Principles and roles of mRNA localization in animal development

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Summary
Intracellular targeting of mRNAs has long been recognized as a means to produce proteins locally, but has only recently emerged as a prevalent mechanism used by a wide variety of polarized cell types. Localization of mRNA molecules within the cytoplasm provides a basis for cell polarization, thus underlying developmental processes such as asymmetric cell division, cell migration, neuronal maturation and embryonic patterning. In this review, we describe and discuss recent advances in our understanding of both the regulation and functions of RNA localization during animal development.

Key words: RNA localization, RNA transport, Local translation, Cell polarity, Post-transcriptional gene regulation

Introduction
Establishment of cell polarity is crucial for the execution of developmental programmes governing key processes, including specification of cell fates, individual or collective cell movements and specialization of somatic cell types. Cell polarization depends on the asymmetric segregation of organelles and various molecules within the cell. Polarized accumulation of RNA molecules was first visualized nearly 30 years ago, when β-actin mRNA was found to be asymmetrically localized within ascidian eggs and embryos (Jeffery et al., 1983). Following this, the discovery of the first localized maternal mRNAs in Xenopus (Rebagliati et al., 1985) and Drosophila oocytes (Frigerio et al., 1986; Berleth et al., 1988) provided evidence for the earlier proposal that localized RNA determinants could be responsible for early embryonic patterning (Kandler-Singer and Kalthoff, 1976). mRNAs were soon found to be asymmetrically distributed within differentiated somatic cells, such as fibroblasts (Lawrence and Singer, 1986), oligodendrocytes (Trapp et al., 1987) and neurons (Garner et al., 1988), and to colocalize with their encoded proteins, establishing intracellular transport of mRNAs as a potential mechanism used to target the production of selected proteins to discrete sites.

Significant improvements in RNA detection methods led to the identification of a growing number of localized mRNAs. Still, in the early 2000s, the set of described targeted mRNAs was limited to ~100 (reviewed by Bashirullah et al., 1998; Palacios and St Johnston, 2001) and the process of intracellular mRNA localization was thought to be restricted to specific cell types. However, recent genome-wide analyses (see Table 1) have changed this view dramatically, and strongly suggest that subcellular targeting of mRNAs is a prevalent mechanism used by polarized cells to establish functionally distinct compartments (Fig. 1). Particularly striking was the discovery that >70% of the 2314 expressed transcripts analysed in a high-resolution in situ hybridization screen were subcellularly localized in Drosophila embryos (Lécuyer et al., 2007). Moreover, hundreds to thousands of mRNAs have been detected in cellular compartments as diverse as the mitotic apparatus (Blower et al., 2007; Sharp et al., 2011), pseudopodia (Mili et al., 2008), dendrites (Moccia et al., 2003; Poon et al., 2006; Zhong et al., 2006; Suzuki et al., 2007; Cajigas et al., 2012) or axons (Andreassi et al., 2010; Zivraj et al., 2010; Gumy et al., 2011). The prevalence of intracellular mRNA targeting is illustrated further by the identification of localized mRNAs in a wide range of organisms outside of the animal kingdom, including bacteria (Keiler, 2011), fungi (Zarnack and Feldbrügge, 2010; Heym and Niessing, 2011) and plants (Crofts et al., 2005).

In this Review, we briefly describe the cellular mechanisms underlying mRNA localization (for more comprehensive reviews, see Martin and Ephrussi, 2009; Bullock, 2011), and focus largely on the developmental processes in which mRNA targeting has been shown to play key roles. This includes early embryonic patterning, asymmetric cell divisions, polarization of epithelia and cell migration, as well as axonal and dendrite morphogenesis and plasticity.

Why localize mRNAs rather than proteins?
Transporting mRNAs rather than proteins presents several significant advantages for a cell. First, transport costs are reduced, as several protein molecules can be translated from a single RNA molecule. Second, transporting mRNAs can prevent proteins from acting ectopically before they reach the appropriate site, which is particularly important in the case of maternal determinants, as spatially inappropriate expression disrupts embryonic patterning. Third, localized translation can facilitate incorporation of proteins into macromolecular complexes by generating high local protein concentrations and allowing co-translation of different subunits (Mingle et al., 2005). Fourth, nascent proteins may have properties distinct from pre-existing copies, by virtue of post-translational modifications or through chaperone-aided folding pathways (Lin and Holt, 2007). Lastly, a major advantage of mRNA targeting is that it allows fine-tuning of gene expression in both space and time. Examples of this include targeting of different splice variants to distinct cellular compartments (Baj et al., 2011) and activation of localized mRNA translation specifically at their destination, in response to signals such as guidance cues, neurotransmitter release or fertilization (Besse and Ephrussi, 2008).

Proposed mechanisms for asymmetric mRNA localization
Three distinct mechanisms have been proposed to account for the asymmetric distribution of mRNAs within cells: localized protection from degradation, diffusion-coupled local entrapment, and directed transport along a polarized cytoskeleton (Fig. 2).
Directed transport of transcripts along a polarized cytoskeletal network is a predominant mechanism to direct mRNA localization and accumulation at the posterior pole of late-stage oocytes (Chang et al., 2004). Directed transport of transcripts is thought to involve specific recognition by trans-acting factors, assembly of localization-competent ribonucleoprotein (RNP) complexes, recruitment of molecular motors and transport along the cytoskeleton, as well as anchoring of the mRNA at the final destination. Finally, tight coupling with translational regulation is required to achieve spatially restricted protein synthesis.

**Cellular mechanisms underlying intracellular mRNA transport**

**Assembly of transport-competent RNPs**

As revealed by proteomic analyses, mRNAs to be transported are packaged within complexes containing a large number of associated proteins (Kanai et al., 2004). Some of these proteins bind to the mRNA upon transcription or splicing, rendering it competent for the future recruitment of the cytoplasmic transport machinery (Marchand et al., 2012). Consistent with a key influence of mRNA nuclear history, nuclear processing events such as splicing, transit through the nucleolus, deposition of key nuclear factors or translocation through specific nucleopore structures have been shown to be required for cytoplasmic targeting of localized mRNAs (Giorgi and Moore, 2007; Marchand et al., 2012). Following export to the cytoplasm, RNP complexes are remodelled, and cytoplasmic factors ensuring translational repression and specific coupling with molecular motors are recruited (Lewis and Mowry, 2007; Besse and Ephrussi, 2008).

The number of mRNA molecules present in a single RNP is still an unresolved question. In favour of a co-packaging of multiple mRNA molecules, oskar mRNA has been shown to multimerize in *Drosophila* oocytes (Hachet and Ephrussi, 2004; Jambor et al., 2011), and differentially tagged *ASH1* and *IST2* mRNAs are co-transported in yeast (Lange et al., 2008). By contrast, RNP complexes found in *Drosophila* embryos or the dendrites of mammalian neurons seem to contain a very limited number of
RNA molecules, suggesting that mRNAs are transported independently of each other in these systems (Mikl et al., 2011; Amrute-Nayak and Bullock, 2012; Batish et al., 2012).

**Cis-regulatory elements and trans-acting factors**

Formation of transport-competent RNP s is initiated via the recognition of cis-regulatory elements present in RNA molecules by specific RNA-binding proteins. These elements, also termed localization elements or zipcodes, are usually (but not exclusively) found in 3′UTR sequences and are necessary and sufficient for efficient mRNA targeting and recruitment of trans-acting factors. Although the molecular mechanisms underlying specific recognition of zipcodes by RNA-binding proteins have long been elusive, recent structural studies have revealed requirements for highly specific motifs and/or structures. For example, a 54-nt sequence required for the targeting of β-actin mRNA in fibroblasts has been shown to contain a bipartite element comprising two RNA motifs recognized by the RNA-binding protein Zbp1 (Chao et al., 2010; Patel et al., 2012). The RNA binding protein Egalitarian, by contrast, does not recognize a specific sequence, but rather the atypical A′-form helices formed by the 44-nt localization element of Drosophila fs(1)K10 transcripts (Bullock et al., 2010). Notably, Egalitarian shows only a modest binding preference for its targets. However, association with BicD protein and formation of a ternary complex significantly enhances its affinity for localizing targets (Dienstbier et al., 2009). A similar synergistic binding has been observed in yeast for the She2p-She3p-ASH1 mRNA complex (Müller et al., 2011), highlighting a role for intermolecular cooperativity in ensuring selective recognition of localizing mRNAs in vivo.

A current limitation to our understanding of localized RNA recognition is the small number of well-characterized localization elements. Although genome-wide analyses have provided large datasets for the discovery of new zipcodes, it has proven difficult to identify common signatures shared by RNA molecules targeted to the same cellular sites. This probably stems from the difficulty of predicting tertiary structures in silico, as well as from the fact that localized mRNAs can contain multiple localizing elements with redundant or complementary functions (Gautreau et al., 1997; Deshler et al., 1998; Macdonald and Kerr, 1998).

**Recruitment of molecular motors and directed transport**

The nature and number of active molecular motors recruited to a target mRNA dictate the cytoskeletal tracks (actin filaments or microtubules) used for mRNA transport, the type of movement (uni- or bidirectional), and the properties (e.g. speed, processivity) of mRNA motion (Bullock, 2011; Gagnon and Mowry, 2011; Marchand et al., 2012). For example, the recruitment of several molecules of the myosin motor Myo4p by multiple localization elements increases the efficiency of ASH1 mRNA transport on actin filaments in yeast (Chung and Takizawa, 2010). Furthermore, dendritically transported RNPs exhibit microtubule-dependent bidirectional movement, suggesting the recruitment and the activity of opposite polarity motors (Doyle and Kiebler, 2011). Consistent with this view, the RNA-binding protein Fmrp has been shown to associate with dendritically localized transcripts, and to bind to KLC (a component of the plus-end motor Kinesin-1) as well as to the dynein-interacting BicD protein (Dictenberg et al., 2008; Bianco et al., 2010). A general trend emerging from live-imaging analyses is that bidirectional transport is commonly used in higher
eukaryotes for mRNA targeting. This might allow RNPs to navigate around obstacles and ensure a constant reassessment and fine-tuning of directional transport.

**mRNA anchoring**

Once transported, mRNAs must be retained at their destinations. In cells with no static pre-localized anchor, this can be achieved via continuous rounds of short-range active transport, as shown for maintenance of **bicoid** mRNA localization at the anterior pole of late-stage **Drosophila** oocytes (Weil et al., 2006). In various cell types, including **Drosophila** oocytes, **Xenopus** oocytes and dividing yeast cells, static anchoring of mRNAs relies on cortical actin and actin-binding proteins (King et al., 2005; Becalska and Gavis, 2009; Heym and Niessing, 2011). Interestingly, alternative actin-independent mechanisms have been discovered: one in mammalian migrating cells, in which accumulation of transcripts in protrusions depends on the tumour-suppressor APC (Mili et al., 2008); one in **Drosophila** blastoderm embryos, in which apical anchoring of pair-rule transcripts requires a motor activity-independent function of dynein (Delanoue and Davis, 2005); and another in ascidian eggs, in which transcripts are associated with a sub-domain of the cortical ER (Paix et al., 2011).

**Translational regulation**

Local protein production requires translational repression of localized mRNAs during transport and subsequent activation at the final destination. Translational repressors have been shown to associate with transport RNPs by directly binding RNA regulatory sequences and blocking translation, largely at the initiation stage (Besse and Ephrussi, 2008). Although the mechanisms regulating local activation of translation are much less clear, a theme emerging from studies in multiple systems is that phosphorylation of repressors at the destination (either directly upon arrival or in response to external signals) can decrease affinity for their target mRNAs, thereby relieving translational blockage. Thus, the RNA-binding protein Zbp1 has been shown to repress the translation of its target mRNA (β-actin) and to exhibit a reduced binding efficiency upon phosphorylation (Hüttelmaier et al., 2005). Furthermore, expression of a non-phosphorylatable form of Zbp1 reduces β-actin protein accumulation at the site of mRNA localization, the cell periphery. Similarly, altering the phosphorylation status of the RNA-binding protein Fmrp (Fmr1 – Mouse Genome Informatics) appears to trigger a translational switch: whereas Fmrp phosphorylation promotes the formation of a RNA-induced silencing complex (RISC)-microRNA (miRNA) inhibitory complex on the dendritically localized **PSD-95** (Dlg4 –

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**Box 1. Live-imaging methods for visualizing mRNA localization**

Over the last decade, methods relying on RNA tagging and high-resolution microscopy have been developed to improve mRNA detection in living cells and organisms (Armitage, 2011). A tethering approach, in which RNA recognition sequences bound by a specific RNA-binding protein are inserted into the transcript of interest, allows dynamic distribution of mRNA in living tissues to be monitored by co-expression of exogenous RNA-binding protein (e.g. MS2, 3N or U1A) fused to a fluorescent protein (FP) (A) (Bertrand et al., 1998). Drawbacks of this technique include background fluorescence produced by unbound chimeric FPs, and the high number of RNA tags necessary for a strong signal, potentially altering mRNA behaviour. A recently developed technique uses RNA motifs (aptamers) that bind fluorogenic dyes. This RNA-fluorophore complex, termed Spinach, emits a green fluorescence comparable in brightness to enhanced GFP (B) (Paige et al., 2011). Spinach has been used for live imaging of abundant RNAs in cultured cells, but utility for in vivo mRNA imaging must yet be demonstrated. Fluorescence imaging techniques have also been developed to follow endogenous mRNAs in live samples. These methods use molecular beacons, which are non-membrane-permeable hairpin-shaped molecules with an internally quenched fluorophore, fluorescence of which is restored upon binding to target RNAs (C) (Bratu et al., 2003). Potential disadvantages include target accessibility and impairment of mRNA function upon binding of multiple beacons. Finally, injection of fluorescently labelled in vitro synthesized RNAs has been used to monitor RNA localization in vivo (D) (Ainger et al., 1993). Potential caveats here are that injected RNAs are not processed by endogenous machineries, and fluorophores might alter the function of labelled RNAs.

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**A** MS2 system

- mRNA
- Fluorescent protein
- RNA-binding protein (MCP)
- MS2 tags

**B** Spinach system

- mRNA
- Fluorogenic dye
- Aptatmer tags

**C** Molecular beacon

- mRNA
- Molecular beacon
- Fluorescent dye
- Quencher

**D** Fluorescently labelled RNA

- mRNA
- Fluorophore
- RNA
- Injection
Mouse Genome Informatics) mRNA, dephosphorylation of Fmrp upon stimulation induces release of RISC from the mRNA and translation activation (Muddashetty et al., 2011).

Together, these mechanisms ensure tight localization of mRNAs, and subsequent protein production, to particular subcellular compartments. In the next sections, we will discuss the functional significance of such localization.

Establishment of embryonic polarity by localized maternal RNA determinants

In many vertebrate and invertebrate organisms, localization of mRNA molecules in oocytes and eggs establishes a spatially restricted pattern of gene expression that acts to specify embryonic axes and cell fates (reviewed by Kumano, 2011).

Axis specification and positional identity during Drosophila oogenesis

Roles for asymmetric RNA localization in embryonic patterning are perhaps best studied in Drosophila, in which localized mRNAs underlie patterning along both the anteroposterior and dorsoventral axes (Fig. 3A). The anteroposterior axis is first established by localization of gurken mRNA to the posterior pole during early oogenesis (González-Reyes et al., 1995; Roth et al., 1995). gurken mRNA, which encodes a TGFα signalling molecule, is also necessary for dorsoventral axis specification by subsequent localization to the anterodorsal corner of the growing oocyte (Neuman-Silberberg and Schüpbach, 1993). Localization of bicoid mRNA to the anterior of the developing oocyte establishes a gradient of transcription factor activity that specifies anterior cell fates (Berleth et al., 1988; Driever and Nüsslein-Volhard, 1988), whereas posterior and germ cell fates are established through localization of oskar mRNA and subsequent posterior accumulation of nanos mRNA (Ephrussi et al., 1991; Kim-Ha et al., 1991; Bergsten and Gavis, 1999).

Germ layer patterning and axis specification in vertebrate oocytes

In Xenopus oocytes, maternal mRNAs localized to the vegetal cortex (Fig. 3B) act in both germ layer patterning and germ cell specification (reviewed by King et al., 2005). Early in oogenesis, mRNAs encoding RNA-binding proteins with roles in germ cell determination, such as Xdazl and Nanos1 (Houston and King, 2000; Lai et al., 2011), are deposited at the vegetal cortex after initial accumulation in the Balbiani body or mitochondrial cloud (Chang et al., 2004). Later in oogenesis, Vg1 and VegT mRNAs are transported to the vegetal cortex and are inherited during cleavage by the vegetal blastomeres (Melton, 1987; Zhang and King, 1996). Vegetally restricted expression of Vg1 and VegT, which encode a TGFβ signalling molecule and a T-box transcription factor, respectively, is crucial for endoderm and mesoderm specification during embryogenesis (Zhang et al., 1998; Birsoy et al., 2006). During oogenesis in zebrafish, many maternal mRNAs are differentially localized along the animal-vegetal axis (Fig. 3C) (Abrams and Mullins, 2009). Whereas several mRNAs, including dazl, are localized to the vegetal pole, pou2 (pou5f1 – Zebrafish Information Network) mRNA, which encodes a transcription factor...
that functions in endoderm specification, is localized to the animal pole (Howley and Ho, 2000; Lunde et al., 2004). bucky ball (buc) mRNA is localized first to the vegetal Balbiani body, and relocates later in oogenesis to the animal pole, along with Vg1 (dvrl - Zebrafish Information Network) mRNA (Marlow and Mullins, 2008). buc mRNA encodes a protein of unknown function that is homologous to Xenopus Xvelo1 (Fig. 3B) and is necessary for animal-vegetal polarity (Bontems et al., 2009).

Axis specification by maternal mRNA localization in marine invertebrates

In eggs of the jellyfish Clytia, mRNAs encoding the Wnt receptor Frizzled1 and its ligand Wnt3 are localized to the animal hemisphere (Fig. 3D), whereas mRNA encoding the negatively acting receptor Frizzled3 is localized to the vegetal hemisphere (Momose and Houlstein, 2007; Momose et al., 2008). The Wnt signalling pathway activated by these localized maternal mRNAs acts to establish the oral-aboral axis during embryogenesis (Momose et al., 2008). In ascidians (including Ciona and Halocynthia), a group of maternal mRNAs termed PEM RNAs (reviewed by Sardet et al., 2005), are localized to the vegetal cortex immediately after fertilization (Fig. 3E). This diverse group of mRNAs includes PEM1, which encodes a protein of unknown function that plays a role in anterodorsal patterning (Yoshida et al., 1996), and the muscle determinant macho1, a zinc-finger transcription factor (Nishida and Sawada, 2001). During cleavage, the PEM RNAs are segregated to the posterior blastomeres and act to specify cell fates and axial polarity during embryogenesis (Sardet et al., 2003).

Evolutionary considerations

As exemplified above, localization of maternal RNA determinants is a widely used strategy for establishing axial polarity during animal development. Although commonalities exist among the localization mechanisms, the molecular identities of localized mRNAs can, in some cases, be rapidly evolving. Studies in the wasp Nasonia showed that anterior patterning is specified by anterior localization of orthodenticle mRNA (Lynch et al., 2006; Olesenicky and Desplan, 2007), rather than bicoid mRNA, as in Drosophila (Berleth et al., 1988). Nonetheless, functional conservation is apparent, as the DNA-binding specificity of the homeodomain transcription factor encoded by orthodenticle is the same as that of bicoid (Wilson et al., 1996). A contrasting view emerges, however, from overlap in molecular identities of localized mRNAs such as dazl, buc/Xvelo1 and Vg1 in Xenopus and zebrafish (Fig. 3), suggesting an evolutionary ancient origin for some patterning circuits directed by mRNA localization.

Specification of cell fate by asymmetric segregation of RNA determinants in dividing cells

Asymmetric cell divisions produce daughter cells with distinct fates, and rely on the asymmetric segregation of key determinants, including localized mRNAs.

Asymmetric RNA inheritance in cleavage-stage embryos

Specific populations of mRNAs are localized for the first time in cleavage-stage embryos, where they are partitioned into only one daughter cell upon cell division. During the early cleavage cycles of the Hymanassa mollusc embryo, for example, a large fraction of mRNAs are localized to one of the two centrosomes and asymmetrically inherited (Fig. 4A) (Lambert and Nagy, 2002). As most of these mRNAs encode developmental patterning genes known for their regulatory functions in other organisms, it is likely that their differential segregation controls cell fate specification (Kingsley et al., 2007).

In mesendoderm cells of the 16-cell stage Halocynthia ascidian embryo, Not mRNA is delivered to the cytoplasm of the future mesoderm-forming pole after nuclear migration, and is asymmetrically partitioned into the mesoderm daughter cell through cytokinesis (Fig. 4B). Not mRNA encodes a transcription
factor that promotes mesoderm fate and suppresses endoderm fate, suggesting that this asymmetric partitioning is responsible for the segregation of germ layer fates (Takatori et al., 2010).

The role of mRNA localization in lineage diversification has recently been extended to mammalian early embryogenesis. During early mouse development, the first cell fate decision is between the pluripotent inner cell mass and the external trophectoderm (Jedrusik et al., 2008). In this context, the trophectoderm determinant-encoding cdx2 mRNA has been shown to concentrate at the apical side of 8- to 16-cell blastomeres, and to be inherited exclusively by outside daughter cells upon division (Jedrusik et al., 2008). Although additional functional studies are required, these results suggest that unequal mRNA distribution might contribute to symmetry breaking between inside and outside cells.

**Asymmetric RNA inheritance in stem cell divisions**

Asymmetric segregation of mRNAs encoding cell fate determinants has also been observed in the context of stem cell divisions. In *Drosophila* embryos, neural precursors (neuroblasts) divide unequally to generate a neuroblast and a smaller ganglion mother cell (GMC). *prospero* mRNA, which encodes a transcription factor that activates GMC-specific gene expression, is localized to the basal pole of neuroblasts during mitosis and is exclusively inherited by the GMC (Li et al., 1997; Broadus et al., 1998). In the absence of mRNA localization, Prospero protein still localizes basally, suggesting that *prospero* mRNA and protein are targeted independently. Functionally, these two processes appear to act redundantly to establish GMC-specific patterns of gene expression (Broadus et al., 1998). Asymmetric mRNA inheritance requires segregation to be coupled with precise orientation of cell division. In *Drosophila* neuroblasts, coupling is mediated by the adapter protein InsCuteable, and *inscuteable* mRNA is targeted apically in interphase neuroblasts (Fig. 4C). Interestingly, mislocalization of *inscuteable* mRNA significantly reduces InsCuteable protein apical accumulation, and is associated with mitotic spindle misorientation (Hughes et al., 2004).

Asymmetric segregation of the glial determinant-encoding glide/gcm (gcm – FlyBase) mRNA has also been observed in early *Drosophila* embryos during neuroglioblast division. Surprisingly, the preferential inheritance of *glide* mRNA by the glioblast does not result in asymmetric inheritance of the Glide protein, but seems to contribute to a glioblast-specific positive autoregulatory loop (Bernardoni et al., 1999).

**Control of epithelial cell polarization by precise mRNA targeting**

Specific localization along the apicobasal axis has been observed for a large number of transcripts (up to 10-15% of the expressed mRNAs in maturing *Drosophila* epithelia) (Lécuyer et al., 2007). Studies on specific transcripts suggest that this process is essential for epithelial cell polarization and functions.

**Apically distributed mRNA encoding cell junction components and cytoskeletal regulators**

Establishment and maintenance of epithelial cell polarity rely on the asymmetric distribution of evolutionarily conserved protein complexes, such as the Crumbs complex. This complex is composed of the transmembrane protein Crumbs (Crb), the scaffolding protein Stardust/MPP5 (Sdt), and the PALS-1 Associated Tight Junction protein (dPatj). *crb, sdt* and *paj* mRNAs have been shown to localize to discrete subapical domains within *Drosophila* embryonic and follicular epithelial cells (Lécuyer et al., 2007; Horne-Badovinac and Bilder, 2008; Li et al., 2008). Remarkably, apical localization of *sdt* mRNA is developmentally regulated through an alternative splicing event and appears to contribute exclusively to the early phase of Sdt and Crb apical accumulation (Fig. 5A) (Horne-Badovinac and Bilder, 2008); at later time points, the mRNA is no longer localized, whereas the protein still is. mRNA targeting coupled to local translation might thus be particularly important in immature epithelia, when polarity is still labile. mRNA localization is also important for epithelial cell polarity in mammals. Most recently, apical localization of the mRNA encoding the zonal occludens-1 (ZO-1; also known as Tjp1) protein has been shown to control tight junction assembly and cell polarity in mammary epithelial cells (Fig. 5B) (Nagaoka et al., 2012).

**Apical mRNA localization might also play crucial roles in the nucleation and positioning of cytoskeletal networks. Indeed, short stop mRNA encoding the *Drosophila* actin-microtubule cross-linker Spectraplakin is apically distributed within the embryonic epithelium (Lécuyer et al., 2007).**

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**Fig. 4. Asymmetrically segregating mRNAs in dividing cells.** (A) In *Ilyanassa* embryos, specific mRNAs (blue) localize to one of the two centrosomes of metaphasic cells at the 4-cell stage (left). Upon division, these mRNAs are differentially inherited by daughter cells (right). (B) Not mRNA (yellow) is delivered to one side of a *Halocynthia* embryo mesendoderm cell by nuclear migration. Not mRNA is inherited by the mesoderm daughter cell, but not the endoderm daughter cell. Adapted from Takatori et al. (Takatori et al., 2010). (C) *Drosophila* embryo neuroblasts (Nb) divide asymmetrically to regenerate a Nb and produce a smaller cell, the ganglion mother cell (GMC). Whereas *inscuteable* (*insc*) mRNA (orange) and InsC protein (red) localize at the apical side of interphasic Nb, *prospero* (*pros*) mRNA (yellow) and Pros protein (green) localize basally at anaphase, thus ensuring a differential inheritance of the two components. A, anterior; Ani, animal; P, posterior; Veg, vegetal.
mRNA, coding for the *Drosophila* actin-nucleating factor Formin, is also accumulated at the apical side of epithelial tubular structures (Massarwa et al., 2009). Whether targeting of these mRNAs is functionally relevant however remains to be studied.

**Functional signalling pathways and transcript localization along the apicobasal axis**

One means of optimizing secretion of signalling molecules in epithelia is to accumulate their transcripts near the site of secretion prior to translation. Transcripts encoding Wingless (Wg), a *Drosophila* member of the Wnt family, are apically localized within epithelial cells of the embryonic ectoderm (Fig. 5C) and salivary glands (Simmonds et al., 2001). Importantly, apical targeting of *wg* mRNA is crucial for autoregulation of Wg protein levels and apical secretion, thus ensuring robustness of the signalling activity. Similarly, *unpaired* (*upd*) mRNA, encoding a cytokine ligand for the JAK/STAT pathway, accumulates at the apical side of polar cells in the *Drosophila* follicular epithelium (Van de Bor et al., 2011). Apical targeting of *upd* mRNA is essential for efficient Upd secretion and signalling to adjacent epithelial cells, triggering their differentiation into migrating cells. Transcripts such as *hairy*, *runt* and *even skipped*, which encode pair-rule transcription factors responsible for *Drosophila* embryonic patterning, are also targeted apically in blastodermic embryos (Fig. 5C). This process is conserved through dipteran evolution and is essential for efficient transcription of patterning genes (Bullock et al., 2004). By targeting translation near apically localized nuclei, mRNA transport could favour the nuclear uptake of encoded transcription factors.

mRNA targeting to basolateral domains of epithelial cells also plays important roles in the maintenance of epithelium integrity. For instance, the *Drosophila* peripheral Golgi protein dGrasp (Grasp65 – FlyBase) is preferentially found in the ZOC (zone of contact), a subcellular domain close to the basal surface of follicular cells, where it is required for αPS1 integrin (Mew – FlyBase) deposition (Fig. 5D). Basal deposition of αPS1 is essential for the formation of focal adhesion sites and the maintenance of epithelial structures, and has been shown to fully depend on the basal targeting of both dgrasp and αPS1 mRNAs to the ZOC (Schotman et al., 2008).

**Regulation of cell migration and guidance by mRNA targeting**

Cellular protrusions in migrating cells and growing neuronal processes accumulate proteins involved in sensing external cues, and regulating cell motility and directionality. mRNA localization has been shown to underlie local translation of some of these proteins in response to environmental signals (Lin and Holt, 2007; Mili and Macara, 2009).

mRNA targeting to migrating cell protrusions

As revealed by a recent global analysis, ~50 mRNAs encoding proteins involved in various functions, including membrane trafficking, signalling and cytoskeleton organization are enriched in cell protrusions of migrating mammalian fibroblasts (Mili et al., 2008). Complementary to this finding, mRNAs encoding β-actin and the seven subunits of the actin-polymerization nucleating Arp2/3 complex have been shown to accumulate together with their corresponding products in protrusions of cultured chicken embryonic fibroblasts (Fig. 6A) (Lawrence and Singer, 1986; Mingle et al., 2005). Asymmetric targeting of these mRNAs is crucial for directional cell migration (Condeéls and Singer, 2005; Liao et al., 2011), and probably promotes the formation of actin nucleation centres at the cell front. Supporting a role for mRNA localization during in vivo cell migration, the conserved RNA-binding protein Zbp1/Vg1RBP, known for its role in mRNA localization in multiple systems, accumulates in the processes of *Xenopus* migratory neural crest cells and is required for their migration (Yaniv et al., 2003). However, mRNA targets for Zbp1/Vg1RBP have not been identified so far.

mRNA localization has also been suggested to influence the invasiveness of tumour cells by regulating the cell orientation necessary for proper chemotaxis (Lapidus et al., 2007), or the targeting of pro-migratory adhesive molecules (Adereth et al.,...
β-actin mRNA (light blue) or mRNAs encoding subunits of the Arp2/3 complex (light green) are targeted to the leading edge of migrating fibroblasts. Local synthesis of their corresponding proteins (dark blue and dark green stars, respectively) contributes to directional migration. β-actin mRNA (light blue) is transported to the side of the axonal growth cone exposed to an attractive guidance cue (red). Locally translated β-actin protein (dark blue stars) accumulates at the same location, promoting the nucleation of actin filaments (purple) and triggering growth cone turning.

Control of dendritic maturation by localized mRNAs

Maturation of neuronal circuits involves remodelling of dendritic trees and refinement of synapse number and strength, two processes controlled by local translation of dendritically targeted mRNAs (Sutton and Schuman, 2006; Doyle and Kiebler, 2011).

Dendritogenesis

The complexity of dendritic trees is a key parameter underlying neuronal activity and connectivity. Strikingly, recent studies have revealed that the transport of specific mRNAs to dendrites is crucial for dendritic branching during development. Targeting of nanos mRNA to dendrites, for example, is required for proper branching of peripheral sensory neurons in Drosophila larvae (Brehmbel and Gavis, 2008). In young mouse hippocampal neurons, inactivation of the RNA-binding protein Staufen1 impairs the transport of β-actin mRNA to dendrites and reduces dendritic length and branching (Vessey et al., 2008). Similarly, hippocampal neurons lacking the RNA-binding protein Zbp1/Vg1RBP exhibit reduced accumulation of β-actin mRNA and protein in distal dendrites, with a concomitant decrease in dendritic branching (Perycz et al., 2011). Interestingly, the function of Zbp1/Vg1RBP is developmentally regulated, as it is required for intensive dendritogenesis in young neurons, but not for dendrite maintenance in mature neurons (Perycz et al., 2011).

In rat hippocampal neurons, differential localization of Bdnf splice variants along dendrites has been shown to lead to spatially restricted effects on dendritic architecture. Whereas Bdnf transcripts restricted to the cell soma and proximal dendrites selectively affect proximal dendritic branching, transcripts with a distal dendritic localization affect peripheral dendrite complexity (Baj et al., 2011). These results have led to a ‘spatial code hypothesis’ (Baj et al., 2011), in which selective targeting of BDNF to distinct dendritic regions through differential mRNA localization allows both a precise shaping of dendritic compartments during development, and spatially restricted control of dendritic plasticity in mature neurons.

Fig. 6. Targeted mRNAs in migrating cells. (A) β-actin mRNA (light blue) or mRNAs encoding subunits of the Arp2/3 complex (light green) are targeted to the leading edge of migrating fibroblasts. Local synthesis of their corresponding proteins (dark blue and dark green stars, respectively) contributes to directional migration. (B) β-actin mRNA (light blue) is transported to the side of the axonal growth cone exposed to an attractive guidance cue (red). Locally translated β-actin protein (dark blue stars) accumulates at the same location, promoting the nucleation of actin filaments (purple) and triggering growth cone turning.
Synapse formation and plasticity
Formation of new synapses is crucial during early development of the nervous system, and is a multistep process involving initial assembly, maturation and stabilization. As shown in cultured Aplysia neurons, recruitment of the neuropeptide-encoding sensorin mRNA to nascent synapses is induced upon recognition of pre- and postsynaptic partners, and is required for further synaptic development and maturation (Lyles et al., 2006). These results illustrate that synaptogenesis not only involves recruitment of proteins or organelles, such as synaptic vesicles, but also requires mRNA targeting. In more mature neurons, local translation of dendritically localized mRNAs encoding proteins such as neurotransmitter receptors, ion channels and signal transduction enzymes is essential for the regulation of synaptic activity (Sutton and Schuman, 2006; Doyle and Kiebler, 2011). Interestingly, specific populations of mRNAs are recruited to dendrites upon synaptic activity (Steward et al., 1998), and their translation can be regulated in a synapse- and stimulus-specific manner (Wang et al., 2009), providing a means of individually tagging activated synapses (Fig. 7).

Although most of the aforementioned studies have been performed ex vivo, evidence has been provided for a functional requirement for dendritically localized protein synthesis in stable forms of synaptic plasticity and memory consolidation in vivo. Key experiments performed in mice have shown that the disruption of Camk2a (encoding CaMKIIα) or Bdnf mRNA dendritic targeting impairs long-term potentiation (Miller et al., 2002; An et al., 2008) and long-term memory (Miller et al., 2002). Moreover, mutations in genes involved in dendritic mRNA targeting or translation have been linked to several human neurological disorders, including the most common cause of inherited mental retardation Fragile X syndrome, consistent with a role for dendritically localized protein synthesis in the regulation of synaptic morphogenesis and plasticity (Liu-Yesucevitz et al., 2011).

Controlling the repertoire of localized mRNAs
The examples discussed above highlight the importance of mRNA localization, as well as its complexity. Given that hundreds of mRNAs can be targeted to diverse subcellular compartments and that their localization can be dynamic, it is clearly essential that the cell can tightly regulate complementary transport machineries in space and time.

Targeting various mRNAs to different cellular locations
Polarized cells must use specific machineries to target mRNAs (or groups of mRNAs) to distinct cellular compartments. For this, combinations of RNA-binding proteins selectively recognize different target mRNAs, ensuring the recruitment of specific molecular motors. In the Drosophila oocyte, for example, oskar and gerken mRNAs assemble into distinct RNP complexes, and their transport to the posterior and anterodorsal poles depends on the activity of kinesin and dynein, respectively (Becalska and Gavis, 2009). How many mRNAs are transported by a given targeting machinery in a given cell type is still unclear, although individual RNA-binding proteins have the capacity to associate with hundreds of functionally related mRNAs (Hogan et al., 2008).

Localizing various mRNAs to distinct cellular locations also implies that these compartments must be provided with a functional translation machinery. Consistent with this, biochemical and electron-microscopy studies have demonstrated that ribosomes are associated with structures as diverse as the mitotic apparatus, mitochondria, neuronal processes and cell adhesion structures (Lécuyer et al., 2009). Whether components of the translation machinery are transported concomitantly with or independently of mRNAs is still unclear, although ribosomal...

Fig. 7. Local translation of dendritic mRNAs in response to synaptic activity. Translation of dendritically targeted mRNAs is activated in response to synaptic activity and is essential for modulation of synaptic activity and dendritic spine morphogenesis. Strikingly, translation can be regulated at the synapse level, and thus represents an efficient way to individually tag activated synapses. Upper left box: representation of the somatodendritic compartment of a mammalian neuron. Lower panel: schematic of the proximal part of a dendrite that roughly corresponds to the region boxed in the upper panel (red rectangle). Proteins synthesized locally in dendritic spines are represented in green.
constituents can be found in localizing RNP complexes (Besse and Ephrussi, 2008).

**Dynamically adjusting the populations of localized mRNAs**

As demonstrated in a variety of cell types, both the number and the identity of localized mRNAs are regulated in response to external stimuli and/or developmental signals (Crimo and Eberwine, 1996; Chicheurel et al., 1998; Steward et al., 1998; Willis et al., 2007; Dicentenberg et al., 2008; Home-Badovina and Bilder, 2008; Zivraj et al., 2010; Gumy et al., 2011). To modulate their repertoire of localized mRNAs, polarized cells must thus dynamically regulate the activity of their mRNA targeting machineries. In mouse hippocampal neurons, transport of the Fmrp cargo Camk2a mRNA to dendrites is increased upon stimulation of metabotropic glutamate (mGlur) receptors (Dicentenberg et al., 2008). Although the underlying mechanisms are still unclear, an increased association between Fmrp and the Kif5 motor is observed after stimulation, suggesting that differential recruitment of molecular motors to RNPs could modulate mRNA trafficking in response to a stimulus. In migrating mammalian cells, two independent pathways controlled by the Zbp1 and Apc proteins can regulate the targeting of mRNAs to the leading edge (Mili and Macara, 2009); their activity has been proposed be modulated in such a way that they are not simultaneously operational.

**Conclusions**

Intracellular mRNA targeting is now recognized as a central mechanism used in many (if not all) polarized cells and, as detailed here, plays a key role in multiple developmental contexts in a wide range of organisms. Strikingly, although the nature of transported mRNAs can vary greatly between cell types and species, mRNA targeting machineries appear to be conserved. For example, the Egl-Bic-Dynein complex is used to target mRNAs in various Drosophila cell types (Bullock and Ish-Horovitz, 2001; Hughes et al., 2004; Van de Bor et al., 2011). Furthermore, the RNA-binding protein Zbp1/Vg1RBP has been shown to promote intracellular mRNA transport in chicken fibroblasts (Ross et al., 1997), mouse axons (Donnelly et al., 2011; Welshans and Bassell, 2011) and Xenopus oocytes (Deshler et al., 1998; Havin et al., 1998).

Despite recent progress in the dissection of mRNA transport mechanisms and the dramatic proliferation of newly identified localized mRNAs, significant challenges remain. First, how cells dynamically regulate transport machineries to control their repertoire of localized mRNAs during development is still unclear. Second, the relative contribution of mRNA and protein targeting must be systematically explored, as they may act in parallel (either synergistically or redundantly) in different contexts. Finally, the extent to which non-coding RNAs are asymmetrically targeted is still largely unknown, although some intriguing studies have suggested that non-coding RNAs with specific distributions might have local regulatory or structural roles (Tiedge et al., 1991; Kloc et al., 2005). Interestingly, recent work has demonstrated a strong interplay between miRNA and proteins binding to localization elements (Koebernick et al., 2010). Answering these questions will require combining high-throughput biochemical and imaging approaches with functional analyses specifically addressing the role of mRNA transport in vivo.

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**Competing interests statement**

The authors declare no competing financial interests.

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