QUANTITATIVE IMAGING OF NUCLEAR FUNCTIONS

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KEY WORDS: life cell imaging, nuclear organisation, FRAP; FRET, FCS, RICS, STED, SMI.

1. ABSTRACT

The cell nucleus is responsible for the storage, propagation, maintenance and expression of the genetic material it contains [1]. Therefore, a highly organized machinery is required for these processes to take place in an extremely condensed nuclear environment. Recent developments in microscopy techniques enabled us to observe macromolecular assemblies in their natural setting: the living cell nucleus [2]. These emerging technologies have revealed novel concepts in nuclear cell biology. In order to further elucidate the biochemistry of gene expression, replication and genome maintenance, the major challenge is now to precisely determine the dynamics of nuclear proteins in the context of the structural organization of the nucleus [3]. We apply Fluorescence Correlation Spectroscopy (FCS), Fluorescence Recovery after Photobleaching (FRAP), Fluorescence Resonance Energy Transfer (FRET), Raster Image Correlation Spectroscopy (RICS) and super-resolution microscopy (STED, SMI) to assess the structure, function and dynamics of subnuclear protein assemblies. Processing these data with mathematical modeling tools provide quantitative frameworks for the assembly of protein complexes [4,5]. Examples of such applications will be presented.

1. REFERENCES

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