SUPERRESOLUTION IMAGING OF CHROMATIN LANDSCAPE IN MEIOSIS PROPHASE I

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Higher-order chromatin structures play a vital role in the regulation of gene expression, and are considered as one of the major emerging concepts to study gene regulation. However, the distribution and organization of chromatin is still a matter of ongoing debate. Electron Microscopy (EM) suggests 10-30 nm chromatin fibres that undergoes higher order folding coincident with formation of Synaptonemal Complex (SC) during meiosis prophase I.

These EM images of radially emanating chromatin loops perpendicular to the lateral elements of SC are highly dependent on sample preparation, and might result in morphologies that are not best representatives of native chromatin fibres. On the other hand, the limitations of conventional Light Microscopy (LM) and lack of an appropriate DNA-specific dye for super-resolution localisation microscopy have so far hampered the application of optical super-resolution microscopy methods for chromatin analysis.

Recently, we observed that UV-induced photoconversion of a couple of commonly used DNA dyes (Hoechst and DAPI) allows for the optical isolation of single, stochastically blinking dye molecules attached to the DNA [1]. We used this unique property of DNA minor groove binders to analyse the distribution of chromatin and several of its post translational modifications along the lateral elements of SC. Taking into account the arrangement and composition of chromatin, as well as the regionspecific distribution of post-translational nucleosomal modifications, we discuss a model of the chromatin architecture along the SC.