**Deciphering the rules of epigenetic regulation during stem cell development**

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The cell fate is controlled by many epigenetic factors including DNA methylation, transcription factor (TF) binding, histone modifications, chromatin remodelers and nuclear RNAs, to name just a few. For the purpose of the current talk I put nucleosome positioning on the top of this scheme. Such a choice is motivated by the fact that if there is no nucleosome at a given position, there are also no histone modifications, and TFs can bind their sites freely. As we will see during the talk, nucleosome positioning is also tightly linked to DNA methylation and nuclear RNAs. I will mostly focus on the interplay of the following three features: DNA methylation/demethylation, TF binding and nucleosome positioning. Our very recent work has provided new insights into this interplay. We have combined high-throughput MNase-seq and ChIP-seq sequencing with theoretical modeling to decipher nucleosome repositioning as a novel feedback mechanism that connects DNA methylation/demethylation with transcription factor binding. As a specific example of a transcription factor utilizing this mechanism I will consider an insulator protein CTCF. Our biophysical model allows predicting quantitative changes of CTCF occupancy during stem cell development as a function of changes in DNA methylation and nucleosome positioning.

References:

1) Teif V.B., Beshnova D.A., Marth C., Vainshtein Y., Mallm J.-P., Höfer T. and Rippe K. (2014). Nucleosome repositioning links DNA (de)methylation and differential CTCF binding during stem cell development. Genome Research. Advance Access. DOI: 10.1101/gr.164418.113

2) Teif V.B., Vainshtein Y., Caudron-Herger M., Mallm J.-P., Marth C., Höfer T., *Rippe K. (2012) Genome-wide nucleosome positioning during embryonic stem cell development. Nature Struct. Mol. Biol. 19, 1185-92.