

SFB 960-/BZR – Kolloquium

19. Mai 2014, 14.00 Uhr

BIO 5.2.38

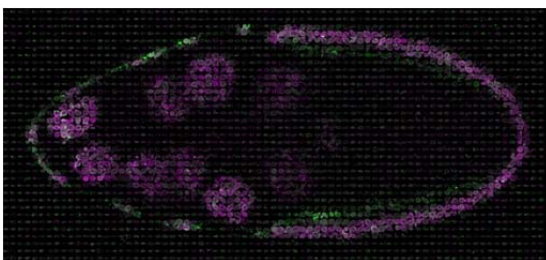
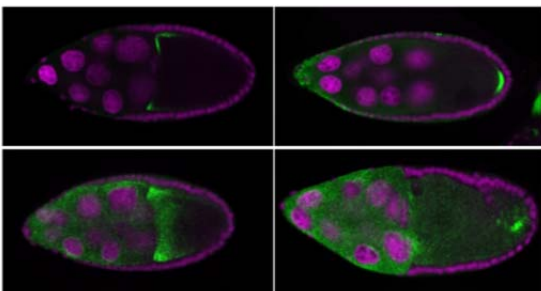


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Spatial control of gene expression - the role of RNA localization in fruit fly ovaries

Segregation of cytoplasmic components during development and cell differentiation is critical in eukaryotic cells for specialization and polarization. A powerful mechanism to generate and maintain intracellular asymmetries is the localization of mRNAs, which in conjunction with restricted translation allows high local concentrations of proteins. We used a genome-wide approach to collect quantitative and qualitative information about individual mRNA localizations over time and discovered that when transcription is stable, cytoplasmic regulation of mRNAs becomes a key mechanism that controls development. Over the course of ovarian development in fruit flies, 20% of the expressed transcripts display subcellular localization and among them are RNAs encoding key oogenesis proteins such as cytoskeletal and cell cycle regulators and axis patterning factors. All cytoplasmic mRNA localizations require an intact microtubule cytoskeleton and known regulators of RNA transport. Despite these similarities, individual mRNA enrichments are not stable and the localization landscape changes dramatically over time suggesting a previously unappreciated complexity of cytoplasmic RNA localization.



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