
Deciphering the role(s) of PRC2-Ezl1 mediated histone H3 modifications in programmed DNA elimination in *Paramecium*

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Abstract

In most eukaryotes, the genetic information remains constant throughout their life cycle. Yet this is not a universal rule. In the unicellular eukaryote *Paramecium*, massive and reproducible elimination of transposable elements and their single-copy remnants occurs, at each sexual cycle, during the development of somatic macronucleus from the germline micronucleus. Understanding how such diverse sequences are recognized and eliminated remains challenging. The DNA elimination process involves small RNA-guided deposition of H3K9me3 and H3K27me3 catalyzed by PRC2-Ezl1 onto transposable elements. In this project, we aim at understanding the precise roles of these two repressive histone modifications. Here, we characterize Chromo2, a chromodomain-containing protein, that we showed is required *in vivo* for correct H3K9me3 and H3K27me3 accumulation and DNA elimination. Using a functional tagged protein, we found that Chromo2 exclusively localizes in the developing macronucleus and that it associates with transposable elements through ChIP-qPCR experiments. Through pulldown and quantitative mass spectrometry, we identified two Chromo2-interacting proteins, whose silencing phenocopy *CHROMO2* knockdown, suggesting a joint action. Further work will shed light on the precise role of Chromo2 and its partners, in relation with histone modifications, during the process of DNA elimination in *Paramecium*.

Keywords: Epigenetics, Histones, Genome stability

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