**RESEARCH ARTICLE**

**Regulation of maternal Wnt mRNA translation in *C. elegans* embryos**

Marieke Oldenbroek¹, Scott M. Robertson¹, Tugba Guven-Ozkan¹,* Caroline Spike², David Greenstein² and Rueyling Lin¹,**

**ABSTRACT**

The restricted spatiotemporal translation of maternal mRNAs, which is crucial for correct cell fate specification in early *C. elegans* embryos, is regulated primarily through the 3′UTR. Although genetic screens have identified many maternally expressed cell fate-controlling RNA-binding proteins (RBPs), their in vivo targets and the mechanism(s) by which they regulate these targets are less clear. These RBPs are translated in oocytes and localize to one or a few blastomeres in a spatially and temporally dynamic fashion unique for each protein and each blastomere. Here, we characterize the translational regulation of maternally supplied *mom-2* mRNA, which encodes a Wnt ligand essential for two separate cell-cell signaling events in early embryos. A GFP reporter that includes only the *mom-2* 3′UTR is translationally repressed properly in oocytes and early embryos, and then correctly translated only in the known Wnt signaling cells. We show that the spatiotemporal translation pattern of this reporter is regulated combinatorially by a set of nine maternally supplied RBPs. These nine proteins all directly bind the *mom-2* 3′UTR in vitro and function as positive or negative regulators of *mom-2* mRNA translation in vivo. The net translational readout for the *mom-2* 3′UTR reporter is determined by competitive binding between positive- and negative-acting RBPs for the 3′UTR, along with the distinct spatiotemporal localization patterns of these regulators. We propose that the 3′UTR of maternal mRNAs contains a combinatorial code that determines the topography of associated RBPs, integrating positive and negative translational inputs.

**KEY WORDS:** 3′UTR, *Caenorhabditis elegans*, Wnt

**INTRODUCTION**

Precise patterns of gene expression during development are regulated predominantly at the level of transcription. In transcription-driven gene regulation, transcriptional activators bind to enhancer elements and orchestrate the colocalization of proteins at the gene promoter to activate transcription. The transcriptional status of a particular gene in a cell or developing tissue is therefore determined primarily by the precise combination of transcription factors that can bind to the enhancer sequence in that specific cell.

There are, however, well-known exceptions to transcription-driven gene regulation. Most notably, in newly fertilized embryos of chicken, fish, flies and worms, early cell divisions and fate specification are primarily controlled by proteins and RNAs deposited into the egg by the mother (Newport and Kirschner, 1982; Edgar and Schubiger, 1986; Powell-Coffman et al., 1996). Even in mammals, maternally contributed factors play an essential role early in preimplantation development (Li et al., 2010).

In *C. elegans* embryogenesis, maternal factors control early cleavage events, including their asymmetric nature, orientation and timing, as well as specific cell-to-cell signaling events (Gönczy and Rose, 2005). The first *C. elegans* embryonic division produces two cells of different sizes and developmental potentials. The larger anterior blastomere, termed AB, will generate only somatic tissues, whereas the smaller posterior blastomere, P1, undergoes three more rounds of asymmetric division, each giving rise to a germline precursor (P2, P3 and P4) and a somatic sister blastomere (Fig. 1A).

The asymmetric localization of maternal proteins to restricted blastomeres, which is an essential step in asymmetric divisions and cell fate-specification in early *C. elegans* embryos, is achieved by various mechanisms, including asymmetric distribution, retention and/or degradation (Reese et al., 2000; Hao et al., 2006; Tenlen et al., 2008; Griffin et al., 2011). Maternal factors can also be deposited into the egg as mRNAs and asymmetrically translated in a subset of blastomeres. This provides a way to prevent the precocious activity of powerful developmental regulators and to delimit their functions in a precise spatiotemporal manner. For example, translation of the maternally supplied *zif-1* transcript begins in 4-cell embryos, and then only in somatic blastomeres (Guven-Ozkan et al., 2010; Oldenbroek et al., 2012). *ZIF-1* is the substrate-binding subunit of an E3 ligase whose many substrates are enriched in germline blastomeres (DeKenzo et al., 2003). Delayed *zif-1* translation ensures that *ZIF-1* protein is present only in cells that have become committed to somatic developmental fates.

Correct spatiotemporal translation of the majority of germline mRNAs in *C. elegans* is controlled via the 3′UTR (Merritt et al., 2008), and we have shown this to be the case for *zif-1* maternal mRNA (Guven-Ozkan et al., 2010; Oldenbroek et al., 2012). Not surprisingly, then, a large proportion of the genes identified through maternal-effect lethal screens as being required for embryonic cell fate specification encode proteins containing RNA-binding motifs (Mello et al., 1994; Draper et al., 1996; Guedes and Priess, 1997; Tabara et al., 1999; Schubert et al., 2000; Gomes et al., 2001). Almost all of these maternally supplied RNA-binding proteins (RBPs) are translated in oocytes, asymmetrically localized after the first mitotic division, and are delimited to one or only a few specific blastomeres following subsequent divisions in a spatially and temporally dynamic fashion that is unique for each protein and each blastomere. Although it is well established that these RBPs are essential for embryogenesis, molecular functions for most of them remain unclear. *In vivo* functional characterization is often complicated by interdependent regulatory
relationships between these RBPs, as well as by the fact that many of them are required for correct blastomere fate specification. RNA binding analyses for several of these proteins have revealed a low sequence specificity for target RNAs, suggesting that specificity in vivo might be achieved by combinatorial binding of multiple proteins (Ryder et al., 2004; Pagano et al., 2007; Farley et al., 2008; Pagano et al., 2009).

We showed previously that the correct spatiotemporal translation of maternal zif-1 mRNA requires seven maternally supplied RBPs: OMA-1, OMA-2, POS-1, SPN-4, MEX-3, MEX-5 and MEX-6 (Oldenbroek et al., 2012). Translation of zif-1 mRNA is repressed by OMA-1 and OMA-2 in oocytes, by MEX-3 and SPN-4 in 1-cell and early 2-cell embryos, and by POS-1 in germline blastomeres P2-P4. In somatic blastomeres, MEX-5 and MEX-6 relieve translational repression by outcompeting POS-1 for binding to the zif-1 3′UTR.

In this study, we characterize the translational regulation of maternally supplied mom-2 mRNA using a reporter carrying the mom-2 3′UTR. mom-2 encodes a Wnt ligand that is essential for two Wnt-mediated cell interactions during C. elegans early embryogenesis (Rocheleau et al., 1997; Thorpe et al., 1997; Park and Priess, 2003; Walston et al., 2004). The first MOM-2/Wnt signal occurs at the 4-cell stage when P2 signals EMS, whereas the second signal occurs at the 8-cell stage when C, the somatic daughter of P2, signals ABar (Fig. 1A). The P2-to-EMS Wnt signal specifies the fate of E, the EMS posterior daughter, as the sole intestinal precursor (Rocheleau et al., 1997; Thorpe et al., 1997; Goldstein, 1992). In embryos deficient in this interaction, EMS adopts the fate of its sister, MS, which produces no intestinal cells. The Wnt signal from C orients the division axis of ABar toward C (Park and Priess, 2003; Walston et al., 2004). P2 and both P2 daughters, namely C and P3, display MOM-2/Wnt signaling activity, whereas no P2 precursor cells or any other cells at the 4-cell or 8-cell stage do (Park and Priess, 2003). However, the mechanism by which MOM-2 activity is spatially and temporally restricted within the early embryo remained unknown. Here we show that maternally supplied MOM-2/Wnt activity is regulated post-transcriptionally through the mom-2 3′UTR. Nine maternally supplied RBPs, many of which were shown previously to also regulate maternal zif-1 expression, bind the mom-2 3′UTR in vitro and combinatorially regulate the proper spatiotemporal translation of a mom-2 3′UTR reporter in vivo. Furthermore, the combinatorial codes are found to be distinct for the expression of the mom-2 and zif-1 reporters.

**RESULTS**

**OMA-1 binds to the mom-2 3′UTR**

OMA-1 and OMA-2 each contain tandem CCCH TIS11-like zinc fingers that can bind to RNAs (Detwiler et al., 2001; Shimada et al., 2002; Jadhav et al., 2008; Li et al., 2009; Guven-Ozkan et al., 2010). OMA-1 and OMA-2 share high sequence similarity and functional redundancy (Detwiler et al., 2001; Shimada et al., 2002) and will be referred to collectively as OMA-1/2 unless stated otherwise. Both proteins are expressed only in oocytes and 1-cell embryos and are degraded soon thereafter. The oma-1(zu405d) mutant results in OMA-1 protein persisting past the 1-cell stage, and this OMA-1 persistence underlies its embryonic lethality (Detwiler et al., 2001; Lin, 2003). Approximately 30% of oma-1(zu405d) embryos lack intestinal cells, similar to embryos defective in the Wnt pathway (Lin, 2003). This shared phenotype suggests that ectopic OMA-1 in zu405d embryos might interfere with the function or expression of one or more components of the Wnt signaling pathway.

In a separate study (to be published elsewhere), we found mom-2 mRNA to be highly enriched in RNP particles that contain OMA-1 protein. In that study, we introduced a rescuing OMA-1::GFP transgene (tnis17) into the null oma-1(zu405d te33) mutant, followed by crossing in the spe-9(hcb88ts) mutation, which has a temperature-sensitive defect in sperm production. The resulting strain, DG2581, produces normal oocytes but no embryos at 25°C. OMA-1::GFP was pulled down from DG2581 worm lysates using anti-GFP antibody and the co-immunoprecipitated (co-IP) RNAs were analyzed using C. elegans Gene Chip Arrays (Affymetrix). mom-2 mRNA was enriched more than 4-fold in the IP fraction compared with the input RNAs. No RNAs corresponding to other genes known to function in the P2-to-EMS signal, including mom-1, mom-3, mom-4, mom-5, gsk-3, apr-1, src-1, wtm-1 and lit-1, were enriched.

The relative abundance of selected transcripts in the OMA-1 IP fraction was also analyzed by RT-qPCR. We assayed mom-2 transcripts along with zif-1 and nos-2 transcripts, which are known targets of OMA-1 (Jadhav et al., 2008; Guven-Ozkan et al., 2010), pie-1 and vit-1 transcripts, which are unlikely to be OMA-1 targets, and mei-1, an mRNA that is regulated by OMA-1 but only in embryos and not in oocytes (Li et al., 2009). The established targets of OMA protein translational repression during oogenesis (zif-1 and nos-2), as well as mom-2, were efficiently recovered compared with negative controls (pie-1 and vit-1) and mei-1 (Fig. 1B).

**Fig. 1. OMA-1 binds to the mom-2 3′UTR in vitro and in vivo.** (A) Illustration of two known MOM-2-dependent interactions (red arrows) in early embryos. Stages of embryos shown in all figures are indicated by the number of blastomeres. Blastomeres exhibiting MOM-2-dependent signaling capability are in yellow. Signal-receiving cells are in orange. Short bars connect sister blastomeres. Germline blastomeres are marked with a thick outline. (B) Recovery of the indicated mRNAs from the input lysate by OMA-1 immunoprecipitation as measured by RT-qPCR. Error bars indicate s.d. (C) In vitro RNA pulldown using MBP-OMA-1 and mom-2 3′UTR RNA was blotted with anti-MBP antibody.
To determine whether the co-IP of mom-2 mRNA with OMA-1 was due to a direct interaction between the mom-2 3′UTR and OMA-1 protein, we performed an in vitro RNA binding assay using purified MBP-OMA-1 protein. Following biotinylation, RNA corresponding to the mom-2 3′UTR was incubated with MBP-OMA-1 and RNA pulled down with streptavidin-conjugated magnetic beads. The amount of MBP-OMA-1 pulled down with the RNA was analyzed by western blot using an anti-MBP antibody. MBP-OMA-1 was selectively pulled down by RNA corresponding to the sense, but not the antisense, strand of the mom-2 3′UTR (Fig. 1C). We conclude that OMA-1 can bind directly to the mom-2 3′UTR and therefore might regulate the expression of MOM-2 protein in vivo.

The mom-2 3′UTR is sufficient to determine the localization pattern of both its mRNA and protein in early embryos

The mechanism by which MOM-2 activity is restricted in early embryos is not known. mom-2 mRNA was detected in oocytes and early embryos by single-molecule fluorescence in situ hybridization (smFISH) (Harterink et al., 2011), which we confirmed (Fig. 2B). We detected uniform mom-2 mRNA levels in oocytes, 1-cell, 2-cell and early 4-cell embryos. The abundance of mom-2 mRNA decreases in somatic blastomeres beginning at the late 4-cell stage. By the 12-cell embryo, mom-2 mRNA was detected at variably decreased levels in different blastomeres but remained relatively unchanged in P3 and C. This preferential degradation in somatic blastomeres has been observed for many, but not all, maternally supplied mRNAs (Seydoux and Fire, 1994).

We generated a reporter construct that expresses nuclear GFP::histone H2B under the control of the germline-specific pie-1 promoter and the mom-2 3′UTR (Ppie-1-gfp::h2b-UTRmom-2) (Fig. 2A). We will refer to the mRNA and GFP::H2B expressed from Ppie-1-gfp::h2b-UTRmom-2 as gfp::h2bmom-2 and GFP::H2Bmom-2, respectively. Using smFISH, gfp::h2bmom-2 was detected in oocytes and early embryos in a pattern similar to that of endogenous mom-2 mRNA (Fig. 2B). Despite gfp::h2bmom-2 being detected at a high level in oocytes and early embryos, GFP::H2Bmom-2 is not detected until the 4-cell stage, initially at a very low level in the P2 blastomere (Fig. 2B,C). The GFP signal is further elevated in P3 and C, which are the daughters of P2, and remains high in all their subsequent descendants. The strong correlation between the onset of GFP::H2Bmom-2 signal and the blastomeres known to exhibit MOM-2 activity argues that the GFP::H2Bmom-2 expression pattern closely parallels that of the endogenous maternal MOM-2 protein. Our analysis also suggests that the mom-2 3′UTR is sufficient to confer correct localization of both its mRNA and protein in early embryos. Owing to the lack of a good MOM-2 antibody, we characterize here how the expression pattern of GFP::H2Bmom-2 is regulated in embryos.

OMA proteins repress GFP::H2Bmom-2 expression in oocytes

Repression of GFP::H2Bmom-2 expression in oocytes depends on OMA-1/2 proteins. High levels of GFP::H2Bmom-2 were observed in oocytes following simultaneous depletion of oma-1 and oma-2 by RNAi (Fig. 2C; 100% animals examined, n=50). Furthermore, ectopic OMA-1 appears to be sufficient to repress GFP::H2Bmom-2 expression in embryos. In oma-1(izu405d) embryos, we observed reduced GFP::H2Bmom-2 expression in P3 and C [55±14% (s.d.) reduction in P3, n=13] (Fig. 2B). Translational repression of maternal mom-2 mRNA by persisting OMA-1 can explain the Wnt phenotype seen in oma-1(izu405d) embryos.

We have shown previously that repression of zif-1 translation by OMA proteins requires the eIF4E-binding protein IFET-1 [previously SPN-2 (Guven-Ozkan et al., 2010)]. IFET-1 binds to both OMA-1 and to the 5′ cap-binding protein elf4E, presumably creating an inhibitory loop that prevents translation initiation (Li et al., 2009). GFP::H2Bmom-2 was derepressed in oocytes of 100% of ifet-1(RNAi) animals (n=25) (Fig. 2C), suggesting that OMA proteins also repress translation of gfp::h2bmom-2 through an IFET-1-dependent mechanism.

Together, our in vitro and in vivo results indicate that OMA-1/2 repress the translation of gfp::h2bmom-2, and presumably the mom-2 mRNA, in oocytes via direct binding to the mom-2 3′UTR.

Expression of GFP::H2Bmom-2 in early embryos requires MEX-1, PIE-1 and POS-1

OMA proteins are degraded soon after the first mitotic division (Lin, 2003). Therefore, repression by OMA proteins cannot account for
the spatiotemporal expression of GFP::H2B<sub>mom-2</sub> in embryos. To identify regulators of MOM-2 expression in embryos, we analyzed GFP::H2B<sub>mom-2</sub> in embryos depleted individually of specific RBPs. All RBPs tested here are maternally supplied and were initially identified genetically to have essential functions in the fate specification of early blastomeres, which could complicate these analyses. In order to exclude RBPs whose effect on GFP::H2B<sub>mom-2</sub> expression could be indirect, possibly via a change in cell fate specification, we first assayed the ability of candidate RBPs to bind to the mom-2 3′UTR. We performed a series of <i>in vitro</i> RNA binding assays using biotinylated mom-2 3′UTR RNA and each candidate RBP. We found that each of these proteins is capable of binding to the mom-2 3′UTR in a sense strand-specific manner (Fig. 3A).

We then analyzed GFP::H2B<sub>mom-2</sub> levels in embryos individually depleted of these candidate RBPs (Fig. 3B, Fig. 5A). Depletion of any of the three germline blastomere-enriched proteins, MEX-1, PIE-1 and POS-1, resulted in a reduction, but not abolishment, of GFP::H2B<sub>mom-2</sub> expression: mex-1(zu121), 50±3% reduction in P3 (n=13); pie-1(zu154), 54±4% reduction in P3 (n=13); pos-1(zu148), 33±4% reduction in P3 (n=12), pos-1(RNAi) in either the pie-1(zu154) or mex-1(zu121) strain resulted in no detectable GFP::H2B<sub>mom-2</sub> in embryos (n=73 and n=59, respectively). Combined depletion of pie-1 and mex-1 (pie-1(RNAi);mex-1(zu121), 55±3% (n=12); pie-1(zu154);mex-1(RNAi), 55±3% (n=12)) did not result in a more severe defect in GFP::H2B<sub>mom-2</sub> expression than either single mutant (Fig. 3B; data not shown). smFISH with probes to either mom-2 or gfp mRNA revealed no gross changes in levels in embryos mutant for any of the three genes (supplementary material Fig. S1). We conclude that PIE-1, MEX-1 and POS-1 function together to promote the translation of gfp::h2b<sub>mom-2</sub> in germline blastomeres.

**Embryos depleted of pie-1, mex-1 or pos-1 exhibit a Wnt signaling-defective phenotype**

Reduced expression of GFP::H2B<sub>mom-2</sub> could indicate a defect in Wnt-mediated processes in mex-1, pie-1 or pos-1 mutant embryos. Both pos-1(zu148) and mex-1(zu121) mutants were previously reported to have endoderm defects (Mello et al., 1992; Tabara et al., 1999). All pos-1(zu148) embryos fail to produce endoderm, whereas mex-1(zu121) mutant embryos have a cold-sensitive, incompletely penetrant defect in endoderm production. However, the E blastomere in pos-1(zu148) or mex-1(zu121) embryos does not undergo a homeotic fate change to the MS blastomere, as is also the case for E in mom-2(orr42) embryos. Specification of MS and the differentiation of MS-derived tissue types requires zygotic transcription (Mango et al., 1994; Broitman-Maduro et al., 2006), which might well be defective in these mutant embryos for reasons unrelated to the translation of maternal mom-2. Therefore, we examined ABar division axis realignment, which is a Wnt-dependent event independent of zygotic transcription (Powell-Coffman et al., 1996).

In wild-type embryos, a Wnt signal from the C blastomere aligns the division axis of ABar toward C, perpendicular to the other three AB-derived blastomeres (Park and Priess, 2003; Walston et al., 2004) (Fig. 4A,B). This alignment was shown to be defective in nearly all mom-2 mutant embryos (Rocheleau et al., 1997; Thorpe et al., 1997), a result we reproduced (96%, n=23). In addition, we observed a similar defect in the ABar division axis in 93% (n=23) of oma-1(zu405d), in 56% (n=27) of pie-1(zu154), in 42% (n=24) of mex-1(zu121) and in 44% (n=16) of pos-1(zu148) embryos. This defect was enhanced when one of the other two positive regulators was also depleted by RNAi in mex-1(zu121) or pos-1(zu148) embryos. There was only modest or no enhancement when RNAi was combined with pie-1(zu154) embryos (Table 1). Although our results suggest that defective Wnt/MOM-2 translation underlies the spindle orientation defect in pos-1, mex-1 and pie-1 mutant embryos, we cannot rule out the possibility of an indirect effect. For example, P2 (and its descendants) is not properly specified in the pie-1 or pos-1 mutant. Furthermore, in the mex-1 mutant the AB lineage develops with irregular timing (Schnabel et al., 1996) and the ABar fate is changed (Mello et al., 1992; Tabara et al., 1999).

**MEX-3/5/6 and SPN-4 repress gfp::h2b<sub>mom-2</sub> translation in embryos**

<i>In vitro</i> analyses showed that the RBPs MEX-3, SPN-4, MEX-5 and MEX-6 have repressive roles in the expression of GFP::H2B<sub>mom-2</sub>. These four proteins are all present at a high levels in oocytes and 1-cell embryos, but are subsequently asymmetrically localized to different subsets of blastomeres (Draper et al., 1996; Schubert et al., 2000; Ogura et al., 2003). Depletion of spn-4 or mex-3 resulted in GFP::H2B<sub>mom-2</sub> expression as early as the 1-cell stage (supplementary material Fig. S2), and in all subsequent blastomeres.
(Fig. 5A). No GFP::H2Bmom-2 was detected in oocytes of mex-3(RNAi) or spn-4(RNAi) animals (not shown). These results suggest that SPN-4 and MEX-3 are both required for the translational repression of gfp::h2bmom-2 in the 1-cell embryo.

MEX-5 and MEX-6 share high sequence similarity, exhibit identical expression patterns and function redundantly in nearly all cases when assayed in vivo (Schubert et al., 2000). Both proteins are highly enriched in AB after the first mitotic division, and localize to all three somatic blastomeres, but not P2, in the 4-cell embryo. In mex-5(RNAi);mex-6(RNAi) embryos, we observed uniform expression of GFP::H2Bmom-2 in all blastomeres as early as the 4-cell stage (Fig. 5A). The spatial localization of MEX-5/6, the derepression of GFP::H2Bmom-2 in mex-5/6(RNAi) embryos, and the in vitro binding of the mom-2 3′UTR by MEX-5, all suggest that MEX-5/6 directly repress translation of gfp::h2bmom-2 mRNA in somatic blastomeres. MEX-5/6 activity is not required for gfp::h2bmom-2 translational repression until the 4-cell stage.

Depletion of either spn-4 or mex-5/6 resulted in mom-2 and gfp::h2bmom-2 mRNAs being uniformly distributed in embryos beyond the 4-cell stage (Fig. 5B; supplementary material Fig. S1), likely the result of defective degradation of these mRNAs in somatic blastomeres. Whereas ectopic gfp::h2bmom-2 mRNA may contribute to the ectopic expression of GFP::H2Bmom-2 in 4-cell and older embryos, it cannot account for the ectopic expression of GFP::H2Bmom-2 in 1- or 2-cell embryos, in which gfp::h2bmom-2 is already high in wild-type embryos.

In mex-5(RNAi);mex-6(RNAi) embryos, PIE-1, MEX-1 and POS-1 are all uniformly localized (Schubert et al., 2000). However, uniform localization of all three positive regulators is not the cause of the uniform expression of GFP::H2Bmom-2 observed in mex-5(RNAi);mex-6(RNAi) embryos. Simultaneous depletion of pie-1 and pos-1 [(pie-1(zu154);pos-1(RNAi)) or of mex-1 and pos-1 [mex-1(zu121);pos-1(RNAi)] in mex-5(RNAi);mex-6(RNAi) embryos resulted in no change to the uniform expression of GFP::H2Bmom-2 (Fig. 5A; supplementary material Fig. S3). Similarly, PIE-1, MEX-1 and POS-1 are not required for the GFP::H2Bmom-2 derepression observed in mex-3(RNAi) or spn-4(RNAi) embryos (Fig. 5A; supplementary material Fig. S3). The observation that the positive regulators PIE-1, MEX-1 and POS-1 are not required for GFP::H2Bmom-2 expression when negative regulators are depleted suggests that these positive regulators promote the expression of GFP::H2Bmom-2 by antagonizing the negative regulators.

MEX-3 binds IFET-1, an eIF4E-binding protein

The GFP::H2Bmom-2 expressed in oocytes of ifet-1(RNAi) animals persists into embryos, precluding a determination of whether IFET-1 activity is also required for the repression of mom-2 in embryos. We did, however, investigate whether any of the RBPs functioning in the embryo bind to IFET-1 in vitro. Like MBP-OMA-1, MBP-MEX-3 efficiently pulled down His-IFET-1 in an in vitro pulldown assay (Fig. 5C). Low, but reproducible, amounts of His-IFET-1 were also pulled down by MBP-MEX-1. No detectable IFET-1 was pulled down with any of the other proteins tested. This suggests that the repression of gfp::h2bmom-2 translation in embryos by MEX-3 is through a mechanism involving IFET-1, similar to the translational repression by OMA-1/2 in oocytes.

Competitive binding of maternal RBPs to the mom-2 3′UTR determines GFP::H2Bmom-2 expression

The seven regulators of GFP::H2Bmom-2 expression in embryos are themselves provided as maternal proteins and are all present in the
1-cell embryo. Beginning with the first embryonic division, these seven proteins exhibit dynamic and different spatiotemporal localization patterns (Fig. 6A) (Draper et al., 1996; Mello et al., 1996; Guedes and Priess, 1997; Tabara et al., 1999; Schubert et al., 2000; Ogura et al., 2003). To better understand how translation of gfp::h2bmom-2 transcripts is determined in cells possessing a combination of both positive and negative regulators, we performed the following two sets of experiments. First, we divided the mom-2′UTR into six equal regions in order to map binding sites for each protein. We generated mom-2′UTR RNAs deleted for one of the six regions (del1-del6 RNAs) and performed binding assays with each of the RBPs (Fig. 3A). SPN-4, MEX-1 and PIE-1 binding was abolished with del3 RNA, suggesting that region 3 contains sequence essential for their binding. PIE-1 binding appears to require sequence present in region 6 as well. The same assay revealed that regions 4 and 6 are essential for POS-1 and MEX-3 binding, respectively. Region 4 and region 6 contain a predicted POS-1 and MEX-3 binding site, respectively (supplementary material Fig. S4) (Farley et al., 2008; Pagano et al., 2009). Consistent with multiple putative MEX-5 binding sites across the entire mom-2′UTR, no single region was found to be essential for MEX-5 binding (Fig. 7D; supplementary material Fig. S4) (Farley et al., 2008; Pagano et al., 2009).

Second, we performed in vitro RNA binding competition experiments. Both a positive and a negative regulator were mixed with the target biotinylated mom-2′UTR RNA to determine whether binding of one protein is favored over the other. P2 and P3 have a high level of the negative regulator SPN-4, as well as the three positive regulators PIE-1, MEX-1 and POS-1 (Fig. 6A). We found that mixing MEX-1 or PIE-1 with SPN-4 immediately prior to the addition of mom-2′UTR RNA resulted in the binding of only MEX-1 or PIE-1, but not SPN-4, to the RNA. This result and the above′UTR domain mapping suggest that PIE-1 and MEX-1 share overlapping binding sites with SPN-4 and that binding of either protein prevents simultaneous binding by SPN-4. In P2 and P3, the high level of MEX-1 and PIE-1 presumably prevents SPN-4 from binding to the mom-2′UTR, thereby antagonizing the SPN-4 repressive effect. In a similar competition RNA binding experiment, we found that binding of POS-1 and SPN-4 to the mom-2′UTR RNA was not affected by the presence of the other protein, consistent with the domain mapping showing that these two proteins bind to distinct regions of the mom-2′UTR (Fig. 3A, Fig. 6B).

EMS, the somatic sister of P2, does not express gfp::H2Bmom-2. Levels of SPN-4, MEX-1, POS-1, MEX-5 and MEX-6 are all initially high in EMS, whereas the first three proteins are degraded by the proteasome later in the cell cycle (Fig. 6A). We found that when MEX-1 or POS-1 was pre-mixed with MEX-5 in the RNA binding reaction, only MEX-5, but not MEX-1 or POS-1, was pulled down by the mom-2′UTR RNA (Fig. 6C). The clear binding preference for MEX-5 over MEX-1 or POS-1, along with the persistence of MEX-5/6 levels in EMS can explain the repression of gfp::h2bmom-2 translation in EMS. The competition assay showed no preference in binding to the mom-2′UTR RNA for MEX-3 versus MEX-1 or POS-1 (Fig. 6D), consistent with these three proteins binding preferentially to different regions as shown in Fig. 3A.

**DISCUSSION**

We show here that a large set of maternally supplied RBPs is required to set up proper MOM-2/Wnt signaling in the *C. elegans* embryo, thereby specifying normal intestinal development and spindle orientation. The 3′UTR of the mom-2 transcript is sufficient to confer localization information for both the gfp::h2bmom-2 mRNA

![Fig. 5. MEX-3, SPN-4 and MEX-5/6 repress GFP::H2Bmom-2 expression.](image-url)

Fluorescence micrographs (A) or smFISH images with gfp probe (B) of embryos expressing GFP::H2Bmom-2 in various RNAi (r) or mutant (–) backgrounds. (C) HiS-FET-1 was mixed with individual MBP-tagged proteins and pulled down with amylose beads. Proteins pulled down were assayed using the indicated antibodies. Scale bar: 10 μm.

**Table 1. Percentage of embryos with a defective ABar division axis**

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<tr>
<th>Genotype</th>
<th>Defective ABar division axis (%)</th>
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<tr>
<td>Wild type</td>
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<td>25</td>
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<td>16</td>
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<tr>
<td>pos-1(-);mex-1(r)</td>
<td>79</td>
<td>19</td>
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<tr>
<td>pos-1(-);pie-1(r)</td>
<td>73</td>
<td>15</td>
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<tr>
<td>oma-1(zu405)</td>
<td>93</td>
<td>23</td>
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<tr>
<td>mom-2(or42)</td>
<td>96</td>
<td>23</td>
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and the corresponding GFP::H2B::mom-2 protein. The gfp::h2bmom-2 mRNA is translationally repressed properly in oocytes and early embryos, and correctly translated in known Wnt signaling cells. We have identified nine maternally supplied RBPs that can all bind in vitro to an RNA corresponding to the mom-2 3′UTR and that suffice to explain the correct spatiotemporal translation of gfp::h2bmom-2 transcripts in vivo. In vitro experiments reveal overlapping binding sites and a hierarchy of binding preferences to the mom-2 3′UTR among these RBPs.

**Common themes governing translational control via the 3′UTR**

Our studies on the mom-2 and zif-1 (Oldenbroek et al., 2012) 3′UTRs reveal two common mechanisms for how positive and negative regulators control translation of these maternal mRNAs via the 3′UTR. First, in the absence of all positive and negative regulators identified to date, the transcripts are translated. Unless additional positive regulator(s) required for translation of gfp::h2bmom-2 are identified, our results suggest that these maternal mRNAs are inherently capable of being translated. Repression of each transcript in oocytes and embryos is maintained by spatially and temporally distinct sets of repressors. Translation occurs when repression is relieved or antagonized by a positive regulator (Fig. 7A). Our demonstration here that OMA proteins repress the translation of gfp::h2bmom-2 suggests that previously characterized Wnt-defective phenotypes in gsk-3(RNAi) and gsk-3(nr2047ts) embryos are likely the result of compromised expression of the Wnt/MOM-2 ligand (Fig. 7C).

**Translational control in oocytes**

We show that OMA-1/2 are required in oocytes to repress gfp::h2bmom-2 mRNA translation, and are capable of continued repression when ectopically present in post-1-cell embryos. This can explain the Wnt-defective phenotype associated with oma-1(zu405d) embryos (Fig. 7A). These results also explain the curious phenotypes of gsk-3(RNAi) and gsk-3(nr2047ts) embryos. In the canonical Wnt pathway, GSK-3 negatively regulates the pathway by phosphorylating β-catenin and promoting its degradation (Wu and Pan, 2010). However, gsk-3(RNAi) and gsk-3(nr2047ts) embryos partially resemble mom-2 mutant embryos, for both β-catenin-dependent and β-catenin-independent phenotypes, suggesting a positive role upstream of β-catenin in the C. elegans Wnt pathway (Schlesinger et al., 1999; Shirayama et al., 2006). We and others have shown that gsk-3(RNAi) and gsk-3(nr2047ts) embryos express ectopic OMA-1 protein, which is likely to underlie their Wnt-defective phenotypes (Nishi and Lin, 2005; Shirayama et al., 2006). Our demonstration here that OMA proteins repress the translation of gfp::h2bmom-2 suggests that previously characterized Wnt-defective phenotypes in gsk-3(RNAi) and gsk-3(nr2047ts) embryos are likely the result of compromised expression of the Wnt/MOM-2 ligand (Fig. 7C).

**Translational control in 1- and 2-cell embryos**

Repression of gfp::h2bmom-2 translation in 1- and 2-cell embryos requires both SPN-4 and MEX-3 (Fig. 7A,B). We showed
previously that repression of the \textit{zif-1} 3′UTR reporter in early germline blastomeres also requires both MEX-3 and SPN-4 (Oldenbroek et al., 2012). In \textit{spn-4(RNAi)}; \textit{mex-3(zu155)} embryos, the \textit{zif-1} reporter is expressed precociously as early as the 2-cell stage. High levels of both MEX-3 and SPN-4 coexist within the same cell only in the 1-cell and (briefly) early 2-cell embryo (Draper et al., 1996; Ogura et al., 2003), thereby limiting translational repression of their joint targets to only these very early stages. Repression would be relieved after the 2-cell stage when MEX-3 and SPN-4 no longer coexist. This distinctive mode of translational repression highlights the unique molecular nature of the 1-cell embryo, with protein regulators of different developmental pathways repressing their joint targets to only these very early stages.

Translational control after the 2-cell stage

In 4-cell embryos, high levels of SPN-4 and MEX-3 are detected in reciprocal patterns, with SPN-4 in both P2 and EMS, and MEX-3 in ABa and ABp (Fig. 6A) (Draper et al., 1996; Ogura et al., 2003). The P2 blastomere also has high levels of MEX-1, PIE-1 and POS-1. A low level of MEX-3 in conjunction with the competitive binding advantage of PIE-1 and MEX-1 over SPN-4 can explain why \textit{mom}-2 is translated in P2 (Fig. 7A,B). Two observations suggest that POS-1 promotes translation of \textit{gfp::h2b}\textsubscript{mom-2} mRNA through a mechanism different from that by MEX-1 and PIE-1.

First, whereas both PIE-1 and MEX-1 share overlapping binding sites with SPN-4, POS-1 appears to bind to a different region. Second, \textit{pos}-1 RNAi in either \textit{pie-1} or \textit{mex-1} mutant embryos enhances the defects in \textit{gfp::H2B}\textsubscript{mom-2} expression. By contrast, little or no enhancement was observed following simultaneous depletion of \textit{mex-1} and \textit{pie-1}. With the caveat that this conclusion is based on experiments using RNAi, it is consistent with POS-1 repressing translation of \textit{gfp::h2b}\textsubscript{mom-2} mRNA through a mechanism that differs from that of MEX-1 and PIE-1.

Our data suggest a model in which the repression of \textit{mom}-2 translation in EMS results from high levels of MEX-5/6, coupled with their competitive binding advantage over MEX-1 and POS-1 for the \textit{mom}-2 3′UTR. The MEX-5 binding advantage could derive from higher numbers of putative binding sites in the \textit{mom}-2 3′UTR (supplementary material Fig. S4). In addition, MEX-5/6 could contribute to \textit{mom}-2 translational repression in somatic blastomeres in at least two other ways. First, MEX-5/6 activity is required to keep the level of \textit{mom}-2 mRNA low in somatic blastomeres, probably by promoting its degradation. Second, it has been shown that MEX-5/6 activity is required to restrict PIE-1, MEX-1 and POS-1 to the germline blastomeres (Schubert et al., 2000).

Intriguingly, whereas POS-1 and MEX-5/6 have essential and antagonistic roles in regulating maternal \textit{zif-1} and \textit{mom}-2 translation, they function in opposite ways on each transcript (Oldenbroek et al., 2012). POS-1 is a negative regulator for \textit{zif-1} translation in P2. The preference for MEX-5/6 binding to the 3′UTR over POS-1 appears to drive translation of \textit{zif-1} in EMS. The contrary is true for \textit{mom}-2, where POS-1 promotes translation in P2 and MEX-5/6 represses translation in EMS. It is currently unclear how POS-1 and MEX-5/6 can exhibit opposite functions within the same cell in the translational regulation of different maternal transcripts.

3′UTRs as post-transcriptional enhancers

In newly fertilized embryos, regulating gene expression at the level of translation provides certain advantages over transcriptional regulation.
First, it uncouples protein expression from transcription, which needs to be repressed for correct specification of germline blastomeres in both flies and worms (Nakamura and Seydoux, 2008). Second, because it does not require transcription, translational control is faster and therefore much better suited to a developmental program in which cell divisions occur every 10-15 minutes.

The importance of 3′UTRs and the RBPs bound to them in regulating the translation of germline transcripts is well established in C. elegans and Drosophila (Wilkie et al., 2003; Piccioni et al., 2005; Merritt et al., 2008). However, the mechanism by which the cohort of maternally supplied RBPs specifies cell fate in early C. elegans embryos via the translational regulation of multiple shared targets remains largely unknown. Our results here lead us to propose that the 3′UTR of maternal mRNAs contains a combinatorial code that determines the precise topography of RBPs, both positive and negative, that are bound to it. Therefore, the spatiotemporal expression pattern of any particular maternal mRNA is determined primarily by the precise combination of RNA-binding regulators present in the cell that are capable of binding to the 3′UTR sequence. By reading the combinatorial code provided by the 3′UTR, this cohort of RBPs specifies cell fate through translational control. This is reminiscent of transcriptional enhancers, whose binding sites provide a combinatorial code for cell-specific regulators that specify cell fate through transcriptional control. Future studies will more precisely define the combinatorial code(s) associated with maternal mRNAs, as well as interrogating RBP codes associated with somatic transcripts.

**MATERIALS AND METHODS**

**Strains**

Genetic markers used were: LGI, spe-9(tc88ts); LGII, mex-1(zu121); tels127(Ppie-1-gfp::h2b-UTRmom-2); LGIII, unc-119(e3); pie-1(zu154); LGIV, oma-1(zu405d), oma-1(zu405d te33); LGV, oma-2(te51), pos-1(zu148), tnlx7(fnc-1(u168)), pCS410 (oma-1:stev:gfpg). Strains used are: TX1377, tels127(Ppie-1-gfp::h2b-UTRmom-2), DG2460 spe-9(tc88ts); oma-1(zu405d te33), DG2581 spe-9(tc88ts); oma-1(zu405d te33); tnlx17, DG2620 unc-119(ed3); oma-1(zu405d te33); oma-2(tc51); tnlx17, tnlx17 resuces oma-1(zu405d te33); oma-2(tc51) sterility. All integrated lines were generated by bombardment (Prairits et al., 2001).

**Plasmid construction**

Most plasmids were constructed using Gateway technology (Guven-Ozkan et al., 2010). A 557 bp genomic sequence beginning 100 bp upstream of the mom-2 stop codon was cloned downstream of pie-1 promoter-driven GFP::H2B in the vector pID3.01B (Guven-Ozkan et al., 2010; Reese et al., 2000). pCS410 was created by modifying plasmid pRL475 (Lin, 2003). GFP::H2B in the vector pID3.01B (Guven-Ozkan et al., 2010; Reese et al., 2000). pCS410 was created by modifying plasmid pRL475 (Lin, 2003).

**RNAi and imaging**

Feeding RNAi was performed by feeding L1 larvae for 2 days at 25°C (Timmons and Fire, 1998). All images were acquired, processed and quantified as described previously (Guven-Ozkan et al., 2008). Spindle orientation was assayed using sequential DIC z-stacks.

**smFISH**

CAL590-coupled probes were purchased from Biosearch Technologies and hybridization was performed as described (Raj and Tyagi, 2010) with a few modifications. Embryos were collected by cutting adult hermaphrodites on poly-lysine-coated slides, squashed with a coverslip, incubated in 3.7% formaldehyde for 15 minutes, and frozen on dry ice. Upon removal of the coverslip, embryos were treated with 95% ethanol for 10 minutes at −20°C, fresh 95% ethanol for 5 minutes at room temperature, 70% ethanol for 3 hours at 4°C, 400 μl wash buffer for 10 minutes, then 100 μl probe (0.1 μM) overnight at 37°C, followed by three 20-minute washes in wash buffer at 37°C, and then mounted.

**Recombinant proteins and RNA binding assays**

Maltose binding protein (MBP)-tagged proteins and HIS-IFET-1 were purified from E. coli and Flag-PIE-1 was purified from HeLa cells (Li et al., 2009; Oldenbroek et al., 2012). Biotinylation of RNA and pulldowns were performed as described (Lee and Schedd, 2001; Guven-Ozkan et al., 2010). The optimal amounts of purified protein and mom-2 3′UTR RNA were empirically determined by titration. A typical binding reaction contained 150 ng purified protein (34.5, 30.3, 34.1, 31.5, 41.5, 36.7 and 76.3 nM, respectively, for MBP-tagged OMA-1, MEX-1, MEX-3, MEX-5, POS-1, SPN-4 and Flag-PIE-1) and 400 ng biotinylated RNA. For the competition binding assays, RNA was kept limiting compared with proteins used (1 μg each MBP-tagged protein and 130 ng RNA, except for the SPN-4/PIE-1 competition, where 750 ng MBP-SPN-4 and 400 ng FLAG-PIE-1 were used).

**Purification of OMA-1 and associated RNAs from adult worms**

OMA-1::S:TEV-GFP was purified as described (Cheeseman et al., 2004; Cheeseman and Desai, 2005) with modifications. Young adults were sonicated in 50 mM HEPEs (pH 7.5), 100 mM KCl, 1 mM MgCl2, 10% glycerol, 0.05% NP40, and protease inhibitors (complete EDTA-free, Roche). OMA-1::S:TEV-GFP was purified from 1 ml medium-speed supernatant (18000 g×2–10 minutes, supplemented to 300 mM KCl and 200 units RNasin (Promega) with 20 μg anti-GFP antibody (NB600-308, Novus Biologicals) cross-linked to 150 μl Dynabeads protein A (Invitrogen) at 4°C for 1 hour. Dynabeads were washed seven times with IP wash buffer (sonication buffer supplemented to 300 mM KCl, 20 units/ml RNasin, 5 mM 2-mercaptopethanol, 5 mM sodium citrate, 10 μM ZnCl2) before incubation with 0.25 μg/ml anti-GFP antibody (Invitrogen) at overnight at 4°C to release immunoprecipitated OMA-1::S protein. RNAs were purified from this supernatant (IP RNA) or from 50 μl of crude lysate (input RNA) using Trizol (Invitrogen) and precipitated with linear acrylamide (Sigma).

**RT-qPCR**

RT-qPCR was performed on IP and input RNA samples from the same DG2581 lysate and an IP RNA sample from a similarly prepared DG2460 lysate, which lacks the OMA-1::S:TEV-GFP fusion protein. Reverse transcription was performed with IP RNA or input RNA using SuperScript II reverse transcriptase (Invitrogen) and random primers according to the manufacturer’s instructions (oligo(dT) primers performed similarly). qPCR was performed using FastStart SYBR Green Master Mix (Roche) on a Mastercycler ep realplex instrument (Invitrogen) in triplicate with 2–[Ct(IP)–Ct(input, corrected)] and 2–[Ct(IP)–Ct(mock IP)] in the latter calculation, the raw Ct value of the input sample was corrected to account for the fact that 0.8% of input sample was used for each RT-PCR reaction. Only fold enrichment relative to input RNA was shown in Fig. 1.

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**Competing interests**

The authors declare no competing financial interests.

**Author contributions**

S.M.R. and R.L. designed the project. T.G.-O. contributed to early results. M.O. performed the experiments pertaining to in vivo and in vitro RBP binding to the mom-2 3′UTR. C.S. and D.G. designed and performed the co-immunoprecipitation of OMA-1 bound RNAs from embryos. S.M.R. and R.L. wrote the paper.

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References


Development