RNA assemblages orchestrate complex cellular processes

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Eukaryotic mRNAs are monocistronic, and therefore mechanisms exist that coordinate the synthesis of multiprotein complexes in order to obtain proper stoichiometry at the appropriate intracellular locations. RNA-binding proteins containing low-complexity sequences are prone to generate liquid droplets via liquid-liquid phase separation, and in this way create cytoplasmic assemblages of functionally related mRNAs. In a recent iCLIP study, we showed that the Drosophila RNA-binding protein Imp, which exhibits a C-terminal low-complexity sequence, increases the formation of F-actin by binding to 3' untranslated regions of mRNAs encoding components participating in F-actin biogenesis. We hypothesize that phase transition is a mechanism the cell employs to increase the local mRNA concentration considerably, and in this way synchronize protein production in cytoplasmic territories, as discussed in the present review.

Keywords:
- post-transcriptional RNA regulon; RNA assemblage; RNA-binding protein; RNP granule; liquid droplet; low-complexity sequence

Introduction

Since 1961, when Jacob and Monod suggested their operon model, the concept of the polycistronic mRNA encoding functionally related proteins has been a paradigm in bacterial and archaeal gene regulation. It is assumed that this mode of co-regulation ensures proportional synthesis of components in multiprotein complexes by translational control, and recent ribosome profiling analysis of global gene expression in Escherichia coli by Weissman and co-workers [1] has shown that this is generally the case. Proportional synthesis avoids dominant-negative effects of excess components that will have to be eliminated by proteolytic quality control. An added bonus of protein synthesis from polycistronic mRNAs is the proximity of the resulting protein products, thus facilitating expedient macromolecular assembly or catalysis.

The prokaryotic mode of creating multiprotein complexes is in sharp contrast to the way the considerably larger eukaryotic cell, encoding monocistronic mRNAs, achieves proximity and stoichiometry, although classical cases of pyrimidine and purine biosynthesis have evolved multifunctional enzymes and enzyme clustering [2, 3]. Faced with this conundrum, Jack Keene [4] suggested that the coordination of gene expression to some extent was delegated from the DNA to the RNA level via the formation of post-transcriptional RNA regulons. The salient feature behind this hypothesis is the pivotal role of a common RNA-binding protein (RBP) associating with mRNAs encoding functionally related proteins and in this way dictating a common fate.

In this review, we describe examples of low-complexity RBPs coordinating RNA metabolism in both mono- and multicellular organisms with an emphasis on cytosolic ribonucleoprotein (RNP) granules (Table 1). We present the available evidence regarding their status as liquid droplets, including our own recent study of the participation of the Drosophila RBP Imp in F-actin formation.

Modular RBPs have a multitude of RNA targets

It is estimated that mammalian cells contain between 800 and 1,600 different RBPs, and about half of these encompasses common RNA-binding modules such as RRMs, KH domains,
CSDs, dsRBDs, RGG motifs, and zinc fingers in various combinations [5–7]. The other half does not contain an easily recognisable module – usually illustrated by the dual behavior of cytosolic aconitate, which switches between high-affinity RNA-binding and catalysis depending on the intracellular iron concentration [8]. From X-ray and NMR studies, a good understanding of the structure of the single RNA-binding module in complex with RNA has emerged [9, 10]. Moreover, several structural examples of truncated multi-domain RBPs in complex with RNA targets are available [11, 12].

There has been a flurry of high-throughput CLIP data on the targetome of full-length RBPs and attempts at defining recognition elements. Besides the well-characterized interaction between Pumilio and its target revealing an 8-nt recognition “code” [13, 14], many RBPs are promiscuous and exhibit low specificity, although the combination of modules within a single RBP will increase the specificity considerably [15]. Because a single RBP may literally have thousands of different interactions with the transcriptome, and hundreds of RBPs may behave in this manner, the complexity is daunting. Nevertheless, the combinatorial binding or competition among RBPs determines the fate of the individual transcript [16, 17].

Are RNP granules membrane-less liquid droplets?
The cell is compartmentalized, and in recent years the participation of RBPs in the formation of membrane-less organelles by phase transition has been examined extensively. Seminal studies were carried out with germ granules (termed P granules) in Caenorhabditis elegans, identifying them as liquid droplets formed by phase separation from the cytoplasm [18], but the concept of phase transition of low-complexity proteins was described earlier for FG-rich nucleoporins [19]. The fortuitous use – by McKnight and co-workers – of a biotinylated isoxazole derivative to stabilize β-strand conformations in intrinsically disordered RBPs paved the way for the biochemical isolation of material within these membrane-less organelles. It turned out that especially low-complexity RBPs such as FUS (Fused in Sarcoma), hnRNPA1 and hnRNPA2B1 were abundant in the droplets/hydrogels [20, 21](Fig. 1). Intriguingly, mRNAs in the hydrogels exhibited a preponderance of long 3’UTRs, which provide a platform for RBP interplay, and could mean that mRNAs in liquid droplets are likely to be regulated mRNA species. An emerging theme in mRNA studies is that extensive 3’UTRs act as scaffolds for post-transcriptional regulatory purposes, and that physiologic responses depend on competing and/or cooperating trans-acting factors [22–24].

P bodies and stress granules contain low-complexity RBPs
P bodies and stress granules are cytoplasmic RNP bodies that exhibit droplet properties. P bodies have been examined in studies of mRNA decay and translational repression, and the marker is usually the decapping enzyme Dcp2 [25]. Stress granules are formed in response to various cellular stresses such as arsenite and glucose deprivation, and are considered to be a pool of mRNPs stalled during translation initiation with TIA-1 as a common marker [26, 27]. However, a clear distinction between the two types of RNP bodies, based on the presence of a particular RBP, is not straightforward [28], and neither type seems to be the cause, but rather a consequence, of polysome disassembly [29–31].

Both types of RNP bodies incorporate low-complexity RBPs. In particular stress granules are regarded as pivotal in the pathogenesis of the neurodegenerative diseases amyotrophic lateral sclerosis (ALS) and frontotemporal dementia (FTD) via fibrillization of RBPs such as hnRNPA1, hnRNPA2B1, FUS and TDP-43 [32–34]. Although the low-complexity sequence from hnRNPA1 is sufficient to mediate liquid-liquid phase separation, the inclusion of the two RRMs in full-length hnRNPA1, and the presence of RNA, favor reversibility rather than fibrillization [35]. This study also showed that fluorescence recovery after photobleaching (FRAP) analysis of hnRNPA1 within liquid droplets exhibited kinetics on the timescale of seconds, both in vitro and in vivo. This is in striking contrast to the near absence of recovery within 15 min in cross-β fibrillar hydrogels, and suggests a more rigid incorporation of hnRNPA1 in the latter. If a zipper motif within the low-complexity sequence of hnRNPA1 is removed (termed delta-hexa mutant), fibrillization is abrogated without affecting liquid droplet formation, thereby uncoupling the two phenomena mechanistically. Moreover, the presence of RNA reduced the necessary critical hnRNPA1 concentration for liquid-liquid phase separation. Finally, a disease-causing hnRNPA1 D262V mutation [36] did not appear to alter molecular interactions that drive phase separation, but increased the propensity toward amyloid-like fibrillization subsequently [35].

Parker and co-workers [37] also examined the propensity of full-length hnRNPA1 and the delta-hexa and D262V mutants to form liquid droplets in vitro, and obtained similar results, namely that a low salt concentration (37.5 mM) and high

### Table 1. RNA-binding proteins discussed in this review

<table>
<thead>
<tr>
<th>Acronym</th>
<th>Organism</th>
<th>RNA-binding domains</th>
<th>Low-complexity sequence</th>
<th>RefSeq</th>
</tr>
</thead>
<tbody>
<tr>
<td>hnRNPA1</td>
<td>human</td>
<td>2 RRMs</td>
<td>Gly and Ser</td>
<td>NP_002127</td>
</tr>
<tr>
<td>hnRNPA2B1</td>
<td>human</td>
<td>2 RRMs</td>
<td>Gly</td>
<td>NP_112533</td>
</tr>
<tr>
<td>FUS</td>
<td>human</td>
<td>2 RRMs</td>
<td>Gly, Ser, and Tyr</td>
<td>NP_004951</td>
</tr>
<tr>
<td>Whi3p</td>
<td>yeast</td>
<td>1 RRM</td>
<td>Gin</td>
<td>NP_014202</td>
</tr>
<tr>
<td>PuF3p</td>
<td>yeast</td>
<td>8 pumilio repeats</td>
<td>Asn and Gln</td>
<td>NP_013088</td>
</tr>
<tr>
<td>Imp</td>
<td>Drosophila</td>
<td>4 KH domains</td>
<td>Gin</td>
<td>NP_511111</td>
</tr>
</tbody>
</table>

Bioessays 38: 674–681, © 2016 The Authors BioEssays Published by WILEY Periodicals, Inc.
Problems & Paradigms of FUS are seen in relation to the neurodegenerative diseases between nucleus and cytoplasm, and importantly, mutations in the terminal low-complexity sequence, an ability to shuttle between regions with varying liquid-liquid compartments both in vitro and in vivo. This is due to several facts: High intracellular concentration, extensive N-terminal low-complexity sequence, an ability to shuttle between nucleus and cytoplasm, and importantly, mutations of FUS are seen in relation to the neurodegenerative diseases.

A transition to more solid-like droplets is accelerated by disease mutations

An emerging theme in studies of liquid droplets is that they evolve into more solid-like entities, and that this transition is greatly accelerated by disease mutations. A controversial issue has been whether conformations of low-complexity sequences in liquid droplets are different from those appearing in more fibrous hydrogels. However, a chemical footprinting experiment with N-acetyl-imidazole has been unable to identify differences in side-chain accessibility of the low-complexity region in hnrNPA2B1, regardless of its presence in liquid droplets, hydrogels – or nuclei for that matter – and suggests cross-β polymerization as a unifying principle [39]. Nevertheless, the physiological relevance of fibrous hydrogels is a pending issue.

Fused in Sarcoma (FUS) is a favorite RBP in studies of liquid droplets in a heterogeneous manner, illustrated by different colors of low-complexity RBPs. The presence of RNA (drawn as “snakes”) together with dynamic, multiple weak interactions between intrinsically disordered protein regions (not shown), seems critical for droplet formation. In hydrogels, the interactions between the disordered regions are less dynamic because of cross-β conformations, and hydrogels appear to exhibit a broad spectrum of reversibility. Formation of amyloid-like inclusions of low reversibility, associated with disease mutations, is shown at the right. Partitioning of RNPs into droplets/hydrogels increases their local concentration by orders of magnitude [38] and thereby the likelihood of fibrillization.

Regardless of whether the wild-type or mutants were analyzed by fluorescence microcopy, a physiological salt concentration (150 mM) resulted in a one-phase system, unless RNA was present together with crowding agents such as polyethylene glycol or Ficoll. However, the kinetics of fibrillization was strikingly different, in that the D262V mutant formed SDS-resistant fibers, whose rate of formation was increased by prior droplet formation, presumably due to an increased protein concentration within the droplets.

Taken together, the crucial players for forming RNP granules via liquid-liquid phase separation appear to be RBPs containing low-complexity sequences and RNA. Multivalency seems to be the key concept behind RNP granule assembly offering synergy between multiple RNA-binding modules in RBPs, multiple RBP target sites on RNA, and multiple low-complexity sequences in RBPs [38].

Whi3p droplet properties depend on RNA identity

In multinucleate large Ashbya cells, the G1 cyclin CLN3 transcript shows a nonrandom spatial clustering due to a glutamine-rich region in the RBP Whi3p, and this inhomogeneous distribution is crucial for cell-cycle timing variability and asynchrony of the nuclei [32]. An additional mRNA target for Whi3p is the BNI1 transcript encoding formin, which is important for establishing polarity [46]. Recombinant Whi3p (28 μM) is able to form protein-only liquid droplets at 75 mM KCl in vitro, but not at physiological salt concentrations. In contrast, the liquid-liquid phase separation of protein-RNA droplets is promoted at physiological salt concentration and protein concentration were necessary for phase separation.
Although entity in terms of high-affinity RNA-binding, granular RNP assembly, and RNA localization [77]. Although Drosophila Imp exhibits rudimentary features of RRMs in minor isoforms, the major isoform of 566 amino acid lacks RRMs. Instead, Drosophila Imp contains a large C-terminal low-complexity glutamine-rich sequence (LCS).

200 nM protein by the presence of RNA in the guise of either CLN3 or BNI1 mRNAs [47]. Moreover, the strict dependence on the RRM domain for Whi3p droplet formation reinforces the important role of RNA. Although both mRNAs encompass five putative UGCAU attachment sites for Whi3p, the viscosity of the two types of protein–RNA droplets, and their propensity to fuse, are different. This implies that the identity of the participating mRNA component could tune the functional specificity and encompass information beyond mere coding ability. Therefore, a combination of low-complexity sequences and multivalent interactions appears to be critical for intracellular phase transition, although the effect of the spacing pattern of Whi3p attachment sites on mRNA targets is unknown. During droplet maturation, the transition from a liquid to a more fibrillar state of glutamine-rich RBPs, such as Whi3p, is diminished considerably by the presence of RNA [40, 47]. In fact, the negatively charged RNA influences the viscoelastic properties of liquid droplets, as measured by micro rheology and FRAP, and gives rise to decreased viscosity within the droplet termed RNA-induced fluidization [44, 47]. The presence of mRNA within these intracellular reactors is therefore crucial for reversibility and, by inference, its subsequent recruitment to the translational apparatus.

Puf3p phosphorylation activates mRNAs encoding mitochondrial proteins

Low-complexity sequences exhibit enrichment of serine and arginine residues [54], thereby providing ample opportunity for post-translational modifications such as phosphorylations and methylations, respectively, that could regulate the reversibility of mRNAs within RNP granules [55]. For example, chemical inhibition of the dual specificity kinase DYRK3 in HeLa cells affects the dissolution of stress granules by preventing autophosphorylation of its own low-complexity N-terminus and phosphorylation of RBPs [56]. Moreover, phosphorylation of intrinsically disordered MEG substrates by the C. elegans DYRK3 homologue drives the dissolution of P granules in embryos, whereas condensation is mediated by a PP2A phosphatase [57]. In the next section, we describe one of the most clear-cut examples of a post-transcriptional RNA regulon that is regulated by environmental cues.

Puf3p associates with cytoplasmic mRNAs encoding mitochondrial proteins in budding yeast [58, 59]. The exact mechanism behind the coordination in terms of localization and/or translatability has been unclear, but a recent study suggests that the participation of RNP granules is pivotal for the physiology of the regulon [60]. Upon glucose starvation, Puf3p becomes heavily phosphorylated, mainly within its N-terminal low-complexity region, and this results in translational activation of bound mRNAs, thereby promoting mitochondrial biogenesis and the capacity for oxidative catabolism of carbon sources [61]. From a mechanistic point of view, it should be noted that phosphorylated Puf3p co-sediments with its target mRNAs in polysomes, suggesting that the translational activation is due to interference with protein–protein, rather than RNA–protein, interactions. Moreover, a phosphomutant containing 24 serine/threonine-to-

RNP granules encompass RNA assemblages

The RNP granule can be regarded as the physical manifestation of the post-transcriptional RNA regulon, because low-complexity sequences in intrinsically disordered regions of RBPs would have an ability to interact both homo- and heterotypically in a dynamic fashion. The concept of an RNP granule is appealing, because this would allow mRNAs encoding functionally related proteins to be stored/transposed in a repressed form and be translated locally in a synchronous manner. The RNP granule concept has been widely accepted among neurobiologists, because mRNAs are transported over considerable distances to obtain local protein synthesis in axons and dendrites [48].

Despite the widespread acclaim of the RNP granule as a mode of harnessing and transporting mRNAs, there are few studies that have identified the molecular motors involved [49–51]. It is generally assumed that long-range movements of RNP granules take place on microtubules and that short-range transport will take place on microfilaments, a concept that is based on disturbances following nocodazole and cytochalasin D treatments, respectively. However, because optical resolution has improved, it is not clear whether RNP granules are co-localizing with microtubules or are tethered via ER/endosomes [52, 53]. An additional question related to RNP granules – at least if based on a solid-like structure – is that of reversibility, i.e. how is the mRNA deployed at the site of translation? The most obvious solution is a signal transduction event leading to a post-translational modification or proteolysis of the RBP. By breaking protein–protein, rather than RNA–protein, interactions, mRNA could be released in an accessible form to the translational apparatus.

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cross-linking sites on the entire transcriptome regardless of experimental approach allows the identification of in vivo followed by immunoprecipitation of lysates [64]. The iCLIP Drosophila coordinates the expression of a subset of mRNAs by creating of hydrogels in a biotinylated isoxazole precipitation assay (Fig. 2). Moreover, passes a C-terminal glutamine-rich low-complexity sequence homologue, we noticed that the latter encom-

In a comparison of the oncofetal RBP IMP family with its Imp coordinates an RNA assemblage Drosophila in terms of time and space is governed by the RBP Puf3p in RNPs accessible to the translational apparatus. The coordina-
tion in terms of time and space is governed by the RBP PuF3p in the appropriate amount – at least at the transcript level – of neurogenesis defects – almost to the point of being stochastic – and even survivors at the pharate adult stage are unable to eclose, suggesting locomotory failure. The broad spectrum of defects is compatible with what was observed in the cell-line: namely that all components appear to be formed in the appropriate amount – at least at the transcript level – regardless of Imp. However, the possibility of producing the components in high local concentrations facilitating macro-
molecular assembly is jeopardized to varying degrees. A study of果 translational RNA regulon – would be in the vicinity of each individual affinities [65, 66], whereas RBP immunoprecipitation on its own preferentially captures stable interactions without pinpointing the precise binding sites within an mRNA. Regardless of the procedure employed, mRNAs encoding components involved in the coordination of F-actin formation were enriched (Fig. 3). To address the physiological significance of the Imp RNA assemblage, we reduced the level of Imp in Drosophila S2 cells by RNA interference and examined the effect on the steady-state F-actin level by staining with phalloidin. S2 cells are spherical without extensive protrusions, but the cellular F-actin level was nevertheless diminished by 36% upon Imp reduction. By carrying out a global transcriptome analysis, we were able to establish that Imp did not alter the global S2 transcriptome, and that the total cytosolic actin monomer concentration was unchanged. We interpret this as an effect of an RBP on local cytoplasmic events rather than on overall cellular post-transcriptional regulation. A simple model would be that Imp defines an RNA assemblage ensuring that functionally related mRNAs – i.e. a post-

Transcripts associated with the Imp-implicated in the formation and maintenance of F-actin in lamellipodia. Several effector proteins are needed to nucleate, elongate, depolymerize, bundle and contract the actin filaments in order to reorganize the shape of the leading edge of a cell in response to external guidance cues. Profilin is responsible for the addition of actin monomers to the barbed end of growing filaments by interacting with the barbed-end protector proteins, the formins and Ena/VASP [78]. Formins and Ena/VASP also ensure continuous growth of the filament by inhibiting the binding of capping proteins, Cap2 and Esp8, otherwise capable of blocking the addition of actin monomers [79, 80]. In lamellipodia, the mesh-

Actin dynamics
R, RhoGDI, Rin, Cdc42, Rac1, Moe, Zip, Pp1-878, Mys, Msn, Chic
Microtubule dynamics
Mapmodulin, Rin, Sept1, Pnut
Vesicle dynamics
Vag, Vha16-1, Vha26, Vha68-2, Vha55, SesB, Surf4, Sar1, Reb11, Reb5, Afp31F
Membrane dynamics and signaling
Sty, Eif, Atj79F, PRL-1, Prominin-like, alpha-Spec, 14-3-3 epsilon, Vsp-33-3, Fox
Translational regulation
Hrb27c, pA5p, 9ot, elf-1A

Drosophila Imp coordinates an RNA assemblage involved in growth cone dynamics

In a comparison of the oncofetal RBP IMP family with its Drosophila homologue, we noticed that the latter encom-
passes a C-terminal glutamine-rich low-complexity sequence (Fig. 2). Moreover, Drosophila Imp has been shown to be part of hydrogels in a biotinylated isoxazole precipitation assay [20]. To address the possibility that this particular RBP coordinates the expression of a subset of mRNAs by creating an RNA assemblage within RNP granules [63], we subjected Drosophila S2 cells to either short or long-wave UV irradiation followed by immunoprecipitation of lysates [64]. The iCLIP experimental approach allows the identification of in vivo cross-linking sites on the entire transcriptome regardless of alanine mutations exhibits entrapment of target mRNAs in RNP granules and a severe growth arrest in response to glucose depletion. Taken together, this study suggests that signal transduction mediated by glucose deprivation unfolds RNP granules (in this case PUF bodies), rendering monomeric RNP granules and a severe growth arrest in response to glucose depletion. Taken together, this study suggests that signal transduction mediated by glucose deprivation unfolds RNP granules (in this case PUF bodies), rendering monomeric RNP granules and a severe growth arrest in response to glucose depletion. Taken together, this study suggests that signal transduction mediated by glucose deprivation unfolds RNP granules (in this case PUF bodies), rendering monomeric...
because defects in mushroom body (somewhat reminiscent of the hippocampus) neurogenesis in Imp-deficient animals can be partially rescued by Chickadee. The latter is the Drosophila homologue of profilin, which is the main facilitator of F-actin formation from G-actin. One would also expect transcripts encoding Rho GTPases, moesin, ena/VASP, and cytosolic actin itself in a post-transcriptional RNA regulon coordinated by Imp and conveying cues from the membrane to the cytoskeleton, and this was actually observed [64]. A recent translational profiling study of the conversion of growth cones into presynaptic terminals in Drosophila photoreceptor R cells has shown that prior to differentiation there is a 40-fold upregulation of Imp. Moreover, all of the actin regulatory proteins encoded by mRNAs, identified in our iCLIP study, are expressed in R cells during synapse formation [69]. Taken together, a picture emerges where one phase transition, namely the partitioning of RNPs into liquid droplets, facilitates a subsequent transition of monomeric actin into F-actin [70].

**The advantages in clustering functionally related mRNAs within an RNA assemblage**

Compared with solid-like cytoplasmic inclusions, liquid droplets offer some intrinsic advantages especially in terms of dynamics, because material can enter and exit the droplet faster but still be concentrated in a small volume [71]. The latter is important, because concomitant release of a high local concentration of related mRNAs to the translational apparatus will facilitate a high local protein concentration of newly synthesized interacting species (Fig. 4). Based on RNP body condensation/dissolution behavior following translational inhibition of either initiation or elongation, respectively [29, 72], it is generally assumed that the translational apparatus does not have access to the droplet interior. However, it should be recalled that ribosomal proteins themselves exhibit intrinsically disordered regions termed “waggly tails” [73]. A few studies have addressed the presence of translating ribosomes in the vicinity of RNP granules [74, 75], and the study by Mili and co-workers [76] actually showed translation within cytoplasmic FUS granules generating local protein production from APC-RNPs in NIH 3T3 protrusions. In general, the understanding of the location and the identity of the ribosomes carrying out the local synthesis is lagging behind, so this should be an important line of enquiry in upcoming studies.

**Conclusions and prospects**

In this essay, we have presented the rationale behind clustering functionally related mRNAs in assemblages, with an emphasis on coordinated and accelerated recruitment to the translational apparatus. An additional bonus of partitioning is fidelity, allowing much less volume and time for aberrant interactions among the resulting protein products. However, this mechanism does not come without a cost, because phase separation of an RBP is a fine balance between physiological assembly and pathological fibrillization.

Recent genome-wide screenings strongly support the concept of RNA assemblages segregated by particular RBPs. To understand the physiological significance of RNA assemblages, we need a deeper understanding of their dynamic behavior and molecular composition. The crucial role of RNA, salt and temperature for droplet dynamics has been obtained from studies in vitro focusing on the biophysical behavior of tagged low-complexity sequences. However, visualization of the interplay between RNP granules and the translational apparatus in vivo is strongly needed. Microscopes are now approaching single RNP particle resolution, so studies should be directed toward endogenous components rather than reporters with various tags. Moreover, low-complexity sequences in homologous RBPs exhibit low levels of conservation, so comparative studies may provide clues to the rationale behind these intrinsically disordered regions in terms of evolutionary rewiring of post-transcriptional regulation.
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A number of granular RBPs have been implicated in neurological diseases. So far we know little about the potential druggability of the conditions, but the concept of modifying particular RNA assemblages is an appealing one, because a complex process might be influenced by a single drug. Blockmirs may be employed to up-regulate RBPs, whereas another possibility would be to prevent granule formation by modulating post-translational modifications, such as phosphorylations, or by introducing RNA sponges. Considering the many ongoing human sequencing initiatives, such as phosphorylations, or by introducing RNA sponges. Considering the many ongoing human sequencing initiatives, such as phosphorylations, or by introducing RNA sponges. Considering the many ongoing human sequencing initiatives, such as phosphorylations, or by introducing RNA sponges.

References

Intrinsically disordered proteins as crucial constituents of cellular transport meets membrane traffic.

Intrinsically disordered proteins (IDPs) are a class of proteins characterized by an absence of well-defined secondary or tertiary structures. These proteins are particularly abundant in eukaryotes, making up a significant fraction of the proteome. IDPs exhibit dynamic structural and functional properties that make them crucial in various cellular processes. They play a pivotal role in several biological functions, including protein-RNA interactions, RNA granule formation, and regulation of RNA metabolism.

One of the key functions of IDPs is their role in protein-RNA interactions. IDPs can bind to RNA molecules, influence their structure, and affect their function. For example, the Puf3 protein, which belongs to the Puf family of RNA-binding proteins, regulates the translational fate of its bound mRNAs, affecting cell cycle and proliferation. This regulatory mechanism is crucial for maintaining cellular homeostasis.

Another important role of IDPs is their involvement in RNA granule formation. RNA granules, also known as RNA-induced silencing complexes (RISCs) or stress granules, are dynamic assemblies of RNA molecules and associated proteins. IDPs actively participate in these granules, contributing to their formation and function. For instance, the Fus protein, a Puf family member, is involved in translation of localized mRNAs in an APC-RNP complex.

IDPs also facilitate RNA transport, affecting the distribution and localization of mRNAs within the cell. This function is particularly evident during the conversion of growth cones to synaptic terminals, where the regulation of mRNA transport is crucial for the proper formation and function of synaptic connections.

In conclusion, intrinsically disordered proteins are essential components in cellular processes involving protein-RNA interactions and RNA granule dynamics. Their dynamic nature and ability to bind to RNA molecules make them versatile regulators of gene expression and cell functions. Further research into the mechanisms and specific roles of IDPs in RNA metabolism will be instrumental in advancing our understanding of cellular biology and disease mechanisms.