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POSTER #2

CHARACTERIZING mRNA EXPORT AT HIGH RESOLUTION IN INDIVIDUAL NUCLEAR PORES IN SINGLE CELLS

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The export of mRNA from the cell nucleus is one of the pillars of the gene expression pathway in eukaryotes. Conventional light microscopy does not allow high resolution analysis of mRNA export in intact cells nor does it enable the examination of specific and functional interactions that exported molecules undergo as they pass from the nuclear side of the nuclear pore complex (NPC), through the inner channel of the pore, and then out to the cytoplasmic side. Such limitations hinder our understanding of the biology of mRNA export within the context of gene expression and its regulation, and require the innovation of new approaches. A key factor involved in the passage of the transcript through the nuclear pore complex is Nuclear Export Factor 1 (NXF1/Tap). We have performed measurements within individual nuclear pores using super-resolution STED microscopy, a FLIM-FRET approach, as well as single mRNA tracking in living human cells. These approaches have allowed the detection and measurements of specific interactions taking place between NXF1 and mRNAs, and between NXF1 and proteins within the NPCs, in intact cells. We are able to discriminate between specific NXF1-NPC interactions under regular conditions and when mRNA export is blocked, and characterize interactions involved in the various stages of mRNA transition through the nuclear pore.