IN BRIEF

NUCLEAR ORGANIZATION

Paraspeckles are subpopulation-specific nuclear bodies that are not essential in mice

Nakagawa, S. *et al. J. Cell Biol.* **193**, 31–39 (2011)

Specific to mammals, paraspeckles appear as distinct dots in the interchromatin space and may affect gene expression. Nakagawa *et al.* studied the expression, in adult mouse tissues, of short and long RNA transcripts generated from the nuclear-enriched abundant transcript 1 (NEAT1) locus (NEAT1_1 and NEAT1_2, respectively), which are thought to function as structural components of paraspeckles. Both transcripts were expressed in a specific subpopulation of cells; however, paraspeckles formed only in a small subpopulation of cells expressing high levels of NEAT1_2. Surprisingly, mice lacking NEAT1 were viable and fertile — the only obvious phenotypic consequence of NEAT1 deficiency was the absence of paraspeckles. Under normal conditions, therefore, paraspeckles seem to be nonessential, and Nakagawa *et al.* hypothesize that their true physiological function becomes apparent under particular environmental conditions, which remains to be determined.

DEVELOPMENT

Self-organizing optic-cup morphogenesis in three-dimensional culture

Eiraku, M. *et al. Nature* **472**, 51–56 (2011)

Eiraku *et al.* have shown that optic cups can be generated autonomously *in vitro* from embryonic stem (ES) cells, in the presence of Matrigel containing extracellular matrix factors. They find that, similarly to events *in vivo*, the ES-derived cells can form retinal epithelium that evaginates and then differentiates along its proximal–distal axis. The proximal region differentiates to form rigid pigment epithelium, and the distal region undergoes subsequent invagination to form an optic cup structure. This striking finding suggests that the optic cup can form in the absence of the lens and surface ectodermal tissue that normally surround the neuroepithelium during eye development. The hope is that this system will now provide a vital tool for analysis of how the eye normally forms and how it is disrupted during disease.

TRANSCRIPTION

The C-terminal domain of RNA polymerase II is modified by site-specific methylation

Sims, R. J. III *et al. Science.* **332**, 99–103 (2011)

Post-translational modifications of the carboxy-terminal domain (CTD) of RNA polymerase II (RNAPII) are essential for transcription initiation and elongation; however, it is largely unknown how CTD modifications are involved in the different roles of RNAPII, which transcribes several classes of RNA. Now, Sims *et al.* find that the CTD is methylated at Arg1810 by co-activator-associated Arg methyltransferase 1 (CARM1) prior to phosphorylation at Ser2 or Ser5 of the CTD consensus repeat — modifications that are associated with elongation and initiation, respectively. Using a mutant of RNAPII that cannot be methylated, the authors show that lack of Arg1810 methylation results in aberrant expression of small nuclear RNAs and small nucleolar RNAs specifically. Thus, modification of the CTD may recruit RNAPII to specific genes, or classes of genes.