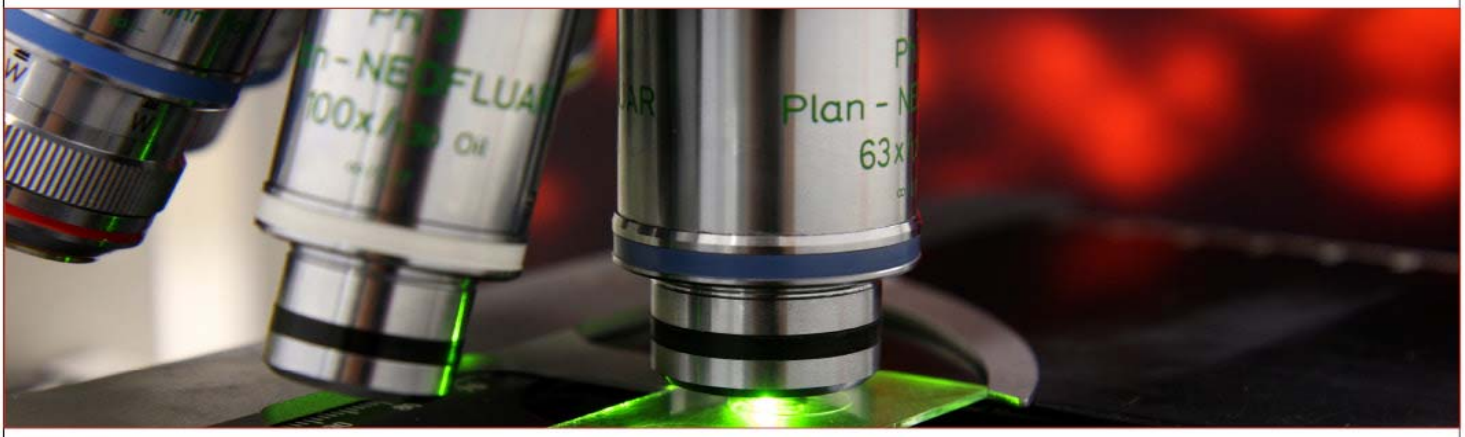
SÉMINAIRES ET CONFÉRENCES



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« Profiling Human Development with Single-Cell RNA-seq»

Embryonic development during the first week is arguably the most critical window of human development. During this time, the first lineages are being established: 1) trophectoderm (TE; prospective placenta), 2) primitive endoderm (PE; prospective yolk sac), and 3) pluripotent epiblast cells (EPI; prospective embryo proper); however, the majority of what we know surrounding this developmental time stems from studies in the mouse. Using single-cell RNA-sequencing, we have now constructed a comprehensive transcriptional map of human embryo development. These data show that cells undergo an intermediate state of co-expression of lineage-specific genes, followed by a concurrent establishment of all three lineages, coinciding with blastocyst formation. Further, we now propose a novel model of X-chromosome dosage compensation, where female cells of all three lineages undergo a dual X-chromosome dosage compensation prior to implantation. The fundamental knowledge elucidated from this study is crucial in identifying mechanistic pathways underlying lineage segregation and the establishment of pluripotency, thus being of great importance for understanding human development and regenerative medicine. Further, we have now established a platform by which the effects of environmental perturbations on embryo development can be elucidated. We envision broad utility of this transcriptional atlas in future studies on human development as well as in stem cell research.

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