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H2A.Z: stable or not stable that is the question

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Nucleosomal structure is repressive therefore; the mechanisms involved in the regulation of nucleosome stability are of great importance in the control of gene expression. It is well established that nucleosome free regions (NFRs) are generated at the transcriptional start sites, flanked by nucleosomes with high turnover rate and of special histone composition. H2A.Z is one of these histone variants, characteristic for the +1 and -1 nucleosomes neighbouring these NFRs, among its other preferential locations. We have developed an *in situ* assay for the measurement of the intrinsic and super helicity dependent nucleosome stability. Using this assay NFR flanking nucleosomes carrying H3K4me3 histone post-translational modification were found to be less stable compared to nucleosomes carrying heterochromatic histone marks. Since H2A.Z can substitute canonical H2A histones in the NFR flanking nucleosomes, we expected that the H2A.Z containing nucleosomes would also be destabilized. Using H2A.Z specific antibodies and fluorophores tagged H2A.Z histones, we observed unusually stable. H2A.Z containing nucleosomes that could be detected in an antibody clone/brand dependent manner. Having compared different antibodies and H2A.Z isotypes we have shown that neither the acetylation of the N-terminal histone tail nor the isotype was responsible for their increased stability. Through the spectacles of super-helicity dependent stability, the unusually stable nucleosomes appear to constitute a sub population of all H2A.Z containing nucleosomes that appears to be of perinucleolar localization.

Recent Publications:

1. Imre et al. (2017) Nucleosome stability measured *in situ* by automated quantitative imaging. Scientific Reports 7(1):12734.

Biography

László Imre completed his MSc studies on the Eötvös Loránd University, Faculty of Science as a molecular biologist. He did his diploma work in the Agricultural Biotechnology Institute investigating the site-specific integration system of the 16-3 phage virus. Then he started to work in the Institute of Isotopes Co., Ltd. as a development engineer and has developed a multiplex microbead assay for the detection of changes in length or sequence of short genomic regions (patented in Hungary). Now he works as a junior research fellow in the Department of Biophysics and Cell Biology, University of Debrecen. He will complete his PhD at the end of 2018 with the supervision of Prof. Gábor Szabó. His field of interest include the effect of epigenetic histone modifications and histone variants on the chromatin structure. He has developed an automated quantitative imaging based method for the evaluation of the intrinsic and superhelicity dependent nucleosome stability and has also developed microbead assays for chromatin studies.

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