Signed, sealed, and delivered: RNA localization and translation at centrosomes

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ABSTRACT **Protein localization is intrinsic to cellular function and specialized activities, such as migration or proliferation. Many localized proteins enrich at defined organelles, forming subdomains of functional activity further specified by interacting protein assemblies. One well-studied organelle showing dynamic, functional changes in protein composition is the centrosome. Centrosomes are microtubule-organizing centers with diverse cellular functions largely defined by the composition of the pericentriolar material, an ordered matrix of proteins organized around a central pair of centrioles. Also localizing to the pericentriolar material are mRNAs. Although RNA was identified at centrosomes decades ago, the characterization of specific RNA transcripts and their functional contributions to centrosome biology remained largely unstudied. While the identification of RNA localized to centrosomes accelerated with the development of high-throughput screening methods, this discovery still outpaces functional characterization. Recent work indicates RNA localized to centrosomes is biologically significant and further implicates centrosomes as sites for local protein synthesis. Distinct RNA localization and translational activities likely contribute to the diversity of centrosome functions within cells.**

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CODING AND DECODING THE MESSAGE

The central dogma is a study in cryptography. First, the DNA code must be transcribed in the nucleus into a premessenger RNA (pre-mRNA) subject to mRNA processing before nuclear export. Once in the cytoplasm, the messages encoded by mature mRNAs are translated by ribosomes to generate protein products. When and where proteins are generated matters. For many cellular responses, such as cell migration or proliferation, rapid adaptation to the cellular environment requires the rapid redistribution of proteins. Conversely, errant synthesis or localization of certain protein products, such as those that define cell fates or contribute to specialized cellular functions, may have deleterious consequences for individual cells or developing tissues. Numerous proteins are translated locally at their site of function, effectively generating subcellular enrichments on demand, and protecting distal sites from ectopic exposure.

Often, local protein synthesis is coupled with RNA localization, whereby mRNAs are enriched at defined subcellular locales. RNA localization is a posttranscriptional paradigm of gene regulation conserved from single-celled bacteria and fungi through complex, multicellular organisms, including humans. Many excellent reviews address mRNA localization and local translation and its importance in diverse cellular responses (Gavis *et al.*, 2007; Martin and Ephrussi, 2009; Meignin and Davis, 2010; Jung *et al.*, 2014; Buxbaum *et al.*, 2015; Ryder and Lerit, 2018; Das *et al.*, 2021). In this Perspective, I provide a primer to RNA localization, then focus on RNA localization and translation at centrosomes and spindle poles, a topic of recently renewed interest.

AN INTRODUCTION TO RNA LOCALIZATION

While many proteins are targeted to defined subcellular compartments, others are synthesized in situ following mRNA localization. Spatial enrichments of RNAs are generated by a variety of mechanisms, including active transport (Long *et al.*, 1997; Takizawa *et al.*, 1997), diffusion and entrapment (Forrest and Gavis, 2003), and local

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Abbreviations used: AHA, azidohomoalanine; Asl, asterless; Asp, abnormal spindles; ASPM, abnormal spindle-like microcephaly-associated; Bcd, bicoid; BICD2, BICD cargo adaptor 2; BONCAT, biorthogonal noncanonical amino acid tagging; CCDC88C, Coiled-coil domain-containing 88C; Cen, centrocortin; Cep350, centrosome protein 350; Cnn, centrosomin; CPEB, cytoplasmic polyadenylation element binding; Cyc B, Cyclin B; FMRP, Fragile-X mental retardation protein; γTub, γ-Tubulin; HMMR, hyaluronan-mediated motility receptor; Mud, mushroom body defective; NUMA1, nuclear mitotic apparatus protein 1; PCM, pericentriolar material; PCNT, pericentrin; PLK4, Polo-like kinase 4; PLP, pericentrin-like protein; Puro-PLA, Puromycylation-proximity ligation; RNA, Ribonucleic acid; 3′-UTR, 3′-untranslated region.

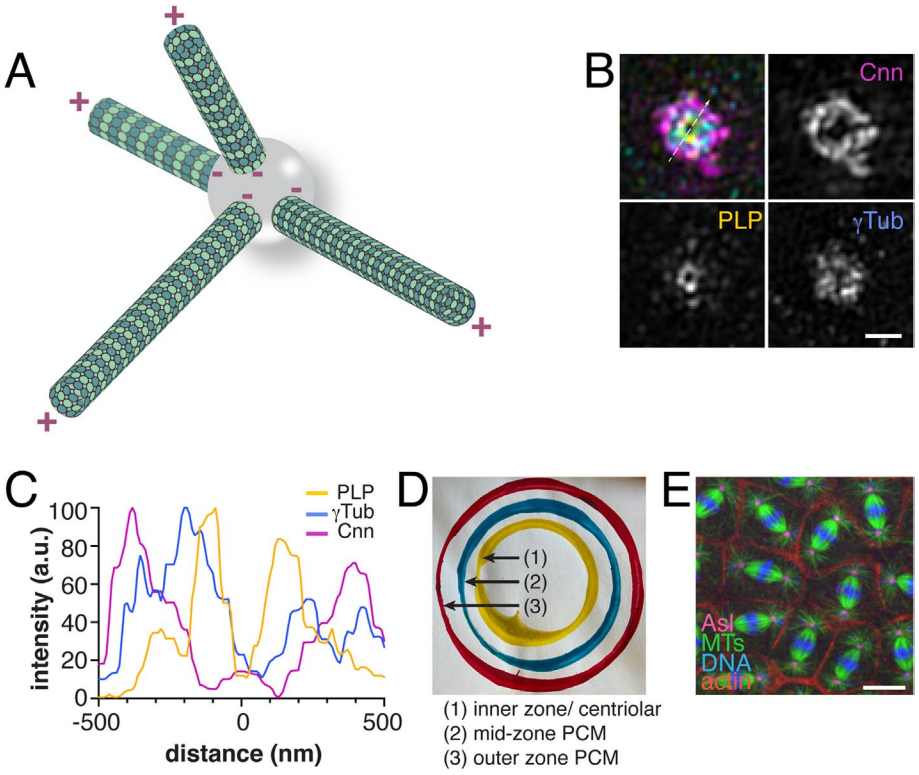

FIGURE 1: The centrosome as a microtubule-organizing center. (A) Cartoon depicts microtubules composed of α- (pale green) and β-tubulin (dark green) heterodimers nucleated from the PCM (gray sphere). Microtubules are polarized structures with minus ends (–) embedded in the PCM and plus ends (+) extending into the cytosol. (B) Structured-illumination microscopy image of a mitotic *Drosophila* embryo centrosome labeled with pericentrin-like protein (PLP; yellow; Martinez-Campos *et al.*, 2004), γTubulin (γTub; blue; Joshi *et al.*, 1992), and centrosomin (Cnn; magenta; Megraw *et al.*, 1999; Vaizel-Ohayon and Schejter, 1999) antibodies. Image courtesy of Nasser Rusan. Dashed arrow shows the direction of the line scan used in (C) to measure the intensity distributions of centrosome proteins. The peak intensity of each protein was normalized to 100 and the distribution is plotted relative to the center of the centriole (0 nm). (D) Artistic rendition of the subconcentric organization of the centrosome, where each color represents the distribution of a centrosome protein. (1) The inner zone (yellow) represents centriolar proteins (e.g., PLP), (2) the midzone (blue) represents PCM proteins residing closer to the centriole, such as γTub, while (3) the outer zone PCM (red) defines proteins at the outer margin of the centrosome, such as Cnn. (E) Organization of mitotic spindles within a *Drosophila* embryo. Magenta centrosomes are marked by Asterless (Asl; Varmark *et al.*, 2007); microtubules (green), actin (red), and DNA (blue) are displayed. Image courtesy of Elías Castro. Bars: (B) 500 nm and (E) 5 μm.

protection from degradation (Ding *et al.*, 1993). Active transport is a prevalent mechanism; and actin, microtubules, and their associated myosin, kinesin, and dynein motors are all implicated in mRNA transport, depending on the specific transcript and destination (reviewed in Bullock, 2011). As the first discovered localized mRNA, *β-actin* mRNA is itself a model for RNA localization mechanism and function (Jeffery *et al.*, 1983). Subsequent work defined *β-actin* mRNA as subcellularly localized to the leading edge of migratory fibroblasts, where it promotes cell migration (Lawrence and Singer, 1986; Kislauskis *et al.*, 1997; Katz *et al.*, 2012). While early observations established the importance of RNA localization for embryonic patterning and neuronal responses, the paradigm is conserved and serves critical functions in diverse cellular settings (Ryder and Lerit, 2018).

RNA localization is remarkably specific, often requiring recognition of sequence or structural motifs within target mRNAs by RNA-binding proteins (Kislauskis and Singer, 1992). Many RNAs are maintained in a translationally repressed state until localized (Gavis and Lehmann, 1994). Other mRNAs, including several localizing to centrosomes, reach their destinations through a cotranslational transport mechanism, whereby RNA localization is coupled to protein synthesis (Sepulveda *et al.*, 2018; Chouaib *et al.*, 2020; Safieddine *et al.*, 2021).

While not all RNAs localize to defined subcellular regions, a large number do. A genome-wide RNA localization screen in early *Drosophila* embryos revealed >70% mRNAs are enriched at defined subcellular compartments (Lecuyer *et al.*, 2007). Spatial transcriptomics in mammalian cells similarly highlights the high prevalence of subcellular RNA localization (Fazal *et al.*, 2019). Taken together, RNA localization is widespread, conserved, and functionally important, as its dysregulation impacts development and disease (reviewed in Holt and Bullock, 2009; Wang *et al.*, 2016).

MESSAGES AT THE CENTROSOME

Centrosomes as microtubule-organizing centers

Among the subcellular depots for RNA localization are specific organelles, including centrosomes. Centrosomes function in microtubule nucleation and organization (Karsenti *et al.*, 1984; Mitchison and Kirschner, 1984) and are key for the fidelity of mitosis. Upon mitotic entry, the duplicated centrosomes organize the bipolar mitotic spindle to ensure faithful segregation of the chromosomes to the two daughter cells (Pihan, 2013). During interphase, centrosomes build a network of polarized microtubules, serving as a highway system for intracellular trafficking and cell polarization. Additionally, in quiescent cells, centrosomes convert into the basal bodies required for ciliogenesis (Kobayashi and Dynlacht, 2011). Indicative of its functional importance, centrosome dysfunction is associated with human developmental disorders and disease, including microcephaly, ciliopathy, and cancer (Nigg and Raff, 2009).

The microtubule-nucleating activity of the centrosome is enabled by the pericentriolar material (PCM; Figure 1A), the levels of which dramatically increase upon mitotic entry (Gould and Borisy, 1977; Khodjakov and Rieder, 1999). The advent of superresolution microscopy uncovered the conserved subconcentric organization of centrosomal proteins within PCM (Figure 1, B and C; Fu and Glover, 2012; Lawo *et al.*, 2012; Mennella *et al.*, 2012; Sonnen *et al.*, 2012). Centriolar components reside near the center, while PCM proteins reside within different or partially overlapping layers radiating out (Figure 1D). The composition and organization of PCM oscillates with the cell cycle, augmenting the microtubule-organizing activity of the centrosome to direct formation of the bipolar mitotic spindle (Figure 1E).

Early evidence for RNA at centrosomes

Initial observations for RNA at centrosomes date back to the 1960s (reviewed in Marshall and Rosenbaum, 2000). Pioneering work indicated purified ciliary basal bodies from the protist *Tetrahymena*

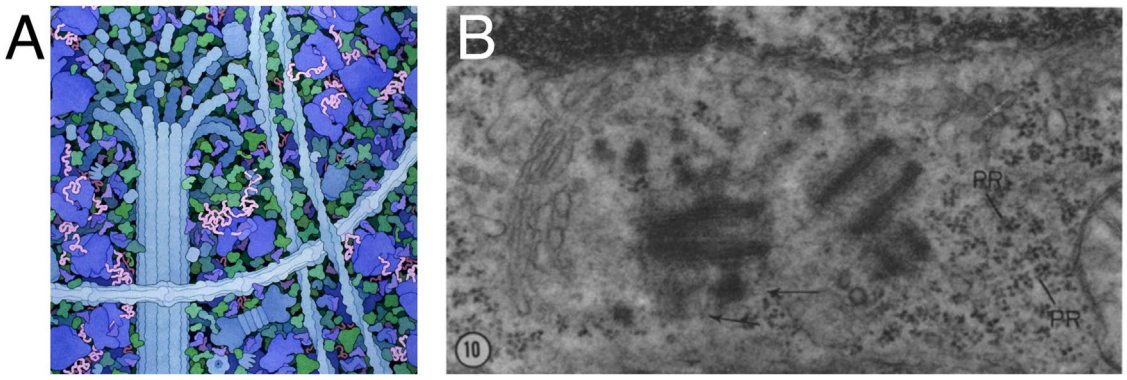

FIGURE 2: The intimate association of the translational machinery with microtubules and centrosomes. (A) Reproduction of "Biosites: Cytoplasm, 2005" illustrated by David S. Goodsell; available online (doi: 10.2210/rcsb_pdb/goodsell-gallery-006). Illustration shows a microtubule filament (light blue, left) juxtaposed to ribosomes (dark blue) synthesizing proteins (pink). (B) Electron micrograph of a rat lymphocyte showing abundant polyribosomes (PR) clustered near the duplicated centrioles from Murray *et al.* (1965) originally published in *Journal of Cell Biology* and reprinted with permission from Rockefeller University Press.

contained approximately 2% of total cellular RNA (Seaman, 1960; Argetsinger, 1965; Hoffman, 1965; Hartman *et al.*, 1974).

While it was debated whether RNA represented a contaminant following cell fractionation, there was also speculation nucleic acids supported centriole duplication (Seaman, 1960; Sagan, 1967). Thus far, there is no evidence supporting a role for RNA in centriole duplication, a process largely regulated by the conserved Polo-like kinase 4 (PLK4; Bettencourt-Dias *et al.*, 2005; Habedanck *et al.*, 2005). As we will discuss below, the function of RNA localized to centrosomes remains relatively underexplored.

Identification of mRNAs at the centrosome

Classically, subcellular RNA localization is visualized through in situ hybridization (Jeffery *et al.*, 1983). Thus, *cyclin B* (*cyc B*) mRNA was first localized to centrosomes within early *Drosophila* embryos (Raff *et al.*, 1990). Later, studies in *Xenopus* suggested local *cyc B* mRNA is important for mitotic progression (Groisman *et al.*, 2000). A genome-wide RNA localization screen similarly detected *cyc B* and other defined mRNAs at *Drosophila* centrosomes (Lecuyer *et al.*, 2007). Recent RNA localization screens employing higher resolution and more quantitative single molecule fluorescence in situ hybridization (smFISH; Femino *et al.*, 1998) identified additional mRNAs localizing to centrosomes (Chouaib *et al.*, 2020; Kwon *et al.*, 2021; Safieddine *et al.*, 2021), consistent with work from our own group (Ryder and Lerit, 2020; Ryder *et al.*, 2020). Transcriptomic methods further enumerate the list of RNAs associated with mitotic spindles (Sharp *et al.*, 2011; Hassine *et al.*, 2020). Similarly, high-throughput analyses reveal several human microtubule-associated and centrosome-localized proteins, including Pericentrin (PCNT) and CDK5RAP2, reside in complex with RNA (Doxsey *et al.*, 1994; Fong *et al.*, 2008; Mallam *et al.*, 2019). These data showcase the prevalence of RNA localized to centrosomes and spindle poles. Moreover, many of the RNAs localizing to centrosomes are conserved across divergent species, arguing for biological significance (recently reviewed in Zein-Sabatto and Lerit, 2021). Notably, most mRNAs identified in these screens encode proteins known to localize to and regulate centrosomes, hinting RNA localization to centrosomes and translation are coupled.

TRANSLATION AT THE CENTROSOME

Compelling evidence indicates local RNA supports protein synthesis at centrosomes. Isolated basal bodies from *Tetrahymena* are capable of protein synthesis (Seaman, 1962). Moreover, ribosomes reside in close proximity to centrioles and basal bodies, as revealed by electron microscopy from intact cells (Figure 2, A and B; Sorokin, 1962). Isolated mitotic spindles from sea urchin, *Xenopus*, and cultured human cells also contain RNA and ribosomes, highlighting the conservation of these associations (Goldman and Rebhun, 1969; Blower *et al.*, 2007). Immunofluorescence likewise shows ribosomal components near centrosomes (Blower *et al.*, 2007; Sepulveda *et al.*, 2018). These data highlight the intimate association of centrosomes, microtubules, and the translational machinery.

More recently, nascent peptide synthesis was directly visualized at centrosomes in *Drosophila* embryos and cultured mammalian cells. Puromycylation-proximity ligation assay (puro-PLA) detects nascent translation based on the physical proximity (~40 nm) of puro-labeled ribosomes and a user-specified protein (tom Dieck *et al.*, 2015). Puro-PLA indicates *Centrocortin* (*Cen*) mRNA is translated near centrosomes in *Drosophila* embryos (Bergalet *et al.*, 2020). Another common tool to detect local protein synthesis is through the incorporation of azidohomoalanine (AHA), also known as biorthogonal noncanonical amino acid tagging (BONCAT; Dieterich *et al.*, 2006). Recent work shows AHA-labeled proteins are enriched at centrosomes and along the spindle, consistent with local protein synthesis (Pascual *et al.*, 2020). RNA localization and local protein synthesis is also noted at the base of, and even within cilia (Hao *et al.*, 2021; Kwon *et al.*, 2021). Additional work is required to determine differences in RNA composition and translation state during the basal body-to-centrosome conversion.

For many transcripts, RNA localization to centrosomes requires intact ribosomes. The localization of *abnormal spindle-like microcephaly-associated* (*ASPM/asp*), *BICD cargo adaptor 2* (*BICD2*), *coiled-coil domain-containing 88C* (*CCDC88C*), *Cen*, *centrosomal protein 350* (*CEP350*), *hyaluronan-mediated motility receptor (HMMR)*, *nuclear mitotic apparatus protein 1* (*NUMA1*)/*mushroom-body defective* (*mud*), and *PCNT/plp* mRNAs to *Drosophila* and cultured human cell centrosomes is puromycin sensitive, supporting a model for cotranslational transport (Sepulveda *et al.*, 2018; Bergalet *et al.*, 2020; Chouaib *et al.*, 2020; Safieddine *et al.*, 2021). Cotranslational transport may expediate the rapid influx of PCM components required for mitotic spindle assembly, for example. Alternatively, cotranslational transport may limit interactions among certain proteins until they reach the centrosome to safeguard microtubule organization.

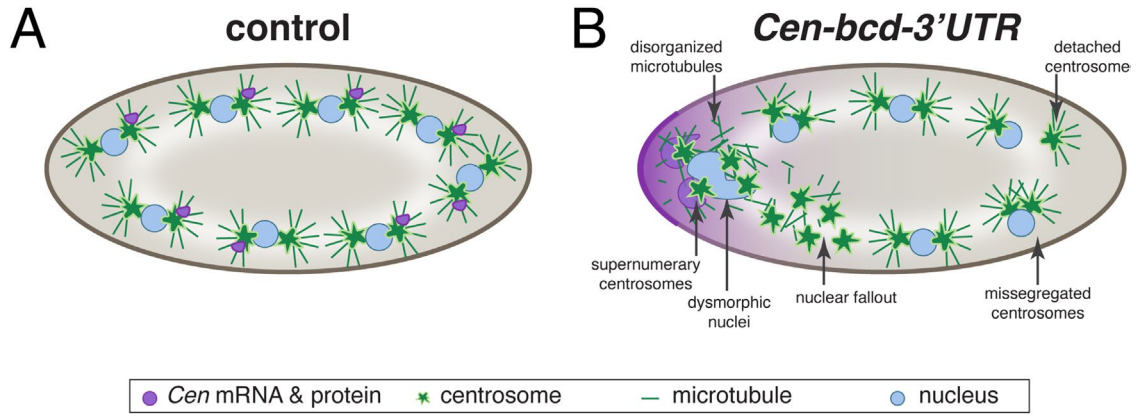

FIGURE 3: Mistargeting *Cen* mRNA in syncytial *Drosophila* embryos impairs centrosome function. Schematic shows *Cen* mRNA and protein localization and associated centrosome-related phenotypes in (A) control and (B) *Cen-bcd-3′UTR* embryos. In control embryos, *Cen* mRNA and protein colocalize as pericentrosomal granules asymmetrically enriched at the mother centrosome. Expression of *Cen-bcd-3′UTR* within otherwise *Cen* null embryos, however, results in the ectopic localization of *Cen* mRNA and protein to the anterior cortex. Mislocalized *Cen* mRNA and protein also form massive centrosome-enriched granules. In contrast, *Cen-bcd-3′UTR* embryos lack *Cen* mRNA or protein at more distal centrosomes near the embryo midregion or posterior. Mistargeting *Cen* mRNA to the anterior cortex significantly disrupts centrosome function, resulting in defects in centrosome position and centrosome–nucleus tethering. More severe phenotypes consistent with mitotic errors are apparent near the anterior, including disorganized microtubules, supernumerary centrosomes, enlarged and dysmorphic nuclei, as well as nuclear fallout, the ejection of damaged nuclei from the syncytial blastoderm cortex. Consequently, *Cen-bcd-3′UTR* embryos also show elevated rates of embryonic lethality. Taken together, these observations indicate the local concentration of *Cen* mRNA is important for centrosome function and mitotic integrity.

Additional evidence for local translation was beautifully demonstrated through live imaging. Translated SunTag sequences are rapidly bound by fluorescent nanobodies, permitting in vivo imaging of active translation when inserted upstream of a protein of interest (Yan *et al.*, 2016). Similarly, SunTag technology permitted detection of cotranslational transport and on-site translation of *ASPM* and *NUMA1* mRNAs at centrosomes (Chouaib *et al.*, 2020; Safieddine *et al.*, 2021). Taken together, these data strongly implicate centrosomes as sites for local translation.

FUNCTIONAL ROLES OF RNAS LOCALIZED TO CENTROSOMES

Early attempts to ascribe function to RNA at centrosomes yielded conflicting results. Basal bodies isolated from *Chlamydomonas* or *Tetrahymena* and injected into unfertilized *Xenopus* eggs organized microtubule asters that were RNase sensitive, suggesting RNA promoted the microtubule-organizing activity of centrosomes (Heidemann *et al.*, 1977). Consistent with these findings, microtubule growth and the abundance of PCM from isolated centrosomes proved to be RNase sensitive in other systems, too (Zackroff *et al.*, 1976; Pepper and Brinkley, 1980). Subsequent work contradicted some of these findings, however (Klotz *et al.*, 1990). Consequently, functional roles for RNA localized to centrosomes remained unclear.

Evidence of a likely role for local RNA influencing centrosome function later arose from the Richter laboratory. Groisman and coworkers mutated sites within the *cyc B* mRNA 3′-untranslated region (3′-UTR) required for RNA localization to spindle poles. Altering these sites or depleting the activity of the cognate RNA-binding protein, cytoplasmic polyadenylation element binding (CPEB), in *Xenopus* oocytes led to diminished *cyc B* mRNA and protein localization to the spindle pole, spindle defects, and mitotic delays (Groisman *et al.*, 2000). This work suggests local *cyc B* mRNA is required for spindle morphogenesis and mitotic progression, perhaps supporting local synthesis of Cyc B protein.

More recently, our group similarly manipulated the RNA-binding protein fragile-X mental retardation protein (FMRP) to investigate consequences for RNA localization and downstream phenotypic responses. *Cen* mRNA localizes to *Drosophila* centrosomes, and this localization requires intact polysomes, consistent with a cotranslational localization mechanism (Lecuyer *et al.*, 2007; Bergalet *et al.*, 2020). We identified FMRP, an RNA-binding protein that functions in translational repression (Darnell *et al.*, 2011), in a biochemical complex with *Cen* mRNA (Ryder *et al.*, 2020). Moreover, loss of *Fmr1*, the gene encoding FMRP, led to increased *Cen* mRNA localization to centrosomes and increased Cen protein translation, suggesting *Cen* mRNA localization and translation are regulated by FMRP (Ryder *et al.*, 2020). Consistently, reducing *Cen* dosage in *Fmr1* mutants partially rescued spindle defects and centrosome separation errors, indicating the titration of local *Cen* mRNA and/or protein dosage at centrosomes is functionally significant.

To directly test the role of local RNA, we mistargeted *Cen* mRNA to the anterior cortex of developing *Drosophila* embryos by fusing the *Cen* coding sequence with the *bicoid* (*bcd*) 3′-UTR (*Cen-bcd-3′-UTR* embryos), sufficient for RNA localization to the anterior cortex (Macdonald and Struhl, 1988). Mistargeting *Cen* mRNA to the anterior pole blocked localization of *Cen* mRNA or protein to distal centrosomes, resulting in phenotypes consistent with *Cen* loss, including centrosome separation errors and spindle defects (Kao and Megraw, 2009; Ryder *et al.*, 2020). This work shows local *Cen* mRNA is required at centrosomes for Cen protein localization and function. Ectopic *Cen* mRNA at the anterior pole also disrupted local microtubule organization and centrosome position, leading to DNA damage, and demonstrating the deleterious effects of excess local *Cen* activity (Figure 3, A and B). Based on the *Cen-bcd-3′-UTR* studies, we conclude local dosage of *Cen* mRNA is finely tuned to ensure normal centrosome function. Going forward, it will be of significant interest to determine whether the local translation of other centrosome-localized mRNAs is likewise required for normal centrosome function.

CONCLUDING REMARKS AND OPEN QUESTIONS

Despite historic debate, the localization of mRNA to centrosomes is now irrefutable. Moreover, recent work from independent laboratories and divergent model systems further implicates centrosomes as sites for local protein synthesis. While local translation is predicted to facilitate the rapid increase in PCM proteins intrinsic to centrosome activation before mitotic onset (i.e., centrosome maturation), further work is required to test this model. Indeed, the discovery of mRNAs localized to the centrosome far outpaces their functional characterization.

To understand the full impact of RNA localized to centrosomes, several critical questions remain to be addressed. The first set of questions relates to identifying which RNAs reside at centrosomes and how they get there. Foremost, for most mRNAs, the molecular machinery required for centrosomal localization, interacting binding partners, and key *cis* elements required for localization are still unknown. Understanding mechanisms of RNA localization will allow researchers to perturb the process and examine consequences to centrosome function. These investigations will also clarify whether cotranslational transport is generalizable to most centrosome-localized RNAs, as currently suggested by the literature, or whether transport mechanisms are transcript specific. Related to RNA transport, do multiple RNAs cotraffic? Transport particles comprising multiple RNAs may efficiently direct multiple RNA transcripts to a common destination. Also, what regulates the cell cycle dynamics of RNA enrichment to centrosomes, and are these oscillations relevant to centrosome activity or function? How do RNA distributions differ at centrosomes versus basal bodies, or in response to external stimuli? Do changes in RNA distribution contribute to centrosome heterogeneity observed in distinct cell types? Resolving these fundamental questions will allow researchers to better understand how RNA localization influences centrosome composition and frame additional experiments to ascertain biological consequences.

Many questions remain pertaining to the biological significance of RNA localized to centrosomes. Why is a specific RNA localized to the centrosome, and does it matter? While evidence supports the idea that some RNAs are subject to translational regulation at the centrosome, as demonstrated for *Drosophila Cen* mRNA, whether this is true for other centrosome-enriched RNAs requires further study. Similarly, details of what regulates translational control at the centrosome, and whether these mechanisms are linked to the cell cycle, are exciting areas of investigation. Do such mechanisms impinge on centrosome maturation, microtubule nucleation, or other processes? Conversely, do RNAs influence centrosome structure? Manipulating RNA localization is one approach to test these ideas.

Continued investigation will unearth the answers.

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REFERENCES

Argetsinger J (1965). The isolation of ciliary basal bodies (kinetosomes) from *TetrahymenaPyriformis*. J Cell Biol 24, 154–157.

Bergalet J, Patel D, Legendre F, Lapointe C, Benoit Bouvrette LP, Chin A, Blanchette M, Kwon E, Lecuyer E (2020). Inter-dependent centrosomal co-localization of the *cen* and *ik2cis*-natural antisense mRNAs in *Drosophila*. Cell Rep 30, 3339–3352.e3336.

Bettencourt-Dias M, Rodrigues-Martins A, Carpenter L, Riparbelli M, Lehmann L, Gatt MK, Carmo N, Balloux F, Callaini G, Glover DM (2005). SAK/PLK4 is required for centriole duplication and flagella development. Curr Biol 15, 2199–2207.

Blower MD, Feric E, Weis K, Heald R (2007). Genome-wide analysis demonstrates conserved localization of messenger RNAs to mitotic microtubules. J Cell Biol 179, 1365–1373.

Bullock SL (2011). Messengers, motors and mysteries: sorting of eukaryotic mRNAs by cytoskeletal transport. Biochem Soc Trans 39, 1161–1165.

Buxbaum AR, Haimovich G, Singer RH (2015). In the right place at the right time: visualizing and understanding mRNA localization. Nat Rev Mol Cell Biol 16, 95–109.

Chouaib R, Safieddine A, Pichon X, Imbert A, Kwon OS, Samacoits A, Traboulsi AM, Robert MC, Tsanov N, Coleno E, *et al*. (2020). A dual protein-mRNA localization screen reveals compartmentalized translation and widespread co-translational RNA targeting. Dev Cell 54, 773–791.e775.

Darnell JC, Van Driesche SJ, Zhang C, Hung KY, Mele A, Fraser CE, Stone EF, Chen C, Fak JJ, Chi SW, *et al*. (2011). FMRP stalls ribosomal translocation on mRNAs linked to synaptic function and autism. Cell 146, 247–261.

Das S, Vera M, Gandin V, Singer RH, Tutucci E (2021). Intracellular mRNA transport and localized translation. Nat Rev Mol Cell Biol 22, 483–504.

Dieterich DC, Link AJ, Graumann J, Tirrell DA, Schuman EM (2006). Selective identification of newly synthesized proteins in mammalian cells using bioorthogonal noncanonical amino acid tagging (BONCAT). Proc Natl Acad Sci USA 103, 9482–9487.

Ding D, Parkhurst SM, Halsell SR, Lipshitz HD (1993). Dynamic *Hsp83* RNA localization during *Drosophila* oogenesis and embryogenesis. Mol Cell Biol 13, 3773–3781.

Doxsey SJ, Stein P, Evans L, Calarco PD, Kirschner M (1994). Pericentrin, a highly conserved centrosome protein involved in microtubule organization. Cell 76, 639–650.

Fazal FM, Han S, Parker KR, Kaewsapsak P, Xu J, Boettiger AN, Chang HY, Ting AY (2019). Atlas of subcellular RNA localization revealed by APEX-Seq. Cell 178, 473–490.e426.

Femino AM, Fay FS, Fogarty K, Singer RH (1998). Visualization of single RNA transcripts in situ. Science 280, 585–590.

Fong KW, Choi YK, Rattner JB, Qi RZ (2008). CDK5RAP2 is a pericentriolar protein that functions in centrosomal attachment of the γ-tubulin ring complex. Mol Biol Cell 19, 115–125.

Forrest KM, Gavis ER (2003). Live imaging of endogenous RNA reveals a diffusion and entrapment mechanism for *nanos* mRNA localization in *Drosophila*. Curr Biol 13, 1159–1168.

Fu J, Glover DM (2012). Structured illumination of the interface between centriole and peri-centriolar material. Open Biol 2, 120104.

Gavis ER, Lehmann R (1994). Translational regulation of nanos by RNA localization. Nature 369, 315–318.

Gavis ER, Singer RH, Huttelmaier S (2007). Localized translation through messenger RNA localization. In: Translational Control in Biology and Medicine, ed. JWB Hershey, Mathews MB, Sonenberg N, Vol. 48. Cold Spring Harbor Press, New York, 687–717.

Goldman RD, Rebhun LI (1969). The structure and some properties of the isolated mitotic apparatus. J Cell Sci 4, 179–209.

Gould RR, Borisy GG (1977). The pericentriolar material in Chinese hamster ovary cells nucleates microtubule formation. J Cell Biol 73, 601–615.

Groisman I, Huang YS, Mendez R, Cao Q, Theurkauf W, Richter JD (2000). CPEB, maskin, and *cyclin B1* mRNA at the mitotic apparatus: implications for local translational control of cell division. Cell 103, 435–447.

Habedanck R, Stierhof YD, Wilkinson CJ, Nigg EA (2005). The Polo kinase Plk4 functions in centriole duplication. Nat Cell Biol 7, 1140–1146.

Hao K, Chen Y, Yan X, Zhu X (2021). Cilia locally synthesize proteins to sustain their ultrastructure and functions. Nat Commun 12, 6971.

Hartman H, Puma JP, Gruney T Jr (1974). Evidence for the association of RNA with the ciliary basal bodies of *Tetrahymena*. J Cell Sci 16, 241–259.

Hassine S, Bonnet-Magnaval F, Benoit Bouvrette LP, Doran B, Ghram M, Bouthillette M, Lecuyer E, DesGroseillers L (2020). Staufen1 localizes to the mitotic spindle and controls the localization of RNA populations to the spindle. J Cell Sci 133, jcs247155.

Heidemann SR, Sander G, Kirschner MW (1977). Evidence for a functional role of RNA in centrioles. Cell 10, 337–350.

Hoffman EJ (1965). The nucleic acids of basal bodies isolated from *Tetrahymenapyriformis*. J Cell Biol 25, 217–228.

Holt CE, Bullock SL (2009). Subcellular mRNA localization in animal cells and why it matters. Science 326, 1212–1216.

Jeffery WR, Tomlinson CR, Brodeur RD (1983). Localization of actin messenger RNA during early ascidian development. Dev Biol 99, 408–417.

Joshi HC, Palacios MJ, McNamara L, Cleveland DW (1992). γ-Tubulin is a centrosomal protein required for cell cycle-dependent microtubule nucleation. Nature 356, 80–83.

Jung H, Gkogkas CG, Sonenberg N, Holt CE (2014). Remote control of gene function by local translation. Cell 157, 26–40.
Kao LR, Megraw TL (2009). Centrocortin cooperates with centrosomin to organize *Drosophila* embryonic cleavage furrows. Curr Biol 19, 937–942.
Karsenti E, Kobayashi S, Mitchison T, Kirschner M (1984). Role of the centrosome in organizing the interphase microtubule array: properties of cytoplasts containing or lacking centrosomes. J Cell Biol 98, 1763–1776.
Katz ZB, Wells AL, Park HY, Wu B, Shenoy SM, Singer RH (2012). β-Actin mRNA compartmentalization enhances focal adhesion stability and directs cell migration. Genes Dev 26, 1885–1890.
Khodjakov A, Rieder CL (1999). The sudden recruitment of gamma-tubulin to the centrosome at the onset of mitosis and its dynamic exchange throughout the cell cycle, do not require microtubules. J Cell Biol 146, 585–596.
Kislauskis EH, Singer RH (1992). Determinants of mRNA localization. Curr Opin Cell Biol 4, 975–978.
Kislauskis EH, Zhu X, Singer RH (1997). β-Actin messenger RNA localization and protein synthesis augment cell motility. J Cell Biol 136, 1263–1270.
Klotz C, Dabauvalle MC, Paintrand M, Weber T, Bornens M, Karsenti E (1990). Parthenogenesis in *Xenopus* eggs requires centrosomal integrity. J Cell Biol 110, 405–415.
Kobayashi T, Dynlacht BD (2011). Regulating the transition from centriole to basal body. J Cell Biol 193, 435–444.
Kwon OS, Mishra R, Safieddine A, Coleno E, Alasseur Q, Faucourt M, Barbosa I, Bertrand E, Spassky N, Le Hir H (2021). Exon junction complex dependent mRNA localization is linked to centrosome organization during ciliogenesis. Nat Commun 12, 1351.
Lawo S, Hasegan M, Gupta GD, Pelletier L (2012). Subdiffraction imaging of centrosomes reveals higher-order organizational features of pericentriolar material. Nat Cell Biol 14, 1148–1158.
Lawrence JB, Singer RH (1986). Intracellular localization of messenger RNAs for cytoskeletal proteins. Cell 45, 407–415.
Lecuyer E, Yoshida H, Parthasarathy N, Alm C, Babak T, Cerovina T, Hughes TR, Tomancak P, Krause HM (2007). Global analysis of mRNA localization reveals a prominent role in organizing cellular architecture and function. Cell 131, 174–187.
Long RM, Singer RH, Meng X, Gonzalez I, Nasmyth K, Jansen RP (1997). Mating type switching in yeast controlled by asymmetric localization of ASH1 mRNA. Science 277, 383–387.
Macdonald PM, Struhl G (1988). *Cis*-acting sequences responsible for anterior localization of *bicoid* mRNA in *Drosophila* embryos. Nature 336, 595–598.
Mallam AL, Sae-Lee W, Schaub JM, Tu F, Battenhouse A, Jang YJ, Kim J, Wallingford JB, Finkelstein IJ, Marcotte EM, Drew K (2019). Systematic discovery of endogenous human ribonucleoprotein complexes. Cell Rep 29, 1351–1368.e1355.
Marshall WF, Rosenbaum JL (2000). Are there nucleic acids in the centrosome? Curr Top Dev Biol 49, 187–205.
Martin KC, Ephrussi A (2009). mRNA localization: gene expression in the spatial dimension. Cell 136, 719–730.
Martinez-Campos M, Basto R, Baker J, Kernan M, Raff JW (2004). The *Drosophila* pericentrin-like protein is essential for cilia/flagella function, but appears to be dispensable for mitosis. J Cell Biol 165, 673–683.
Megraw TL, Li K, Kao LR, Kaufman TC (1999). The centrosomin protein is required for centrosome assembly and function during cleavage in *Drosophila*. Development 126, 2829–2839.
Meignin C, Davis I (2010). Transmitting the message: intracellular mRNA localization. Curr Opin Cell Biol 22, 112–119.
Mennella V, Keszthelyi B, McDonald KL, Chhun B, Kan F, Rogers GC, Huang B, Agard DA (2012). Subdiffraction-resolution fluorescence microscopy reveals a domain of the centrosome critical for pericentriolar material organization. Nat Cell Biol 14, 1159–1168.
Mitchison T, Kirschner M (1984). Microtubule assembly nucleated by isolated centrosomes. Nature 312, 232–237.
Murray RG, Murray AS, Pizzo A (1965). The fine structure of mitosis in rat thymic lymphocytes. J Cell Biol 26, 601–619.
Nigg EA, Raff JW (2009). Centrioles, centrosomes, and cilia in health and disease. Cell 139, 663–678.
Pascual R, Segura-Morales C, Omerzu M, Bellora N, Belloc E, Castellazzi CL, Reina O, Eyras E, Maurice MM, Millanes-Romero A, Mendez R (2020). mRNA spindle localization and mitotic translational regulation by CPEB1 and CPEB4. RNA 27, 291–302.
Pepper DA, Brinkley BR (1980). Tubulin nucleation and assembly in mitotic cells: evidence for nucleic acids in kinetochores and centrosomes. Cell Motil 1, 1–15.
Pihan GA (2013). Centrosome dysfunction contributes to chromosome instability, chromoanagenesis, and genome reprograming in cancer. Front Oncol 3, 277.
Raff JW, Whitfield WG, Glover DM (1990). Two distinct mechanisms localise *cyclinB* transcripts in syncytial *Drosophila* embryos. Development 110, 1249–1261.
Ryder PV, Fang J, Lerit DA (2020). *centrocortin* RNA localization to centrosomes is regulated by FMRP and facilitates error-free mitosis. J Cell Biol 219, e202004101.
Ryder PV, Lerit DA (2018). RNA localization regulates diverse and dynamic cellular processes. Traffic 19, 496–502.
Ryder PV, Lerit DA (2020). Quantitative analysis of subcellular distributions with an open-source, object-based tool. Biol Open 9, bio055228.
Safieddine A, Coleno E, Salloum S, Imbert A, Traboulsi AM, Kwon OS, Lionneton F, Georget V, Robert MC, Gostan T, *et al*. (2021). A choreography of centrosomal mRNAs reveals a conserved localization mechanism involving active polysome transport. Nat Commun 12, 1352.
Sagan L (1967). On the origin of mitosing cells. J Theor Biol 14, 255–274.
Seaman GR (1960). Large-scale isolation of kinetosomes from the ciliated protozoan *Tetrahymenapyriformis*. Exp Cell Res 21, 292–302.
Seaman GR (1962). Protein synthesis by kinetosomes isolated from the protozoan *Tetrahymena*. Biochim Biophys Acta 55, 889–899.
Sepulveda G, Antkowiak M, Brust-Mascher I, Mahe K, Ou T, Castro NM, Christensen LN, Cheung L, Jiang X, Yoon D, *et al*. (2018). Co-translational protein targeting facilitates centrosomal recruitment of PCNT during centrosome maturation in vertebrates. eLife 7, e34959.
Sharp JA, Plant JJ, Ohsumi TK, Borowsky M, Blower MD (2011). Functional analysis of the microtubule-interacting transcriptome. Mol Biol Cell 22, 4312–4323.
Sonnen KF, Schermelleh L, Leonhardt H, Nigg EA (2012). 3D-structured illumination microscopy provides novel insight into architecture of human centrosomes. Biol Open 1, 965–976.
Sorokin S (1962). Centrioles and the formation of rudimentary cilia by fibroblasts and smooth muscle cells. J Cell Biol 15, 363–377.
Takizawa PA, Sil A, Swedlow JR, Herskowitz I, Vale RD (1997). Actin-dependent localization of an RNA encoding a cell-fate determinant in yeast. Nature 389, 90–93.
tom Dieck S, Kochen L, Hanus C, Heumuller M, Bartnik I, Nassim-Assir B, Merk K, Mosler T, Garg S, Bunse S, *et al*. (2015). Direct visualization of newly synthesized target proteins in situ. Nat Methods 12, 411–414.
Vaizel-Ohayon D, Schejter ED (1999). Mutations in *centrosomin* reveal requirements for centrosomal function during early *Drosophila* embryogenesis. Curr Biol 9, 889–898.
Varmark H, Llamazares S, Rebollo E, Lange B, Reina J, Schwarz H, Gonzalez C (2007). Asterless is a centriolar protein required for centrosome function and embryo development in *Drosophila*. Curr Biol 17, 1735–1745.
Wang ET, Taliaferro JM, Lee JA, Sudhakaran IP, Rossoll W, Gross C, Moss KR, Bassell GJ (2016). Dysregulation of mRNA localization and translation in genetic disease. J Neurosci 36, 11418–11426.
Yan X, Hoek TA, Vale RD, Tanenbaum ME (2016). Dynamics of translation of single mRNA molecules in vivo. Cell 165, 976–989.
Zackroff RV, Rosenfeld AC, Weisenberg RC (1976). Effects of RNase and RNA on in vitro aster assembly. J Supramol Struct 5, 577–589.
Zein-Sabatto H, Lerit DA (2021). The identification and functional analysis of mRNA localizing to centrosomes. Front Cell Dev Biol 9, 782802.