The micro and macro of RNA function

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The central dogma uniquely positions RNA as the key molecular player for translating genetic software into protein hardware. But it has become increasingly clear that RNA also plays an essential regulatory role within cells. MicroRNAs in particular have emerged as ubiquitous and still poorly understood molecules involved in the control of a wide variety of biological processes. RNA has also recently been shown to have important roles in structural assembly within cells. A diverse set of speakers at the Minisymposium on Micro- and Coding RNA highlighted some of these new and often unexpected roles of RNA across a range of length scales.

Tracy Johnson (University of California–San Diego) discussed her lab's work on cotranscriptional mRNA splicing. Her talk underscored the importance of ATP-dependent RNA helicases in rearranging RNA secondary structure and the integral role for chromatin modification in coordinating RNA rearrangements with transcription in space and time.

Albert Rosana (Owttrim lab, University of Alberta) also discussed RNA helicases within the fascinating context of temperature fluctuations of cyanobacteria. He described his work on the altered expression of the oligomeric RNA helicase CrhR as a temperature stress response. His work provides new insights into RNA regulation, suggesting CrhR autoregulates its expression through a combination of RNA processing and RNA–protein stabilization mechanisms, which in turn leads to temperature-dependent regulation of small regulatory RNAs.

Several presentations explored how RNAs play a role in the assembly of large-scale intracellular structures. **Magdalena Strzelecka** (Heald lab, University of California–Berkeley) discussed her work on RNAs in the assembly of the mitotic spindle. She utilized *Xenopus* egg extracts and next-generation sequencing approaches to demonstrate a surprising role for splicing factors in mitosis. This suggests the intriguing possibility that RNA processing plays a regulatory role in cell division.

Moving to even larger scales, **Cliff Brangwynne** (Princeton University) discussed his lab's work on the biophysics of ribonucleoprotein (RNP) bodies—large, non–membrane bound assemblies that behave as liquid-phase droplets of RNA and protein. This work exploits the nucleus of *Xenopus* oocytes to study the nucleolus, an RNP droplet involved in ribosome biogenesis. The presentation revealed some unexpected biophysical consequences of the large length scales involved, with important implications for nuclear RNP organization and function.

The nucleolus was also the central theme of a talk by **Thoru Pederson** (University of Massachusetts Medical School), who summarized his lab's recently published work on a subset of microRNAs localized in the nucleolus of rat myoblasts. He also reported new results on the nucleolar presence of certain mRNAs in these cells, proposing there might be microRNA–mRNA interactions in the nucleolus to pre-set the translational status of exported mRNAs.

The remaining talk of the session, by **Rebecca Holmes** (Tollervey lab, University of Edinburgh), focused on the yeast protein Npl3, a member of the large SR family of RNA-binding proteins with diverse functions in pre-mRNA processing. She described experiments utilizing in vivo cross-linking and deep sequencing, which revealed the binding of Npl3 to a surprising variety of RNA species. Her data suggest an unexpected role for Npl3 in regulating noncoding RNAs (ncRNAs), with consequences for the expression of surrounding genes. These results raise the possibility that other previously described functions of Npl3 may, in fact, be consequences of Npl3 regulation of ncRNAs.

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