STUDYING DNA LOOP EXTRUSION BY COHESIN AND CONDENSIN USING A SINGLE-MOLECULE TECHNIQUE

DIRECTEURS DE THESE :

- WILFRIED GRANGE

  INSTITUT DE PHYSIQUE ET CHIMIE DES MATERIAUX DE STRASBOURG,
  23, RUE DU LOESS, 67034 STRASBOURG
  wilfried.grange@ipcms.unistra.fr

- MARIE LAURE DURAND ET CHRISTOPHE ROMIER

  INSTITUT DE GÉNÉTIQUE ET DE BIOLOGIE MOLÉCULAIRE ET CELLULAIRE
  1, RUE LAURENT FRIES, B.P. 10142, 67404 ILLKIRCH CEDEX
  durandm@igbmc.fr, romier@igbmc.fr

BACKGROUND Chromatin organization plays a central role in the regulation of most nuclear processes and, consequently, participates in cellular homeostasis. Both Cohesin and Condensin complexes are key to these mechanisms as they organize chromatin by forming and extending chromatin loops in an ATP hydrolysis dependent manner. However, whether these complexes have similar mechanisms during this loop extrusion process is unclear and requires further studies.

APPROACH

- Utilizing proteins from the simplified eukaryotic model organism *Encephalitozoon cuniculi*, an intracellular parasite. *E. cuniculi*'s proteins are smaller than their yeast or human paralogs and are thus more amenable to biochemical and biophysical studies
- Employing Magnetic tweezers (MT) that have emerged as a method of choice for studying in depth loop extrusion, revealing the physical and molecular mechanisms of this process. We will benefit from the high bandwidth of our MT device (400 Hz versus 50 Hz as used in recent MT experiments)

EXPECTED RESULTS Using single-molecule approaches, we will resolve minute changes in DNA length that occur upon loop extrusion and will identify key rate-limiting steps.