# An exciting time to study the nucleus

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Some exciting new findings were reported at the Minisymposium "The Cell Biology of Genetic Information" held at the 2015 annual meeting of the American Society for Cell Biology. **G. V. Shivashankar** (Mechanobiology Institute, Singapore) spoke about how geometric constraints, such as extracellular matrix stiffness, can regulate nuclear organization in mammalian cells, from nuclear shape to chromatin dynamics and gene expression. The regulation is mediated by a pathway that includes focal adhesion, perinuclear actin, and chromatin modulations. Reduction of adhesion was found to reduce perinuclear actin filaments and increase the turnover of core histones (Toh *et al.*, 2015), suggesting that gene expression and chromatin state tightly couple with changes of extracellular conditions. In another system, **K. Weis** (ETH Zurich Institute of Biochemistry, Switzerland) showed that nutritional or pH conditions could affect nuclear stiffness and chromatin dynamics in yeast. Genome organization and expression can also be regulated by nucleolar function (**S. Huang**, Northwestern University) and by differentiation (**A. Wood**, Northwestern University). Chromatin state, in turn, was shown to play a key role in shaping physical properties of the nucleus (**A. D. Stephens**, Northwestern University). A more euchromatic genome associates with a more elastic nucleus. These reports demonstrate dynamic functional coordination between the organization of the genetic material in the nucleus and cytoplasmic and extracellular function in response to environmental changes.

The MCM helicase was reported to play important roles in preventing early replication stress– and loss-of-function–induced mitotic missegregation and genome rearrangement in fission yeast, resembling micronuclei in cancer cells (**S. L. Forsburg**, University of Southern California; Sabatinos *et al.*, 2015). Micronucleolus formation, on the other hand, was shown by **A. Spektor** (Dana-Farber Cancer Institute) to be one of the causes of chromothripsis common in cancer cells (Zhang *et al.*, 2015). **Y. Kim** (University of California, Berkeley) showed the activity of CHK-2 to be part of a conserved feedback mechanism that is important for meiosis and is facilitated by HORMA-domain proteins within the chromosome axis in *C. elegans* (Kim *et al.*, 2015). Single RNA tracking in live cells defined the kinetics of mRNA export and demonstrated that mRNA remained associated with the outside of the nuclear envelope for an extended time upon exiting the nucleus in budding yeast (**A. Lari**, University of Alberta, Canada; Smith *et al.*, 2015). Influenza virus mRNAs were shown by **A. Mor** (University of Texas Southwestern Medical Center) to be spliced and exported through nuclear speckles—nuclear organelles highly enriched with factors for pre-mRNA splicing.

The reports on development of innovative methods provided exciting and more precise tools for future studies of nuclear functions. **R. E. Kleiner** (Rockefeller University) showed a novel chemical proteomics approach for quantitative profiling of direct binders to phosphorylated γ-H2AX (Kleiner *et al.*, 2015) or other proteins in the future. **Y. Chen** (University of Illinois, Urbana–Champaign) spoke of a specific cross-link method, TSA-Seq, for measuring cytological distance in micrometers between genes and specific nuclear organelles, which can also be used to identify DNAs associated with specific nuclear organelles. **D. S. Nelles** (University of California, San Diego) showed that clustered regularly interspaced short palindromic repeats (CRISPR)/Cas9 technology can be suited for tracking RNA in living cells without modifying the targeted RNA (Nelles *et al.*, 2015).

These findings provided glances at current studies and future research trajectories. There remain many black boxes regarding nuclear structure, function, and coordination between the nucleus, cytoplasm, and extracellular environment in normal and diseased conditions. The increasingly sophisticated tools make it an exciting time to explore these mysteries.

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