EU-India S&T Cooperation Days
4-6 November 2009 New Delhi
www.euindiacoop.org

Thursday 5 November
EU-India PARTNERING EVENT

Theme: *Health*

RESEARCHER'S NAME: Làszlò Tora RESEARCHER'S ORGANISATION: Institut de Génétique et de Biologie Moléculaire et Cellulaire (IGBMC)

CNRS, INSERM, Université de Strasbourg (UdS), Illkirch, France

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SEVENTH FRAMEWORK PROGRAMME

RESEARCH CENTRE

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Resources made available to the groups:

-DNA sequencing, high throughput sequencing

-peptide synthesis, mass spectrometry,

-antibody facilities and services

- cell culture facilities and services

-baculovirus overexpression service

-transgenic animals, ES cell facility,

-crystallography, NMR, electromicroscopy,

-imaging platform and service

-bioinformatics platform

The **IGBMC** is a mixed research unit of CNRS/INSERM/University of Strasbourg with approximately 600 people, in **44 research groups** including 300 researchers, post-doctoral fellows and PhD students. IGBMC is structured in 5 **departments**, which in turn are supported by 5 **technological platforms**, and 12 highly developed common **facilities**, occupies an eminent position in the landscape of biological and medical research in France, both due to its unique structure and its research of international reputation.

The current activities of the IGBMC cover a spectrum of disciplines on the following issues:

-Regulation of basal and activated RNA polymerase II transcription

-Biochemistry, genetics and molecular biology of nuclear receptors

-Structure determination of proteins and nucleic acids

-Biology and molecular genetics of different cancers

-Human molecular genetics

-Developmental and molecular biology of *C. elegans, Drosophila*, zebrafish and mouse

- Neurobiology

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Functional and genome wide characterization of chromatin remodelling complexes in normal, embryonic stem and cancer cells

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One of the most appealing questions in eukaryotic mRNA transcription regulation are :

a) how stem cells can regulate their transcription networks to maintain their pluripotency and how these regulatory networks change when stem cells differentiate to various cell types or when they become cancer cells.

b) how activators can transmit their signals to the general transcription machinery to stimulate transcription in the context of a chromatin environment.

Stem cells have recently become the focus of intensive research, because they may be used in the future to generate cells and tissues for therapeutic purposes.

To answer the above exposed two fundamental questions, in our present project we propose:

a) to perform the biochemical and cellular characterization of chromatin remodelling complexes in normal, emryonic stem cells (ESCs) and cancer cells by using **proteomics** to identify a) the subunit composition of these complexes b) the normal ES and cancer cell interactome of chromatin remodelling complexes c) the post-translational modifications of the identified subunits

b) to identify direct binding sites in the genome of these chromatin remodelling complexes in normal, ES and cancer cells by using chromatin immunoprecipiattion coupled **high throughput sequencing** (ChIP-seq)

c) to identify direct target genes for these complexes in the genome in normal, ES and cancer cells by using knockdown approaches coupled to **global transcriptomic** analyses

d) to identify deregulated pathways, networks and hubs regulated by the chromatin remodelling complexes in ESCs and cancer cells, by using **system biology** including **high throughput** and **newly developed bioinformatics techniques, tools and platforms**.

The present project will be built on the combined strengths of the partners, including molecular biology, chromatin, cell and cancer biology, systems biology, genome research and bioinformatics.

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Potential partner expertise:

Eukaryotic transcription regulation,

Cell biology, stem cell biology,

Cancer biology,

.rge scale genome research and bioinformatic

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