic distribution of human histone H1 subtypes

10:40-11.20 ***Coffee break and poster session sponsored by Covalab***

Session II. *Chair: Alfred Cortés (CRESIB)*

11.20-11.40 **15min +5**
Ma José Barrero (CMRB-PRBB)
Determinants of H1 recruitment during differentiation

11.40-12.00 **15min +5**
Joan-Ramon Daban (UAB)
The energy components of stacked chromatin layers explain the morphology, dimensions and mechanical properties of metaphase chromosomes

12.00-12.20 **15min +5**
Alejandro Vaquero (PEBC-IDIBELL)
A new role for SIRT6 in the regulation of NF-kB

12.20-12.40 **15min +5**
Joaquim Roca (IBMB-CSIC-PCB)
The topology of DNA at the point centromere of budding yeast

12.40-13.00 **15min +5**
Montserrat Corominas (IBUB-UB)
Gene expression, transcriptional stability and histone modifications

13.00-13.20 **15min +5**
Jordi Bernués (IBMB-CSIC-PCB)
Functional analysis of Drosophila melanogaster Histone H1

13.30-15:00 Lunch at restaurant

Session III-BCC. Non-coding RNA and heterochromatin

Chair: Sonia Forcales (IMPPC)

15.00-15.10 Sponsor' talk **7min +3**
Sarantis Chlamydas (Active Motif)
Active Motif's toolbox for non-coding RNA studies

15.10-15.40 **25min +5**
Gunnar Schotta (Ludwig Maximilian Universität, Munich, Germany)
Establishment and maintenance of heterochromatin requires Atrx

15.40-16.10 **25min +5**
Natalia Azpiazu (CBM-CSIC)
Contribution of transcription factors to heterochromatin assembly in Drosophila

16.10-16.20 Short talk **7min +3**
Attila Nemeth (University of Regensburg, Germany)
Characterisation of the RNA- and DNA-binding domains of the heterochromatin regulator protein Tip5

16.20-16.30 Short talk **7min +3**
Céline Duc (CNRS, Clermont Université, INSERM, France)
Histone H3 dynamics in heterochromatin organization

16:30-17.00 Coffee break and poster session sponsored by Active motif

Session IV. *Chair: Jorge Ferrer (IDIBAPS)*

17:00-17.20 **15min +5**
Ángel Barco (IN-UMH/CSIC)
Genomic landscape of histone acetylation in the adult hippocampus: Implications in neuroplasticity and brain disorders

17.20-17.40 **15min +5**
Miguel A. Peinado (IMPPC)
Insights into the epigenetic architecture of the cancer cell

17.40-18.00 **15min +5**
Esteban Ballestar (PEBC-IDIBELL)
Interplay between transcription factors and DNA methylation changes in myeloid differentiation

18.00-18.20 **15min +5**
Melike Lakadamyali (ICFO)
Super-resolution imaging of nucleosome organization in vivo

18.20-18.40 **15min +5**
Miguel Beato (CRG-PRBB)
Chromatin dynamics and nuclear ATP synthesis

18.40-19:00 **15min +5**
Guillaume Filion (CRG-PRBB)
Promoters interpret the chromatin context in different ways

19.00-19.20 **15min +5**
Marc A. Marti-Renom (CRG-PRBB, CNAG-PCB)
Does color has a structure? Modeling 3D domains of the fly genome

19.25 Farewell and meet together for a beer

Secretaries of SCB:

Mariàngels Gallego and Maite Sánchez
Societat Catalana de Biologia
C/ Maria Aurèlia Capmany, 14-16, 08001 Barcelona.
Tel. 933 248 584; A/e: *scb@iec.cat*

Organized by:

Albert Jordan Vallès
Coordinator of the Molecular Biology section of the SCB
Dept. Molecular Genomics, Institut de Biologia Molecular de Barcelona (IBMB-CSIC), Parc Científic de Barcelona
A/e: *albert.jordan@ibmb.csic.es*

Coorganized by:

Sonia Forcales and Marcus Buschbeck
Coordinators of the Barcelona Chromatin Club
Institut de Medicina Predictiva i Personalitzada del Càncer (IMPPC)
A/e: *bcc@imppc.org*

ABSTRACTS
ORAL COMMUNICATIONS

Session I.

Lorenzo Pasquali (IGTP-IJC)
3D chromatin structure and cis regulatory networks in human pancreatic islets

---

UNDERWINDING AND KINKING DNA WITH HMG PROTEINS

Raquel Sánchez-Giraldo, Francisco Acosta-Reyes, Nuria Saperas y **J. Lourdes Campos**
Departament d'Enginyeria Química, Universitat Politècnica de Catalunya, Barcelona, 08028, Spain

http://macrom.upc.edu Lourdes.campos@upc.edu

The high mobility group HMG proteins act as architectural proteins that affect cellular functions by modulating chromatin structure and thereby gene expression in eukaryotic cells. HMGB proteins are one of the three members of this family and are defined by their DNA binding motifs, HMGB1 contains two DNA binding domains, box A and box B, which have little sequence specificity but remarkable abilities to underwind and bend DNA. Here we will present the structure of two HMGB1 box A bound to an AT-rich DNA fragment determined by x-ray crystallography at 2 Å resolution. Both of them collaborate in an unusual configuration where two domains stack together and intercalate to the same CG base pair generating highly kinked DNA. This is a novel mode of DNA recognition for HMGB proteins and reveals a mechanism by which structure-specific HMG boxes kink and underwind linear DNA.

ENVIRONMENTAL EFFECTS DURING EARLY DEVELOPMENT MEDIATED BY EPIGENETIC MECHANISMS IN FISH

Francesc Piferrer, Dafni Anastasiadi, Noelia Díaz, Ivet Sucarrats

Institute of Marine Sciences (ICM-CSIC). Passeig Marítim, 37-49, 08003 Barcelona

In contrast to mammals, fertilization and embryonic development are external in fish. Thus, fish are ideal models for studying how environmental information received during early development is integrated through epigenetic mechanisms. Epigenetic modifications can affect gene expression permanently and this may influence the potential of an organism to respond to these environmental cues later in life, with consequences not only for the sustainability of natural populations in a scenario of global change but also for optimizing animal production. Recently, we showed that in one-year-old European sea bass the DNA methylation levels in the promoter of gonadal aromatase were higher when the fish were exposed to elevated temperature from 0 to 60 days post fertilization (dpf) compared to fish raised at natural temperature (Navarro-Martín et al. 2011. *PLoS Genetics* 7(12): e1002447). In order to narrow down the developmental period which is crucial for the establishment of DNA methylation marks by temperature, we studied global DNA

methylation in larvae having experienced high temperature exposure at different time-points and for variable duration up to 60 dpf. Moving on to another perspective, we have also studied the effects of temperature treatment during larval development, as well as the ones of farming conditions in the muscle and testis of 3-year-old fish. We detected differentially methylated cytosines (DMC) in both tissues and both experiments, most of which neighboring genes and their regulatory elements, while attempting to correlate these data with their corresponding transcriptomic profile, with regard to establishing a functional relationship. Furthermore, we conducted experiments to explore the potential implication of histone modifications in the regulation of expression of key genes. In addition, we are currently examining the DNA methylation levels of a panel of 40 functionally important genes in gonads and muscle of immature, reproductively active and senescent fish. Our experiments together highlight the significance of the early environment an organism experiences for the establishment of epigenetic marks with long lasting phenotypic consequences. *Supported by MINECO grant AGL2013-41047-R "Epifarm" to FP.*

X-CHROMOSOME REACTIVATION DURING MOUSE DEVELOPMENT AND STEM CELL REPROGRAMMING

Bernhard Payer

Gene Regulation, Stem Cells and Cancer Programme, Centre for Genomic Regulation (CRG), Barcelona, Spain

Female mammals inactivate one of two X-chromosomes to achieve equal gene dosage with males with only one X. This X-inactivation process is closely linked to the differentiated state and is reversed in pluripotent stem cells, during development and in the germ cell lineage, where both X-chromosomes are active. X-reactivation thereby serves three major functions:

1. Switch between different forms of X-inactivation during embryonic development, where initially only the paternal X-chromosome is inactivated (imprinted). After X-reactivation, the inactivated X is chosen randomly, allowing to alleviate effects of X-linked mutations in females.
2. Resetting of the inactive X in the germ cell lineage to allow inheritance of an active X to the next generation, a requirement for embryonic development.
3. As distinct epigenetic hallmark of naïve pluripotent stem cells – commonly used to assess the quality of human pluripotent stem cells.

How the X-chromosome is reactivated and how this is developmentally regulated is largely unclear.

In a candidate approach, we studied the role of the germ line determinant PRDM14 and the noncoding RNA gene *Tsix*, a known regulator of X-inactivation. We found that both genes control X-reactivation in mouse blastocyst embryos and that PRDM14 has important functions for X-reactivation and self-renewal of induced pluripotent stem cells (iPSCs). We elucidated the X–reactivation mechanism of PRDM14 in which it represses the X-inactivation regulator *Rnf12* through recruitment of polycomb repressive complex 2 (PRC2). Furthermore, we found that Tsix enables PRDM14 to bind to the X-inactivation master regulator *Xist*, which needs to be repressed to allow X-reactivation. Therefore we have shown that PRDM14 and Tsix are key factors in the X-reactivation process and we are now pursuing further approaches to gain a more comprehensive picture of this epigenetic reprogramming event, which will have wider implications on regenerative and reproductive medicine.

SPECIFICITIES ON THE GENOMIC DISTRIBUTION OF HUMAN HISTONE H1 SUBTYPES

Andrea Izquierdo-Bouldstridge, Lluis Millan-Ariño, Regina Mayor, Alberto Bustillos, Jean-Michel Terme & Albert Jordan

Institut de Biologia Molecular de Barcelona (IBMB-CSIC), Barcelona, Spain
albert.jordan@ibmb.csic.es

Seven linker histone H1 variants exist in human somatic cells (H1.1 to H1.5 being expressed in a replication-dependent manner, whereas H1.0 and H1X are replication-independent), with distinct prevalence depending on the cell type analyzed and along differentiation. H1 bind to linker DNA contributing to higher order chromatin compaction. In addition, H1 seems to be actively involved in the regulation of gene expression. It is not well known whether the different variants have specific roles, are distributed differentially along the genome, or regulate specific promoters. We explored this by inducible shRNA-mediated knock-down of each of the H1 variants. Thus, specific phenotypes are observed in breast cancer cells depleted of individual histone H1 variants. Moreover, knock-down of each H1 variant alters expression of a different, reduced subset of genes, with more genes being repressed than activated, suggesting a local positive role of H1 on gene expression control. Using variant-specific antibodies to H1 and HA-tagged recombinant H1 variants expressed in breast cancer cells, we have investigated the distribution of six H1 variants in promoters and genome-wide. H1 is depleted at promoters depending on its transcriptional status and differs between variants. We show that histone H1 variants are not distributed uniformly along the genome and there are differences between variants, H1.2 being the one showing the most specific pattern and strongest correlation with low gene expression. H1.2 is enriched at chromosomal domains characterized by low GC content and is associated with lamina-associated domains. Meanwhile, other variants are associated with higher GC-content, CpG islands and gene-rich domains and chromosomes. Moreover, we have found H1.0 to be enriched at nucleolus-associated DNA repeats and chromatin domains, whereas H1X is associated with coding regions, RNA polymerase II-enriched regions and hypomethylated CpG islands. Further, H1X accumulates within constitutive or included exons and retained introns, and towards the 3' end of expressed genes. We conclude that H1 variants are not distributed evenly across the genome and may participate with some specificity in chromatin domain organization or gene regulation.

Session II.

DETERMINANTS OF H1 RECRUITMENT DURING DIFFERENTIATION

Maria J. Barrero
Spanish National Cancer Research Center (CNIO),
C/ Melchor Fernández Almagro, 3. 28029 Madrid, Spain.
mjbarrero@cnio.es

Chromatin structure plays fundamental roles in the regulation of gene expression during development and differentiation. We have previously reported a critical role for linker histone H1 in the silencing of pluripotency-related genes during the differentiation of human embryonic stem cells. We now explore the molecular mechanisms that facilitate H1 recruitment to pluripotency-related genes to mediate their silencing. Alterations of these regulatory mechanisms cause important defects in the differentiation of human pluripotent cells.

THE ENERGY COMPONENTS OF STACKED CHROMATIN LAYERS EXPLAIN THE MORPHOLOGY, DIMENSIONS AND MECHANICAL PROPERTIES OF METAPHASE CHROMOSOMES

Joan-Ramon Daban
Departament de Bioquímica i Biologia Molecular, Facultat de Biociències, Universitat Autònoma de Barcelona.
joanramon.daban@uab.cat

The measurement of the dimensions of metaphase chromosomes in different animal and plant karyotypes prepared in different laboratories indicates that chromatids have a great variety of sizes which are dependent on the amount of DNA that they contain. However, all chromatids are elongated cylinders that have relatively similar shape proportions (length to diameter ratio ~13). To explain this geometry it is considered that chromosomes are self-organizing structures formed by stacked layers of planar chromatin and that the energy of nucleosome-nucleosome interactions between chromatin layers inside the chromatid is ~3.6×10^{-20} J per nucleosome, which is the value reported by other authors for internucleosome interactions in chromatin fibers. Nucleosomes in the periphery of the chromatid are in contact with the medium; they cannot fully interact with bulk chromatin within layers and this generates a surface potential that destabilizes the structure. Chromatids are smooth cylinders because this morphology has a lower surface energy than structures having irregular surfaces. The elongated shape of chromatids can be explained if the destabilizing surface potential is higher in the telomeres (~0.16 mJ/m^2) than in the lateral surface (~0.012 mJ/m^2). The results obtained by other authors in experimental studies of chromosome mechanics have been used to test the proposed supramolecular structure. It is demonstrated quantitatively that internucleosome interactions between chromatin layers can justify the work required for elastic chromosome stretching (~0.1 pJ for large chromosomes). The high amount of work (up to ~10 pJ) required for large chromosome extensions is probably absorbed by chromatin layers through a mechanism involving nucleosome unwrapping. Chromosomes can be considered as hydrogels with a lamellar liquid crystal organization. These hydrogels have outstanding elastic properties because, in addition to the covalent bonds of the DNA backbone, they have attractive ionic interactions between nucleosomes that can be regenerated when the chromosome suffers a deformation. This self-healing capacity has been observed in nanotechnology studies of other hydrogels stabilized by ionic interactions. In the cell, this may be useful for the maintenance of chromosome integrity during mitosis. A complete description of this work can be found in reference (1).

(1) JR. Daban, J. Royal Soc. Interface, 11 (2014) 20131043.

A NEW ROLE FOR SIRT6 IN THE REGULATION OF NF-KB

Alejandro Vaquero
Chromatin Biology Lab, Cancer Epigenetics and Biology Program (PEBC), Bellvitge Biomedical Research Institute (IDIBELL) , Av Gran via de l´Hospitalet, L´Hospitalet de Llobregat, Barcelona, SPAIN, E. mail : avaquero@idibell.cat

Detecting and efficiently responding to potentially fatal environmental changes is a major challenge for all organisms. Said changes, such as calorie restriction, are intimately associated to metabolic fluctuations and certain forms of stress (e.g. oxidative or genotoxic) (1). Over the past decade, evidence has suggested that the members of the Sirtuin family are major players in sensing and coordinating the responses geared to chromatin and to mitochondria(2-5). The importance of the role of Sirtuins in these processes is reflected by their involvement in a wide range of human pathologies including cancer, endocrine-associated pathologies such as diabetes, cardiovascular diseases, and

neurodegenerative diseases, among others (6). Mammals have seven Sirtuins (SirT1- 7). These exhibit great functional diversification, which has led to two different enzymatic activities (NAD^+-dependent deacetylation and ADP-ribosylation of proteins), a myriad of substrates and a highly diverse pattern of cellular localization (7). Sirtuins SirT1 to 7 have adapted during evolution by acquiring new roles, including deacetylation of histone and non-histone proteins in gene expression, cell survival and metabolic regulation (8). Among Sirtuins, SirT6 is a nuclear protein involved in both metabolic homeostasis and genomic stability through a role in DNA damage signaling and repair as well as in telomere structure (9-10). Interestingly, it has been proposed that SirT6 regulates the majority of these processes through deacetylation of a histone mark, H3K9Ac (10). SirT6 acts as a tumor suppressor and *SIRT6*$^{-/-}$ mice show an accelerated aging phenotype associated to overactivation of the Nf-kB pathway (11). Thus, SirT6 regulates the ability of Nf-kB to induce the expression of a set of specific genes. Here we will provide evidence that suggest a novel mechanism for SirT6 in the regulation of Nf-kB-dependent stress response though a functional link to the histone methyltransferase Suv39h1.

References

1. Vaquero, A., and Reinberg, D., Genes Dev, 26, 5505, 2009.
2. Schwer B and Verdin E. Cell Metab., 7, 104, 2008
3. Vaquero, A., Sternglanz, R., and Reinberg, D., Oncogene., 26, 5505, 2007.
4. Imai S, et al, Nature, 403, 795-800, 2000
5. Landry J, et al. Proc Natl Acad Sci U S A. 97, 5807, 2000.
6. Finkel T, Deng CX, Mostoslavsky R. Nature. 460, 587, 2009.
7. Vaquero A. Int J Dev Biol.53, 303, 2009.
8. Martínez-Redondo, P., and Vaquero, A. Genes & Cancer 4, 148, 2013
9. Mostoslavsky, R. et al., Cell, 124, 315, 2006
10. Michishita E, et al. Nature, 452, 492-6. 2008
11. Kawahara TL, et al. Cell, 136, 62-74, 2009

THE TOPOLOGY OF DNA AT THE POINT CENTROMERE OF BUDDING YEAST

Ofelia Díaz-Ingelmo, Belén Martínez, Xavier Fernández, Joana Segura, Antonio Valdés, Joaquim Roca
Institut de Biología Molecular de Barcelona-CSIC. Parc Cientific de Barcelona. joaquim.roca@ibmb.csic.es

The structure of the centromeric nucleosomes that contain the histone variant cen-H3 is controversial since recent years. Several experimental observations indicate that these nucleosomes do not have histone octamers, but cenH3/H4/H2B/H2A hemisomes. Other observations suggest that DNA wraps in a right-handed orientation in such hemisomes, although $(cenH3/H4/H2B/H2A)_2$ octamers are found to be left-handed as in conventional nucleosomes. To this regard, we have conducted a deep analysis of the DNA topology at the single cen-H3 nucleosome that occupies the point centromere of budding yeast. Our results indicate that the intrinsic architecture of the yeast centromere firmly stabilizes a DNA linking number difference of +0.6 units; and that this topology is determined by the protein complexes that interact with the CDEII and CDEIII sequences, but not the CDEI sequence of the CEN DNA. We propose a model, in which the CBF3 complex bound to CDEIII enforces a positive DNA supercoil without requiring the intervening hemisome bound to CDEII to be inherently right-handed.

Montserrat Corominas (IBUB-UB)
Gene expression, transcriptional stability and histone modifications

---

Jordi Bernués (IBMB-CSIC-PCB)
Functional analysis of Drosophila melanogaster Histone H1

Session III.

Sponsor' talk
Sarantis Chlamydas (Active Motif)
Active Motif's toolbox for non-coding RNA studies

Gunnar Schotta (Ludwig Maximilian Universität, Munich, Germany)
Establishment and maintenance of heterochromatin requires Atrx

---

Natalia Azpiazu (CBM-CSIC)
Contribution of transcription factors to heterochromatin assembly in Drosophila

---

CHARACTERISATION OF THE RNA- AND DNA-BINDING DOMAINS OF THE HETEROCHROMATIN REGULATOR PROTEIN TIP5

Attila Nemeth

Department of Biochemistry III Biochemistry Center Regensburg
University of Regensburg , Universitaetsstr. 31, D-93053 Regensburg
Germany

The Nucleolar Remodelling Complex is involved in centromeric, telomeric and rDNA heterochromatin formation and its activity can be regulated by non-coding RNA. This regulation is mediated by Tip5, the large subunit of NoRC. Tip5 contains a variety of nucleic acid-binding domains, including a TAM domain, four AT-hooks, and a newly discovered extended AT-hook (eAT-hook). The involvement of these domains in facilitating Tip5's function will be discussed and the possible role of the eAT-hook as a novel RNA-binding motif will be highlighted.

HISTONE H3 DYNAMICS IN HETEROCHROMATIN ORGANIZATION

Céline Duc

Génétique, Reproduction et Développement, UMR CNRS 6293, Clermont Université, INSERM U1103, 24 Avenue des Landais, BP 80026, 63171 Aubière Cedex, France

Eukaryotic DNA is organized in chromatin that packages the long nuclear DNA molecules and functions as carrier of epigenetic information. Local chromatin features such as nucleosome composition impact the organization of higher-order chromatin structures that occupy specific positions in nuclear space. A paradigm for such higher-order organization is the formation of repressive chromatin domains termed heterochromatin, which play a critical role in genome stability by preventing expression of repetitive elements and their illegitimate recombination. We are investigating the role of H3 histone variants and their post-translational modifications in heterochromatin organization and function. For this purpose, we use *Arabidopsis thaliana* as a model system, in which heterochromatin domains cluster into cytological visible chromocenters in interphase nuclei. Hence, they can be easily tracked microscopically. We showed that defective histone deposition in plants lacking either the Chromatin Assembly Factor 1 (CAF-1) or the HIR (Histone Regulator) complex affects nucleosome occupancy and transcriptional silencing of heterochromatic repeats. Furthermore, by investigating formation of chromocenters during post-germination development, we found that enrichment of repetitive elements in repressive marks H3K9me2 and H3K27me1 and the canonical histone H3.1 precedes chromocenter formation. During chromocenter formation, levels of the canonical histone H3.1 increase specifically at heterochromatic repeats. This H3.1 enrichment and chromocenter formation require the CAF-1 chaperone complex but not the HIR complex, demonstrating a critical function for CAF-1-mediated histone deposition and concomitant modification of histone tails in chromocenter formation. Taken together, our results illustrate the importance of histone chaperones for histone handing, correct nucleosome composition and histone modifications and ultimately higher-order chromatin organization and function.

Session IV.

Ángel Barco (IN-UMH/CSIC)
Genomic landscape of histone acetylation in the adult hippocampus: Implications in neuroplasticity and brain disorders

---

INSIGHTS INTO THE EPIGENETIC ARCHITECTURE OF THE CANCER CELL.

Joaquin Custodio, Mar Muñoz, Eva Musulen, Eva Martinez-Balibrea, Jaume Farres, Miguel A. Peinado.
Institute of Predictive and Personalized Medicine of Cancer (IMPPC), Institute Germans Trias i Pujol (IGTP), Campus Can Ruti, Badalona; Autonomous University of Barcelona (UAB), Bellaterra.

The control and fine-tuning of gene expression is a complex process orchestrated by multiple players, including transcription factors, epigenetic modifications and chromatin architecture. The cancer phenotypes are largely explained by aberrant expression of multiple genes and therefore characterization of the mechanisms involved in gene regulation is essential to understand the grounds of malignant transformation and tumor progression.

In a genome-wide screening in human colorectal cancer we identified epigenetic alterations and aberrant regulation of a cluster of genes of the AKR1B family. We have characterized the epigenetic landscape of the region and investigated the relationships with the expression of the corresponding genes and the encoded proteins. We show that deregulation of members of the AKR1B1 gene family affects most colorectal cancers, resulting in a disruption of the retinoic acid metabolic pathway and affecting cancer cell biology. Analysis of AKR1B1 gene family and other enzymes involved in the metabolism of retinoic acid may have diagnostic and prognostic applications in colorectal cancer.

INTERPLAY BETWEEN TRANSCRIPTION FACTORS AND DNA METHYLATION CHANGES IN MYELOID DIFFERENTIATION

Esteban Ballestar
Chromatin and Disease Group, Cancer Epigenetics and Biology Programme (PEBC), Bellvitge Biomedical Research Institute (IDIBELL), Barcelona, Spain. E-mail: eballestar@idibell.cat

Cell differentiation from progenitors involves sequential decision steps where transcription factors play a fundamental role. One of the best studied systems for cell differentiation is hematopoietic differentiation where the sets of transcription factors involved in each step are very well characterized. Transcription factors, different elements of post-transcriptional control and epigenetic modifications (histone modifications and DNA methylation) form complex networks in driving differentiation. In these processes, DNA methylation plays a key role by stabilizing gene activity during cell-fate decisions. By examining differentiation of closely related cell types it is possible to dissect the specific role and relationship between transcription factors and their connections with epigenetic machinery. One of such examples is terminal differentiation from monocytes into macrophages, dendritic cells (DCs) and osteoclasts (OC). These differentiation processes not only are relevant under physiological conditions but also in the context of disease, like in various autoimmune diseases. This presentation will focus on our DNA methylation studies on differentiation towards OC, DC and macrophages and the interplay between transcription factors and elements of the DNA methylation (and demethylation) machinery. Our results open up perspectives on the elements that target these DNA (de)methylation enzymes but also provide novel targets for potential modulation of the differentiation commitment towards these different related cell types.

Melike Lakadamyali (ICFO)
Super-resolution imaging of nucleosome organization in vivo

Miguel Beato (CRG-PRBB)
Chromatin dynamics and nuclear ATP synthesis

Guillaume Filion (CRG-PRBB)
Promoters interpret the chromatin context in different ways

DOES COLOR HAS A STRUCTURE? MODELING 3D DOMAINS OF THE FLY GENOME

Marc A. Marti-Renom, ICREA Research Professor
Genome Biology Group, Centre Nacional d'Anàlis Genòmica (CNAG, http://cnag.org), Barcelona, Spain.
Structural Genomics Group, Centre de Regulació Genòmica (CRG, http://crg.cat), Barcelna, Spain.

We will introduce the TADbit computational library for modeling and analyzing the structure genomes and genomic domains. TADbit, which has been applied to the modeling the fly genome, uses interaction data [1] to build three-dimensional (3D) models of genomic domains. The results indicate that the colors of the chromatin [2], that is, its protein occupancy, determine structural properties of the genome.

[1] Dekker, J., Marti-Renom, M. A., & Mirny, L. A. (2013). Nature Reviews Genetics, 14(6), 390–403. doi:10.1038/nrg3454
[2] Filion, G. J., et al. (2010). Cell, 143(2), 212–224. doi:10.1016/j.cell.2010.09.009

1) GENOME-WIDE DNA METHYLATION CHANGES DUE TO TEMPERATURE AND FARMING CONDITIONS IN THE EUROPEAN SEA BASS

Dafni Anastasiadi and Francesc Piferrer

Institute of Marine Sciences (ICM-CSIC). Passeig Marítim, 37–49, 08003 Barcelona

The environment an organism experiences during early development may have a long lasting impact mediated by epigenetic mechanisms. From one hand, temperature is an environmental factor shown to be related with changes in DNA methylation levels and lasting alterations of gene expression. From the other hand, farming conditions result in changes in the gene expression level in fish. Here, we surveyed genome-wide DNA methylation changes in adult European sea bass (*Dicentrarchus labrax*) related to temperature and/or farming conditions using next generation sequencing (NGS) technology. In order to study temperature effects, 3-year-old fish raised at low (17^{o}C) or at high (21^{o}C) temperature during the thermosensitive period were used and for the effects of farming fish sampled in the wild were compared to farmed fish raised at low temperature. We employed Reduced Representation Bisulfite Sequencing (RRBS) to measure DNA methylation levels, where, in brief, after digestion with a methylation-sensitive restriction enzyme *MspI* and bisulfite conversion, libraries are constructed and sequenced by Illumina HiSeq2000. Bioinformatic analysis was adapted to a non-model species genome and performed using R and RRBS-specific packages. Temperature was found to affect ~3500 cytosines in testis and ~12000 cytosines in muscle. Farming conditions affected more CpG sites than only temperature, with testis presenting ~4000 differentially methylated CpGs (DMC) and muscle presenting ~15000 DMCs. The majority of the DMCs in both comparisons were located close to genes and their regulatory elements, as well as in a distance of up to 5000 bp upstream the transcription start site (TSS). In this study, we have shown that the environmental conditions during the early development of sea bass produce changes on DNA methylation that are detected later in life. We are currently using RNA-seq to determine possible alterations in gene expression associated with these changes in DNA methylation. *Supported by MINECO grant AGL2013-41047-R "Epifarm" to FP.*

---

2) EPIGENETIC AND EXPRESSION PROFILE OF KLK LOCUS CONTRIBUTE TO THYROID CANCER CLASSIFICATION

Raquel Buj, Mireia Roca, Anna Díez-Villanueva, Izaskun Mallona, Miquel A. Peinado1, Mireia Jordà

Institute of Predictive and Personalized Medicine of Cancer (IMPPC). Ctra. de Can Ruti, Camí de les Escoles s/n, 08916. Badalona, Barcelona, Spain.
RB e-mail: rbuj@imppc.org

Thyroid cancer (TC) is the most common endocrine neoplasia and although most patients survive the disease, there is a need of new preoperative markers for early diagnosis and prognostic assessment. In this regard, many authors have proposed the mutagenic analysis as an important tool to stratify the risk and to determine the extent of surgery in TC patients.
It is well known that the two main driver mutations in TC ($BRAF^{V600E}$ and RAS) are mutually exclusive and produce distinct signaling effects that give rise to different transcriptional outputs. Furthermore, they are associated with distinct clinicopathological characteristics.

In our previous DNA methylation genome-wide study (Mancikova et al., 2014) we identified numerous epigenetic alterations in TC. In particular, we found that the promoter region of KLK10 was specifically hypomethylated in BRAF-mutated tumors, which correlated with KLK10 overexpression. KLK10 is a member of the Tissue Kallikrein family (KLK), a group of 15 secreted serine-peptidases that cluster together in the 19q13.3-4 region. Interestingly, many members of these family are involved in several cancers, but nothing is known regarding thyroid cancer.
The analysis of KLK gene cluster using TCGA data revealed that not only KLK10 but all the cluster displayed a specific epigenetic and transcriptional profile strongly associated with the mutational status. Taking advantage of the different behavior of KLK gene cluster in BRAF and RAS tumors, we have developed a decision tree that allows to classify no mutated tumors as BRAF- or RAS-like, which reflects more accurately their underlying signaling, and could lead to improve their pathological classification as well as the management of the disease.

---

3) MUSCLE CELL IDENTITY REQUIRES LINEAGE-SPECIFIC DNA DEMETHYLATION

Elvira Carrió[1], Alessandro Magli[2], Mar Muñoz[1], Miquel Angel Peinado[1], Rita Perlingeiro[2] and Mònica Suelves[1]
1 Institute of Predictive and Personalized Medicine of Cancer, Badalona, Spain
2 Lillehei Heart Institute, Department of Medicine, University of Minnesota, Minneapolis, Minnesota, USA

Skeletal muscle stem cells enable the formation, growth, maintenance, and regeneration of skeletal muscle throughout life. Under pathological conditions, muscle stem cells regenerative potential is compromised being therefore myogenic-inducible embryonic stem (ES) or inducible pluripotent stem (iPS) cells new therapeutic sources of myoblast progenitors. DNA methylation is an epigenetic modification associated with transcriptional repression essential for shaping and stabilizing cell fate decisions. In the present study we addressed the DNA methylation dynamics of the principal genes orchestrating the myogenic determination and differentiation programs by comparing ESCs with primary myoblasts (in a quiescent, activated and differentiated state), as well as with induced Pax7-ES-derived myogenic precursors. The results showed a common DNA methylation signature required to acquire and maintain the muscle-cell identity. In addition, the integrative analysis of DNA methylation profiles together with public ChIP-seq data revealed different epigenetic dynamics taking place during myogenesis according to the CpG content of the underlying DNA sequence. In one hand, CpG island promoters of myogenic determination genes were unmethylated and showed a bivalent poised state declined toward the positive mark H3K4me3 upon myogenic differentiation. On the other hand, a myogenic-specific DNA demethylation of CpG poor myogenic regulatory regions was observed upon skeletal muscle-lineage commitment consistent with an active or poised transcriptional state modulated by polycomb repressive complex 2. Interestingly, the down-regulation of the cytidine deaminase Apobec2 in muscle progenitor cells reduced the myogenic-associated DNA demethylation, abolishing the expression of differentiation markers and impairing muscle differentiation. All together, these findings revealed the epigenetic dynamics orchestrating the myogenic process, and led to the identification of muscle epimarkers that could be used to ensure the efficient and safe reprogramming of ES- and iPS-derived myogenic progenitors for future therapeutic applications in muscle pathologies.

Acknowledgements
This project has been supported by Ministerio de Ciencia e Innovación (SAF2009-08128 and SAF2012-37427) and from Generalitat de Catalunya (2009 SGR1356). EC is a FPI Fellow (MCINN).

---

4) CHROMATIN ORGANIZATION AND TRANSCRIPTIONAL REGULATION OF A PERICENTROMERIC REPETITIVE ELEMENT IN COLORECTAL CANCER

Gabrijela Dumbovic, Johanna K. Samuelsson, Sergio Alonso, Sonia Forcales and Manuel Perucho

We identified a frequently hypomethylated genomic region in colorectal tumors that belongs to the family of a moderately repetitive pericentromeric element called SST1. 15% of the tumors analyzed exhibited an age-dependent demethylation that follows our "wear & tear" model linking aging with cancer through gradual demethylation. However, 7% of the patients displayed a more severe age-independent demethylation.

Methylated SST1 shows low H3K27me3 and high H3K9me3 levels, while demethylated SST1 co-occurs with an increase of H3K27me3, lower levels of H3K9me3 and increased transcription. This upregulated SST1 transcription in the presence of an increased polycomb-repressive mark (H3K27me3) was puzzling. To gain insight on the mechanisms underlying this peculiar transcription, a DNA demethylation treatment with 5-aza-2'-deoxycytidine (AZA) was performed in combination with the inhibition of the PRC2 complex (GSK126). In the absence of a functional PRC2, the expression of SST1 elements was higher than in cells treated only with AZA. However, when AZA treatment was followed by Trichostatin A (TSA), which inhibits histone deacetylases, the SST1 expression was much more increased. This epigenetic reprogramming also occurs in ovary and breast cancer cell lines and importantly in primary colorectal tumors.

Further characterization of the RNA originating from SST1 elements shows that it is predominantly non-polyA, transcribed by RNA polymerase II and it is mainly associated to the chromatin, which reinforces a non-coding role. The results gathered in this study indicate that DNA methylation and histone deacetylation contribute to the silencing of the SST1 elements in different tissues. Our hypothesis is that upon demethylation in cancer (by a yet unidentified mechanism), the SST1 elements acquire the polycomb repressive mark H3K27me3 in an attempt to maintain the region silenced. However, this mechanism cannot fully repress SST1 expression as DNA methylation does. Further disruption of histone deacetylation at hypomethylated SST1 region in normal colon epithelium could lead to aberrant overexpression of SST1 elements, with yet unknown consequences.

---

5) JMJD3 HISTONE DEMETHYLASE PARTICIPATES IN TGFB-TRIGGERED TRANSCRIPTION ELONGATION ON NEURAL GENES AND ENHANCERS

Raquel Fueyo[1], Conchi Estarás[2], Sergi Lois[3], Xavier de la Cruz[3,4] and Marian Martínez-Balbás[1]

[1]Instituto de Biología Molecular de Barcelona (IBMB- CSIC), Parc Científic de Barcelona. [2]Regulatory Biology Laboratory, Salk Institute for Biological Studies, La Jolla, CA 92037-1099 [3]Passeig de la Vall d'Hebron, 119; Barcelona, Spain. [4]Institut Català per la Recerca i Estudis Avançats (ICREA). Barcelona 08018, Spain

RNA polymerase II (RNAPII) transcription is an extremely regulated multi-step process in which several proteins and signaling pathways are involved. Previous studies have pointed to TGFß pathway as a major regulator of neural development. Recently, our lab has demonstrated the interaction of SMAD3 (main effector of the pathway) with the histone demethylase JMJD3 in mice neural stem cells and the importance of this cooperation in neural differentiation *in vivo*. Here, we show that JMJD3 activates the neural program not only acting on promoters but operating on TGFß-triggered coding gene elongation and enhancer activation.

6) COULD MICRORNA MODULATION OVERCOME SENESCENCE PROCESS IN SAMP8 STRAIN?

C.Griñán-Ferré, Veronica Palomera-Avalos, María J. Alvarez-López, M. Cosín-Tomás, A. Camins, P. Kaliman and M. Pallàs
Dep. Farmacologia i Quim. Terapèutica. Facultad de Farmacia. Instituto de Biomedicina, Universidad de Barcelona.

Aging is a multifaceted process that characterized by an intricate and irreversible accumulation of physiological changes and is associated with an increase in transcriptional noise, aberrant production and maturation of many mRNAs. Epigenetic role in control of transcriptional mechanisms are one of the earliest emerging fields in senescence processes. These aging-associated transcriptional signatures seem to be controlled by non-coding RNAs, as microRNAs (miRNA). These miRNAs are small molecules (22 nucleotides approximately) that regulate gene expression by binding to its target messenger RNA (mRNA) inhibiting its translation, or, less frequently, promoting its degradation. In brain, miRNAs play an important role in the developing nervous system, neurogenesis, synapsis and plasticity, etc. Because progressive neurological dysfunction and neurological disorders such as Alzheimer's disease (AD) are a key aspect of human aging, miRNAs are indispensable actors for explain the impairment in brain functions such as learning, memory and emotion regulation.

The spontaneous senescence-accelerated P8 mouse model (SAMP8) were established via phenotypic selection of the AKR/J mouse strain and exhibits age-related deterioration in learning and memory abilities compared with mice with nonaccelerated aging that were established from the same AKR/J strain (SAMR1). It is assumed that the abnormality in senescence and memory function observed in SAMP8 mice depend on several factors, such as morphological, neurochemical and neuropathological changes and oxidative stress. It is feasible that differences among SAM strain could be explained on the basis of epigenetics.

For this reason, we focus on SAMP8 epigenetic alterations through the 84 mature miRNAs screening expression in hippocampus of females SAMR1 and SAMP8 (1 and 9 months) by using the *miScript*® miRNA PCR Array-Neurological Development and Disease miRNA PCR Array (Qiagen). These miRNAs were chosen because they are differentially expressed during the progression of neurological diseases.

The results of microarray analysis showed that family of let-7, miR-26b-5p, miR-29a-3p, miR-29c-3p, miR-146a-5p, miR-151a-3p, miR-181a-5p miR-191-5p, miR-298, miR-485-5p were all differentially expressed depending on the strain and age. The mirDB is an online database for miRNA target prediction and functional annotations and its analysis showed that these microRNAs may be involved in the emotional disorders, inflammation, apoptosis, neurogenesis, regulation of epigenetical enzymes and ß-amyloid processing. At the same time, we have analyzed the APP processing that is considered a key event in the pathological cascade leading to Alzheimer's disease. Western blotting and qPCR analysis showed that BACE1, ADAM10, sAPPα and sAPPß levels correlated with changes in key role miRNAs on this pathway. Results were validates by quantitative real-time PCR. Data obtained pointed out several miRNAs that participated as regulators of aging and neurodegeneration in females SAMP8 mice.

ACKNOWLEDGEMENTS: SAF2012-39852 "Ministerio de Educación y Ciencia". Spain

7) WANDERER, AN INTERACTIVE VIEWER TO EXPLORE DNA METHYLATION AND GENE EXPRESSION DATA IN HUMAN CANCER

Anna Díez-Villanueva, Izaskun Mallona and Miguel A. Peinado

Institut de Medicina Predictiva I Personalitzada del Càncer (IMPPC) and Institut d'Investigació en Ciències de la Salut Germans Trias i Pujol
Badalona

The Cancer Genome Atlas (TCGA) initiative is an ambitious project aiming to accelerate our understanding of the molecular basis of cancer by providing large-scale genome information from thousands of clinically characterized cancer samples. However, wet lab experimentalists have very limited access to these data because sophisticated bioinformatics skills are required to manage and analyze such large datasets. Hence, development of interfaces facilitating the visualization and analysis of the information to non-bioinformaticians is essential to get a broad exploitation of this gigantic effort.

To overcome this limitation we developed Wanderer, a very simple and intuitive web tool allowing real time access and visualization of gene expression and DNA methylation profiles from TCGA data using gene targeted queries.

For any given gene selected by the investigator, the tool provides detailed individual profiles of gene expression, exon by exon, and DNA methylation of all the probes inside or in the vicinity of the gene. Graphs for normal and tumor samples from any of the 19 available TCGA datasets are readily produced. Summarizing plots and tables are also generated, allowing further data analysis or representation using any software the investigator is used to (e.g.: Excel or any other spreadsheet or graphing tool). In addition, statistical analysis is applied to identify differential gene expression or DNA methylation between normal and tumor samples at either the single exon or the DNA methylation probe level, respectively. The tool allows local navigation and zoom in/out within the region of interest, as well as simple graph customization. Resulting graphs and tables may be downloaded and an application programming interface (API) allows data sharing, automatable query of multiple instances and direct linkage from external servers.

---

8) PARENTAL ASYMMETRY OF EU- AND HETEROCHROMATIC HISTONE MODIFICATIONS IN THE ARABIDOPSIS SEED ENDOSPERM

Jordi Moreno-Romero, Juan Santos-González and Claudia Köhler
Department of Plant Biology, Uppsala BioCenter, Swedish University of Agricultural Sciences and Linnean Center of Plant Biology, Uppsala, Sweden. jordi.moreno@slu.se

Seed development in flowering plants is initiated after a double fertilization event that leads to the formation of the two fertilization products, the zygotic embryo and the endosperm, which are surrounded by the maternally derived seed coat. The endosperm is an ephemeral tissue that nourishes the embryo, similar as the placenta does in mammals. Parental genomes in the endosperm are marked by differential DNA methylation and are therefore epigenetically distinct. This epigenetic asymmetry is established in the gametes and maintained after fertilization by unknown mechanisms. To decipher the mechanisms that maintain epigenetic asymmetry after fertilization, we have established genome-wide profiles of eu-and heterochromatic histone modifications and DNA methylation in the early endosperm. Using maternal and paternal sequence polymorphisms we were able to differentiate the parental origin of those modifications. The data reveal that Polycomb Repressive Complex2 (PRC2)-mediated H3 lysine 27 trimethylation (H3K27m3) has a

centromeric and pericentromeric distribution in the endosperm, unlike the euchromatic distribution of this silencing mark in vegetative tissues. Several DNA hypomethylated transposable elements (TEs) are targeted by H3K27m3 in the endosperm, revealing a general role of PRC2 to target and possibly silence TEs. Importantly, H3K27m3 is differentially distributed in the parental genomes and follows the differential DNA methylation patterns of the parental genomes, suggesting that parental-specific H3K27m3 distribution is a consequence of differential DNA methylation. We furthermore show that paternal-specific H3K27m3 is co-localized with the heterochromatic marks H3 lysine 9 dimethylation (H3K9m2) and H3 lysine 27 monomethylation (H3K27m1), suggesting that H3K27m3 supports heterochromatin formation of the paternal genome after fertilization.

---

9) A CBX8-CONTAINING POLYCOMB COMPLEX FACILITATES GENE ACTIVATION DURING ES CELL DIFFERENTIATION

Anna Palau, Catherine Creppe, Roberto Malinverni, Vanesa Valero and Marcus Buschbeck

Institut de Medicina Predictiva i Personalitzada del Càncer (IMPPC), Ctra de Can Ruti, Camí de les Escoles s/n 08916 Badalona (Barcelona). apalau@imppc.org

Polycomb proteins play an essential role in maintaining the repression of developmental genes in self-renewing embryonic stem cells. The exact mechanism allowing the derepression of polycomb target genes during cell differentiation remains unclear. Here, we show that several differentiation genes transiently recruit a Cbx8-containing Polycomb repressive complex (PRC) 1 during their early activation. Depletion of Cbx8 partially impairs the transcriptional activation of these genes. Prolonged gene activation results in eviction of PRC1 despite persisting H3K27me3. We further demonstrate that the exchange of Cbx7 for Cbx8 occurring during differentiation is required for effective gene activation. Taken together our results establish a function for a Cbx8-containing complex in facilitating the transition from a Polycomb-repressed chromatin state to an active state.
As this affects several key regulatory differentiation genes this mechanism contributes to the robust execution of differentiation programs.

---

10) WNT-PATHWAY MODULATION IN SAMP8: IS THERE A ROLE IN NEUROGENESIS DURING AGEING PROCESS?

Veronica Palomera-Avalos, C.Griñán-Ferré, S. Bayod, A.M Canudas, M. Pallàs
Dep. Farmacologia i Quim. Terapèutica. Facultad de Farmacia. Instituto de Biomedicina, Universidad de Barcelona.

In the mature nervous system, the canonical Wnt (Wnt/ß-catenin) signaling pathway is involved in learning and memory processes, modulating neuronal function, hippocampal neurogenesis and synaptic plasticity. Therefore, downregulation of Wnt signaling could be involved in the cognitive decline associated with aging and also with neurodegenerative diseases such as Alzheimer's disease. Here, we examined Wnt signaling in hippocampus of the model of accelerated senescence SAMP8 mice, as well as in its control-strain SAMR1 mice. Due to the possible participation of metabolic stress in neurodegenerative process, we also were interested in the influence of a high fat diet (as a metabolic stressor) in Wnt signalling and its role in neurogenesis. We found that SAMP8 showed with age an increase of Dickkopf-1 protein levels, in addition to GSK-3 activation. Consequently, higher ß-catenin phosphorylation at $Ser^{33,37}$ and Thr^{41}, which promotes its degradation, along with a decrease of Active ß-catenin (ABC) in the nucleus, were observed in SAMP8. Finally, we determined the expression levels of chromatin modifying enzymes in SAMR1 and SAMP8 in

hippocampus. These results indicated lower neurogenesis gated to SAMP8 in reference to SAMR1 at early ages. When a stressing metabolic stimulus was added (mice feed by high fat diet), we observed an impairment in working cognitive skills in novel object recognition test, accompanied by changes in Wnt/neurogenesis markers.

ACKNOWLEDGEMENTS: SAF2012-39852 "Ministerio de Educación y Ciencia". Spain

---

11) EPIGENETIC CONTROL OF REGENERATION IN *Drosophila*

Vizcaya, E; Fernández-Guerrero, M; Serras, F and Corominas, M.
Departament de Genètica, Facultat de Biologia and Institut de Biomedicina (IBUB), Universitat de Barcelona
Av. Diagonal 645, 08028 Barcelona, España
elenavizcayamolina@gmail.com

Regeneration is the ability to restore damaged or lost body parts and tissues. This process is highly regulated and requires a combination of signaling and chromatin events to promote gene expression changes and tissue reprogramming. However, the mechanisms underlying transcriptional regulation during regeneration remain unclear. Chromatin modifying enzymes are crucial modulators in transcriptional regulation and cell memory. Thus, epigenetic modifications are important players in the activation and silencing of genes underlying the ability for a cell to rebuild the lost part. Here we study the role of histone methylation and acethylation role in *Drosophila* imaginal disc regeneration. *Drosophila* is an excellent model to approach this question as imaginal discs have the intrinsic competence to restore itself after injury giving rise to normal adult structures. The levels of chromatin modifications have been analyzed in regenerating wing discs through Western blots and immunostaining. Moreover, experiments using heterozygous mutant backgrounds for chromatin modifying enzymes, such as histone methyltransferases (HMTs), acetyltransferases (HATs), histone demethylases (HDMTs), and deacetylases (HDACs), demonstrate that these enzymes are essential during wing disc regeneration.

PARTICIPANTS

Nom	Cognom	Institució
Erik	Abner	IBMB - CSIC
Ildem	Akerman	IDIBAPS
Rocío	Amoretti	UB
Dafni	Anastasiadi	ICM-CSIC
Ester	Anton	UAB
Foix	Aragones	IMPPC
Gemma	Armengol	UAB
Alba	Azagra	PEBC (IDIBELL)
Ferran	Azorín	CSIC
Natalia	Azpiazu	CBM-CSIC
Esteban	Ballestar	PEBC-IDIBELL
Cristina	Bancells	CRESIB-ISGLOBAL
Angel	Barco	UMH-CSIC
Maria Jose	Barrero	CNIO
Alex	Bayona	IBMB-CSIC
Miguel	Beato	CRG-PRBB
Malte	Beringer	CRG
Jordi	Bernués	IBMB-CSIC
Carles	Bonet-costa	IBMB-CSIC
Laia	Bosch	IDIBELL
Raquel	Buj Gómez	IMPPC
Marcus	Buschbeck	IJC
Alcides	Bustillos	IBMB-CSIC
Oriol	Cabré Fabré	UAB
J.lourdes	Campos	UPC
Cristina	Camprubí	-
Elvira	Carrio Gaspar	IMPCC
Anna	Casas	IRB-CSIC
Joan Pau	Cebrià Costa	fIMIM
Paul	Chammas	CRG
Andrea	Chicano	UAB
Sarantis	Chlamydas	Active Motif
Carles	Ciudad	UB
Paula	Climent	IRB
Laura	Coch	IRB
Montserrat	Corominas	UB
Alfred	Cortés	CRESIB-ISGlobal
Joaquin	Custodio	IMPPC
Joan-Ramon	Daban	UAB
Ofelia	Diaz	IBMB
Céline	Duc	CNRS, France
Gabrijela	Dumbovic	IMPPC
Gustavo	Egea	UB

M Lluisa	Espinàs	IBMB-CSIC
David	Expósito	UB
Elisa	Fanunza	IBMB-CSIC
Xavier	Fernandez	IBMB-CSIC
Marc	Fernández	
Irene	Fernandez-Duran	University of Edinburgh
Elisabet	Figuerola	Hospital Sant Joan de Deu
Guillaume	Filion	CRG
Sonia	Forcales	IMPPC
Ujué	Fresán	IBMB-CSIC
Raquel	Fueyo	IBMB-CSIC
Alejandra	Garcia	IBMB
Soledad	Gómez	Fundació Sant Joan de Déu
Christian	Griñan	UB
Carmen	Hernandez	IMPPC
Ane	Iturbide	fIMIM
Andrea	Izquierdo	IBMB-CSIC
Mireia	Jordà	IMPPC
Albert	Jordan	IBMB-CSIC
Andreas	Lackner	CRG
Melike	Lakadamyali	ICFO
Oriol	Llorà Batlle	CRESIB - ISGlobal
Roberto	Malinverni	IMPPC
Anna	Mallol	UAB
Izaskun	Mallona	IMPPC
Anna	Manzano	UB
Berta	Martin	IMPPC
Marian	Martínez-Balbás	IBMB-CSIC
Belen	Martinez	IBMB-CSIC
Marc A.	Marti-Renom	ICREA-CNAG-CRG
Aina Maria	Mas	IRB
David	Mas	UAB
Irene	Miguel-Escalada	IDIBAPS
Olga	Moreno	IBMB-CSIC / IRB Barcelona
Jordi	Moreno	Swedish University of Agricultural Sciences
Mar	Muñoz	IMPPC
Ana Mª	Muñoz-Mármol	Hospital Germans Trias i Pujol
Attila	Nemeth	University of Regensburg, Germany
Sergio	Niñerola	Universidad de Barcelona
Yaiza	Núñez	IMPPC
Rafael	Oliva	IDIBAPS
Ulf	Orom	Max Planck Institute for Molecular Genetics
Modesto	Orozco	Institut for Research in Biomedicine
Anna	Palau	IJC
Mercè	Pallàs	UB
Veronica	Palomera	UB
Stella	Pappa	IBMB-CSIC
Laura	Pascual	IMIM

Lorenzo	Pasquali	IGTP-IJC
Bernhard	Payer	CRG
Miguel A.	Peinado	IMPPC
Sandra	Peiro	IMIM
Núria	Pell Vidal	IBMB-CSIC
Sílvia	Pérez Lluch	CRG
Salvador	Pérez-Montero	IBMB-CSIC
Francesc	Piferrer	ICM-CSIC
Inmaculada	Ponte	UAB
Roser	Pujol	UAB
Jessica	Querol	FIMIM
Natalia	Ramírez	PEBC (IDIBELL)
George	Rasti	IDIBELL
Helena	Raurell	IGTP-IJC
Laia	Ribas	ICM-CSIC
Maria Àngels	Rigola	UAB
Joaquim	Roca	IBMB-CSIC
Maria	Rodríguez	IBMB-CSIC
Meritxell	Rovira	IDIBAPS
Núria	Rovira	CRESIB-ISGLOBAL
Marina	Ruiz	UB
Alexandra	Santanach	CRG
Núria	Saperas	ETSEIB, UPC
Zaida	Sarrate	UAB
Eva	Satovic	IRB Barcelona
Gunnar	Schotta	Ludwing Maximilian Universität, Germany
Joana	Segura	IBMB-CSIC
Gemma	Serra	fIMIM
Priyanka	Sharma	CRG
Carolina	Soriano	IMIM
Pere	Suau León	UAB
Juan Antonio	Subirana	UPC-IMIM
Mònica	Suelves	IMPPC
Elisabet	Tintó	CRESIB - ISGlobal
Antonio	Valdés	IBMB-CSIC
Alex	Vaquero	IDIBELL
Elena	Vizcaya	UB
Juergen	Walther	IRB
Irene	Zapata	UB