**11th course on epigenetics, 2015, Institute Curie, Paris, FR. 11-18.03.2015**

**Andrew Moore**- BioEssays, DE. Editor

1. “Read abstracts from the bottom”

**Saadi Khochbin**- Molecular Basis of post-meiotic male genome programming, Institute albert Bennoit, FR.

1. Claims that histones can be extracted from the chromatin by mechanical pressure caused by protein-protein interactions on both sides of the histone

**Leonid Mirny**- Physical pronciples of genome folding, Harvard, MIT, USA

1. Presented the inference problem- inferring the polymer model from HiC encountersignals
2. Simulates polymers with hydrodynamic forces inside a cylinder
3. Compares the resulting encounter frequencies to the experimental data

**Maxim Dahan** – Single molecule approach for probing the nuclear architecture, Institute Curie

1. Develops new microscopy techniques
2. Examines DNA target search by proteins and measures their dynamics, mean first passage time, etc…
3. Target finding happens up to 100 times faster than expected by pure diffusion
4. Did not offer a search strategy which is new, but the 1D sliding-3D diffusion model

**Edith Heard-** X-chromosome inactivation: a model for monoallelic gene expression, Institute Curie

1. Absence of X-inactivation is leathal
2. Xist orchestrate the inactivation process in mouse ESC.
3. Some genes where found to be active on the inactive X chromosome.
4. Some genes get switched on again after inactivation
5. Paternal X is always the one which shuts down (at first it is not random inactivation), but during development it is reactivated and then a random inactivation takes place
6. Looping out of the densely packed X chromosome might be the mechanism which helps genes escape inactivation on the silent X

**Francois Spitz** - Managing long range distance (regulatory) relationship, European molecular Biology Laboratory, DE

1. During embryogenesis in mouse, after 5 days almost all cells are committed.
2. Enhancers are located 01-1 Mb from the initiation site
3. Characterizes regulatory elements

**Arturo Londono Vallejo**- Epigenetics at the tips, Institute Curie

1. Telomeres length are heterogeneous
2. What defines difference in length?
3. There is some evidence for the epigenetic effect on telomeres length
4. **LF**: recombination at the telomeres
5. The distance between nucleosomes at the telomeres is shorter than in other parts of the chromosomes
6. There is a T loop (or D loop) at the end of the telomere
7. Late replicating telomeres are located close to the nuclear membrane (lamina associating?)
8. **LF**: recruitment process in biology
9. The homologeous recombination process is facilitated using APB which serve as a stable basis on which telomere attach and exchange genomic content
10. LF: telomere position effect
11. Long range interactions at the telomeres disappear with cell age

**Patrick Heun** – Dissecting the centromere specific histone CENP-A in drosophila, Welcome trust center for biology, UK

1. A sequence of 125bp motif is enough to define the centromere in drosophila
2. In human this motif is much longer
3. However, one element is conserved, CSE4 protein in many species
4. Fusion of chromosome can lead to dicentromeric structure
5. Microtubules connect to both centromeres in this case
6. **LF**: timing in biological processes
7. it is unknown how is the second centromere gets cancelled

**Valerie Borde**- chromatin and recombination in meiosis, I curie

1. works on budding yeasts
2. the structure of the chromosome is thought to be a main axis and loops stemming from it

**Doug Higgs** – Switching genes on and off, Oxford, UK

1. How do genes switched on and off during lineage commitment?
2. 90% of the genes gets transcribed-> are functional
3. There are about 2 million enhancers but the number of genes is much larger
4. **LF**: cis/trans elements
5. “super enhancers” – occupy larger genomic sections and regulate genes which determine cell identity
6. Transcription factors are enriched in position of super enhancers
7. Enhancers work cooperatively to compensate inactivation
8. He finds no synergistic effect for super enhancers, nor is there an additive effect
9. **LF**: enhancers and how they regulate genes
10. as genes become more transcribed they become more methylated
11. Higgs claims that there aren’t any “super enhancers”

**General comments:**

1. **LF**: [European Research Area](http://ec.europa.eu/research/era/index_en.htm)(ERA)
2. **LF**: [Euraxess](http://ec.europa.eu/euraxess/) (website)
3. **LF**: [Epigenesys](http://www.epigenesys.eu/en/) (network)
4. **LF**: single cell epigenetic workshop June 22-23