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Investigation of the role of the Trithorax group protein ASH1 in the recovery of transcriptional patterns after cell division

Nancy Gutierrez Hernandez[1], Waltraud Müller[1], Davide Mazza[2], Leonie Ringrose[1]

[1] Humboldt University of Berlin, Germany
[2] Scientific Institute for Research, Hospitalization and Healthcare, San Raffaele Scientific Institute, Italy

Presenter: Nancy Gutierrez Hernandez (ESR1)

Global chromatin compaction and transcriptional down regulation are part of the events taking place during mitosis in which the duplicated genetic material is divided between the two cells arising from cell division. The recovery of the chromatin landscape and transcriptional program after this event is key to maintain the identity of fully differentiated and self-renewing pluripotent cells. However, mitosis is also a time window of opportunity for cell fate decisions during embryonic development, but the molecular mechanisms of memory maintenance or plasticity are not fully yet understood. Polycomb and Trithorax are epigenetic multiproteic complexes that regulate the correct gene expression in time and space contributing to a correct pattern formation during embryonic development. Live imaging experiments from my host laboratory have demonstrated the robust binding of the Trithorax component ASH1 to mitotic chromosomes in early Drosophila embryos. The mutation of the BAH and the AT hook domains lead to a reduction of ASH1 binding to mitotic chromatin, deregulation of target genes and affection of adult fly survival. During my PhD, we aim to study the participation of ASH1 in the recovery of transcriptional patterns after cell division in pluripotent cells and in cell fate decisions. We hypothesize that ASH1 is acting as a mitotic bookmarking factor that facilitates the fast and accurate recovery of transcriptional programs upon mitotic exit. The combination of molecular biology techniques, single molecule tracking and mathematical modelling will allow us to study the dynamic behavior of this protein and understand its contribution on the maintenance of epigenetic memory and in cell fate decisions after mitosis in Drosophila.