Titre du sujet de stage :

**Functional impact of chromatin loop organization on recombinational DNA repair and genome stability**

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**Sujet de stage :**

DNA break threaten cell viability and genome stability. Homologous recombination repairs DNA break using an intact dsDNA molecule as a template, which has to be identified in the genome. Since, repair off a non-allelic template can cause chromosomal rearrangements, a layer of genome maintenance consists in suppressing identification and usage of non-allelic homologous sequences. Cohesin is a conserved motor complex that thread along DNA bidirectionally, extruding chromatin loops along the way. We recently showed that cohesin regulates the chances of encounter between a DNA break and non-allelic donors, suppressing template identification on other chromosomes, and stimulating template identification near the break site. We now wish to broaden this observation and establish how factors that regulate the distance travelled by cohesin influence the formation of chromosomal rearrangements by performing mutation accumulation experiments followed by high-throughput sequencing in various mutants. This project has the potential to demonstrate, for the first time, how 3D genome organization regulates genome plasticity/stability.

**Technologies utilisées** : Hi-C, Capture-C, Nanopore sequencing, Illumina sequencing

**Mots clés** : DNA damage, Genomic stability, 3D genome

**Publications d’intérêt** :

  **Delineation of two multi-invasion-induced rearrangement pathways that differently affect genome stability**
  BioRxiv (in revision at Genes & Dev).

  **Cohesin regulates homology search during recombinational DNA repair**
  Nature Cell Biology - co-first and co-corresponding