

Laboratory of RNA Biology

Pre-mRNA splicing, spliceosome, epigenetics, nuclear architecture, retinitis pigmentosa

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Our long-term interest is to determine how cells decode information stored in the genome. We focus on the molecules called mRNAs that serve as messengers between DNA and proteins. Information for protein synthesis in our genome is fragmented and the coding sequences are joined together after transcription of DNA into RNA in a process called RNA splicing. In our laboratory, we analyse how the protein coding fragments are recognized and joined together. We mainly focus on how the nuclear environment and mainly chromatin influence RNA splicing, and the quality control mechanisms that ensure that the splicing machinery is correctly formed on proper RNA. These studies also help us to understand why mutations in proteins that catalyse RNA splicing cause retinitis pigmentosa, a human genetic disease characterized by photoreceptor cell degeneration. As we mostly study all these processes directly in living cells, we widely employ cell culture and various microscopy techniques (e.g. super-resolution fluorescence microscopy, live cell imaging, high-content microscopy, and other).

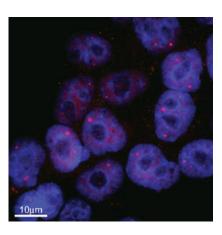


Fig. 1. Distribution of the splicing factor LSm4 [red] in cancer cells. The cell nucleus is visualized by DNA staining [blue], Cajal bodies are the bright red spots. Classical fluorescence microscoov.

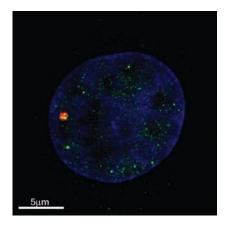


Fig. 2. Localization of the splicing factor U2 snRNA (green) in the cell nucleus (blue - DNA) and in Cajal bodies (red) using structured illumination-based superresolution microscopy. One cancer cell shown only.

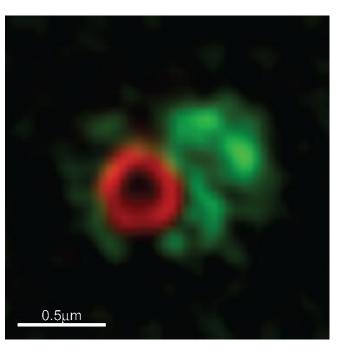


Fig. 3. Two spliceosome assembly proteins (SART3 and SMN) visualized in the Cajal body by structured illumination-based super-resolution microscopy.

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Not in the picture: David Staněk, PhD / Head of Laboratory, Samira Hozeifi, MSc / PhD Student (until 2014), Ivan Novotný, PhD / Postdoctoral Fellow (until 2013), Daniel Matějů / Diploma Student (until 2013)