The Secret Life of Dnmt1

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Abstract

DNA methylation plays a critical role during development, particularly in repressing retrotransposons. The mammalian methylation landscape is dependent on the combined activities of the canonical maintenance enzyme Dnmt1 and the de novo Dnmts, 3a and 3b. Here, we demonstrate that Dnmt1 displays de novo methylation activity in vitro and in vivo with specific retrotransposon targeting in mouse. We used whole-genome bisulfite and long-read Nanopore sequencing to provide an in-depth assessment and quantification of this activity. Our data demonstrate that Dnmt1 can catalyze DNA methylation in both a de novo and maintenance context, especially at retrotransposons, where this mechanism may provide additional stability for long-term repression and epigenetic propagation throughout development.

Bio-sketch

Helene studied Biomathematics at the University of Greifswald and did her PhD in Bioinformatics from 2012-2016 at the University of Leipzig with Prof. Peter Stadler. Here, she developed methods for DNA methylation sequencing analysis and their application to cancer data in the framework of the ICGC.

In late 2017, she joined as a Postdoc Alexander Meissner's group at the Max Planck Institute for Molecular Genetics in Berlin. Here, she heads the lab-intern bioinformatics group and focuses on using single-cell RNAseq and DNA methylation to study how epigenetic factors regulate early mammalian embryonic development, as well as analyzing the epigenetic footprint of cancer.