Celf1 regulation of dmrt2a is required for somite symmetry and left-right patterning during zebrafish development

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SUMMARY

RNA-binding proteins (RBPs) bind to numerous and diverse mRNAs to control gene expression post-transcriptionally, although the in vivo functions of specific RBP-mRNA interactions remain largely unknown. Here, we show that an RBP named Cugbp, Elav-like family member 1 (Celf1) controls expression of a gene named doublesex and mab-3 related transcription factor 2a (dmrt2a), which is essential for somite symmetry and left-right patterning during zebrafish development. Celf1 promotes dmrt2a mRNA decay by binding to UGU repeats in the 3’UTR of dmrt2a mRNA, leading to asymmetric somitogenesis and laterality defects. Furthermore, blocking the Celf1-dmrt2a mRNA interaction by a target protector morpholino alleviates failures in somite symmetry and left-right patterning that are caused by celf1 overexpression. Our results therefore demonstrate that Celf1-dependent fine-tuning of dmrt2a expression is essential for generating bilateral symmetry of somites and left-right asymmetric patterning during zebrafish development.

KEY WORDS: RNA-binding protein, Post-transcriptional regulation, Symmetric somitogenesis, Left-right patterning, Target protector morpholino, Zebrafish

INTRODUCTION

Transcriptional control has important roles in generating a properly organized body during vertebrate development (Naiche et al., 2005; Schier and Talbot, 2005; Shivdasani, 2002). However, levels of particular transcripts are highly variable in space and time during development because of the stochastic nature and the spatiotemporal regulation of transcription (Blake et al., 2003; Elowitz et al., 2002). Embryos must therefore have systems that precisely control the amounts of proteins, to regulate multiple developmental processes at post-transcriptional levels (Gebauer and Hentze, 2004). RNA-binding proteins (RBPs) are known to provide such a mechanism. For instance, an RBP named Cugbp Elav-like family member 1 (Celf1) controls gene expression at multiple post-transcriptional levels, including alternative splicing, deadenylation and mRNA decay, and fine-tunes the abundance of proteins that are synthesized from its target mRNAs (Barreau et al., 2006; Vlasova et al., 2008).

Celf1 target mRNAs have been identified by a yeast three-hybrid screen, a SELEX (systematic evolution of ligands by exponential enrichment) approach, an in vitro binding assay and RNA immunoprecipitation assays (Lee et al., 2010; Marquis et al., 2006; Mori et al., 2008; Rattenbacher et al., 2010; Suzuki et al., 2002; Takahashi et al., 2000). In HeLa cells, Celf1 binds to >600 short-lived mRNAs that are involved in cell growth, motility and apoptosis (Rattenbacher et al., 2010), suggesting that Celf1 coordinately regulates protein expression from multiple mRNAs. Analyses of the conserved sequences among these mRNAs reveal that UG-rich elements or UGU repeats, such as UGUUGUUUGU and UUGUGUGUGU, are the binding sequences of Celf1 (Rattenbacher et al., 2010); these sequences are similar to target elements identified by other methods in human, mouse and frog (Lee et al., 2010; Marquis et al., 2006; Mori et al., 2008; Takahashi et al., 2000).

Celf1 is broadly expressed in early vertebrate embryos, whereas Celf1 expression is restricted to specific regions, such as eyes and somites (Gautier-Courteille et al., 2004; Hashimoto et al., 2006; Kress et al., 2007), suggesting a role(s) for Celf1 in the regulation of developmental processes. However, loss of Celf1 function in either frog or mouse embryos has only minor effects on their development; knockdown of the Xenopus Celf1 ortholog EDEN-BP results in only a defect of somite segmentation (Gautier-Courteille et al., 2004). Some Celf1-knockout mice are viable to the adult stage, although they display growth retardation (Kress et al., 2007). These mild effects on development may be explained by redundant actions among Celfs and/or by high abundance of proteins synthesized from Celf1 target mRNAs. Therefore, the physiological roles for Celf1 in the regulation of vertebrate development remain largely unclear.

A possible strategy to explore such a role for Celf1 is to deplete proteins synthesized from Celf1 target mRNAs. We thus overexpressed celf1 in zebrafish embryos to intensify Celf1-mediated post-transcriptional regulation. This manipulation resulted in failures of bilateral symmetric somitogenesis and left-right (LR) asymmetric patterning, defects which are similar to the phenotype induced by knockdown of a single gene named doublesex and mab-3 related transcription factor 2a (dmrt2a, formerly terra) (Saude et al., 2005). We also found that Celf1 downregulates dmrt2a expression by binding to the 3’UTR of dmrt2a mRNA. Furthermore, blocking the interaction between Celf1 and dmrt2a mRNA reduced the effects of celf1 overexpression on both somite symmetry and LR asymmetric patterning. Our results therefore identify a crucial role of the specific Celf1-mRNA pair in generating a properly organized body during vertebrate development, and provide a powerful tool for analyzing the roles of specific RBP-mRNA pairs in various experimental settings.
mRNA and morpholino injections
pCS2-celf1 (long form), pCS2-celf1 linker, pCS2-dmrt2a and pCS2-monomeric red fluorescent protein (mRFP) were used in this study. celf1, celf1 linker, dmrt2a and mRFP mRNA were synthesized using the SP6 mMessage mMachine System (Ambion). Either 50 or 150 pg celf1 mRNA was injected into one-cell-stage zebrafish embryos; as a control, either 50 or 150 pg mRFP mRNA was injected.

Because a deletion mutant of the linker domain of human or frog Celf1 (Celf1 linker) is known to lose its functional activity by losing RNA-binding activity or by preventing oligomerization (Takahashi et al., 2000; Cosson et al., 2006), we used zebrafish celf1 linker as a negative control in this study. To confirm its protein expression in embryos, we injected 50 pg celf1 linker mRNA into one-cell-stage zebrafish embryos, and found that a 26 kDa protein, equivalent to that of mutant protein, was expressed in the manipulated embryos (supplementary material Fig. S1B). To test its functional activity, we performed quantitative PCR for dmrt2a in celf1 linker overexpressing embryos and showed that Celf1 linker does not affect dmrt2a expression in vivo (Fig. 5A). These observations suggest that Celf1 linker acts as a loss-of-function mutant in our experimental settings.

To generate a Celf1-resistant dmrt2a mRNA, we engineered the plasmid pCS2-dmrt2a, which harbors only the coding region of dmrt2a and does not include the Celf1-binding site within the 3' UTR. We thus used mRNA synthesized from the pCS2-dmrt2a as the Celf1-resistant dmrt2a mRNA. Antisense MO oligonucleotides named celf1 short-MO, celf1 short-MO linker, dmrt2a-MO, dmrt2a-TP-MO or control MO were obtained from Gene Tools. celf1 long-MO, celf1 short-MO, dmrt2a-MO, dmrt2a-TP-MO or control MO were designed to target the AUG initiation codon of these mRNAs. dmrt2a-TP-MO was designed to target the UGU repeats within the 3' UTR of dmrt2a mRNA.

The MO sequences were as follows: control-MO, 5'-CCCTTCTACGTTACTAATTATA-3'; celf1 long-MO, 5'-GCTCTCAGC- TTGGAATCTAC-3'; celf1 short-MO, 5'-GGTGGTCAAGACCCATTACATCTT-3'; dmrt2a-MO, 5'-AGATCCGTGATTTTCTGAGGCA- GGCTA-3' (Saude et al., 2005); dmrt2a-TP-MO, 5'-ACATTACAT- AAATACACATCCAC-3'.

To knock down celf1, we co-injected 2.5 ng celf1 long-MO and 2.5 ng celf1 short-MO (5 ng celf1-MOs) into one-cell-stage zebrafish embryos. To protect dmrt2a mRNA from Celf1, we injected 5 ng dmrt2a-MO into one-cell-stage zebrafish embryos; as a control, we injected 5 ng control-MO. To confirm the specificity of dmrt2a-TP-MO, dmrt2a-MO (5 ng) was co-injected with either dmrt2a-MO (0.5 ng and 1 ng) or control-MO (1 ng) into one-cell-stage embryos. For rescue experiments, a combination of celf1 mRNA (50 pg) with either dmrt2a-MO (2.5 ng and 5 ng), control-MO (5 ng), dmrt2a mRNA (1.25 pg and 2.5 pg) or mRFP mRNA (2.5 pg) were co-injected into one-cell-stage embryos. Defects of somite symmetry and LR patterning in these embryos were evaluated by in situ hybridization for uncx4.1 and mle2a, respectively.

The specificity and efficacy of celf1 long-MO and celf1 short-MO was tested by co-injection of RNAs encoding GFP-tagged celf1 long or celf1 short (celf1L-GFP or celf1S-GFP) with the cognate MO into zebrafish embryos and by western blotting using anti-Celf1 antibody, respectively (supplementary material Fig. S1B). The efficacy of dmrt2a-MO was confirmed in vivo by its ability to recapitulate the phenotype of dmrt2a morphants, as shown previously (Saude et al., 2005). The efficacy and specificity of dmrt2a-TP-MO were evaluated by RNA immunoprecipitation assay and quantitative PCR assay (Fig. 4C, Fig. 5A).

Western blotting
Embryos at 12-14 hours post-fertilization (hpf) were squeezed using glass slides to remove the yolk and to dissociate cells. Dissociated cells were lysed with lysis buffer (PBS containing 1% Triton X-100, 0.2% SDS, 150 mM NaCl and 5 mM EDTA). Cell lysates were subjected to SDS-PAGE, and then transferred to Hybond-P membrane (GE Healthcare). To detect Celf1, the membrane was incubated with rabbit anti-Celf1 antisera (a gift from Dr Kunio Inoue, Kobe University, Japan). After extensive washing, the membrane was incubated with HRP-conjugated anti-rabbit antibody (Jackson ImmunoResearch Laboratories), and the immune complex was visualized with ChemiLumi One L (Nacalai Tesque). After stripping, the membrane was incubated with mouse anti-β-actin antibody (Sigma), and then with HRP-conjugated anti-mouse antibody (Jackson ImmunoResearch Laboratories).

In vitro binding assay
Cos7 cells were transfected with pCS2-celf1 using Trans-IT LT-1 (Mirus) according to the manufacturer’s protocol. After 48 hours cultivation, cells were lysed with binding buffer [10 mM Tris-HCl (pH8.0), 150 mM NaCl, 1 mM MgCl2, 0.1 mM CaCl2, 0.5% NP-40 and 5% glycerol]. Biotinylated RNA oligonucleotides (Gene Design) were pre-mixed with streptavidin-Sepharose beads (GE Healthcare) for 10 minutes, and mixed with cell lysate for 30 minutes at room temperature. The beads were washed three times with binding buffer, and pulled-down proteins were subjected to western blotting using anti-Celf1 antisera.

The sequences of RNA oligonucleotides were as follows: dmrt2a wildtype, 5'-auguagugauuuuuguauuuauuuu-3'; dmrt2a 3p mut, 5'-augCguagauuuuacGcauauuuauuuu-3'; dmrt2a 7p mut, 5'-acGCGCagauuuuacGcauauuuauuuu-3'; s0 (negative control), 5'-agauccugccgugccugucgaucagc-3' (Marquis et al., 2006); EDEN (positive control), 5'-guauugauuuuuguauuuuauuuu-3' (Marquis et al., 2006) (intact nucleotides in lower case, substituted nucleotides in uppercase).

RNA immunoprecipitation (RIP)
According to the manufacturer’s protocol of the RIP-Assay Kit (MBL), complexes that consist of mRNAs and Celf1 were isolated from either un.injected embryos or dmrt2a-TP-MO-injected embryos at 12-14 hpf using rabbit anti-Celf1 antisera. Normal rabbit serum (Thermo Scientific) was used as a control. In vivo interaction between Celf1 and dmrt2a mRNA, myod mRNA, a known target of Celf1 in a mouse myoblast cell line C2C12 (Lee et al., 2010), or suppressor of hairless (rbpja or rbpjb) in zebrafish mRNA, a known target in frog (Cibis et al., 2010; Gauthier-Courteille et al., 2004), was tested by quantitative PCR (see below). We also tested interaction of Celf1 with non-target mRNAs (β-actin and cyclinA1) as negative controls.

Quantitative PCR (qPCR) and measurement of mRNA half life
Embryos injected with control-MO, celf1-MOs or dmrt2a-TP-MO were grown to 12-14 hpf. To measure mRNA half life, embryos injected with control-MO, celf1-MOs or dmrt2a-TP-MO were grown to 11 hpf, treated with 8 µg/ml Actinomycin-D (Nacalai Tesque) for 1 hour and collected at the indicated time points following the incubation.

Total RNAs of embryos were isolated using Sepasol RNA I (Nacalai Tesque). First-strand cDNAs were synthesized from total RNA with SuperScript II (Invitrogen) and oligo-dT primers (Invitrogen). Quantitative real-time PCR using gene-specific primers (see below) was performed in either MX3000p (Agilent Technologies) using SYBR-Green PCR Master Mix (Takara Bio) or LightCycler 480 system II (Roche Diagnostics) using LightCycler 480 SYBR Green I Master (Roche Diagnostics).

The sequences of gene-specific primers were as follows: dmrt2a-F, 5'-CGTTGTTTGTACTGTTTTGG-3'; dmrt2a-R, 5'-CGCCTGATC- ATGCCATCTC-3'; myod-F, 5'-ACTCTCAATGACACCAAAATG-3'; myod-R, 5'-CATGCAGAGGACTCTGTGGGA-3'; rbpja-F, 5'-TTTACCCT- CCAACCTACAGT-3'; rbpja-R, 5'-ACGCGAGATGCAGGAAACC- 3'; rbpjb-F, 5'-ACAGAACATCTTCCAACTG-3'; rbpjb-R, 5'- ATGCTCTCCACACCTG-3'; cyclin A1-F, 5'-CAATATCTGC- CATCCCAAGCC-3'; cyclin A1-R, 5'-AATCAGAGCCAG- AGATGAAACAG-3'; β-actin-F, 5'-GCTGTGTCTCCATCTGTTG- 3'; β-actin-R, 5'-TCTTGTCCTCCTCAGCCACAT-3'.
RESULTS

celf1 controls somite symmetry and LR asymmetric patterning in zebrafish

Overexpression of celf1, by injection of 50 pg celf1 mRNA into one-cell-stage zebrafish embryos, often resulted in an uneven number of somites on the left and right sides at 12-14 hpf (56%, n=89; Fig. 1B-D). Sixty percent of the defective embryos had one or more excess somites on the left side (Fig. 1B,D) and 40% had an excess on the right side (Fig. 1C,D), suggesting that this asymmetry was not biased towards either side. However, injection of 50 pg celf1Δlinker mRNA, which encodes a loss-of-function mutant of Celf1 (for details, see Materials and methods), did not alter somite symmetry (Fig. 1D). As LR asymmetric somitogenesis can be caused by loss of synchrony of the segmentation clock, including the Notch effector her1, between the left and right presomitic mesoderm (Kawakami et al., 2005; Saude et al., 2005;...

DEVELOPMENT
Vermot et al., 2005; Vermot and Pourquie, 2005), we investigated next whether celf1 overexpression affects the synchrony of her1 oscillatory expression. her1 oscillation was observed in all celf1-overexpressing embryos, but more than half of the embryos showed asynchronous her1 oscillation between the left and right presomitic mesoderm (58%, n = 98; Fig. 1F-H).

Defects in LR axis determination yield an uneven number of somites without bias to either side (Kawakami et al., 2005; Oishi et al., 2006; Saude et al., 2005). By contrast, loss of retinoic acid signaling leads to strongly biased asymmetric somitogenesis: almost all embryos have excess somites on the left side (Kawakami et al., 2005; Vermot et al., 2005; Vermot and Pourquie, 2005).

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**Fig. 3. Knockdown of celf1 leads to defects in somite symmetry and LR patterning.** (A-C) Representative images of uncx4.1 expression demonstrating symmetric (uninjected; A), right-biased (celf1-MOs; B) or left-biased (dmrt2a-TP-MO; C) asymmetric somitogenesis in zebrafish embryos at 12-14 hpf. Dorsal view, anterior to the top. Asterisks mark the last-formed somite. (D) Percentages of symmetric (L=R), left-biased (L>R) or right-biased (L<R) asymmetric somitogenesis in embryos injected with 5 ng control-MO (n=121), 5 ng celf1-MOs (n=102), 5 ng dmrt2a-TP-MO (n=90), 5 ng dmrt2a-TP-MO plus 1 ng control-MO (n=40), 5 ng dmrt2a-TP-MO plus 0.5 ng dmrt2a-MO (n=60) or 5 ng dmrt2a-TP-MO plus 1 ng dmrt2a-MO (n=68). (E-G) Representative images of mlc2a expression showing L-jog (uninjected; E), no-jog (celf1-MOs; F) or R-jog (dmrt2a-TP-MO; G) of the heart in embryos at 24-28 hpf. Dorsal view, anterior to the top. Arrows indicate the direction of heart jogging. (H) Percentages of L-jog, R-jog, no-jog or cardia bifida of the heart in embryos injected with 5 ng control-MO (n=152), 5 ng celf1-MOs (n=90), 5 ng dmrt2a-TP-MO (n=76), 5 ng dmrt2a-TP-MO plus 1 ng control-MO (n=46), 5 ng dmrt2a-TP-MO plus 0.5 ng dmrt2a-MO (n=47) or 5 ng dmrt2a-TP-MO plus 1 ng dmrt2a-MO (n=46). Scale bars: 200 μm.

**Fig. 4. Celf1 binds to dmrt2a mRNA in vitro and in vivo.** (A) Sequences of RNA oligonucleotide probes used in vitro binding assay. Underlines mark UGU repeats and capital letters indicate substituted nucleotides. (B) Binding of Celf1 with specific RNA was tested by in vitro binding assay. Lane 1: dmrt2a_wildtype; lane2: dmrt2a_3p mut; lane 3: dmrt2a_7p mut; lane 4: empty; lane 5: s0 (negative control); lane 6: EDEN (positive control). Interaction between Celf1 and either dmrt2a_wildtype (lane 1) or EDEN (lane 6) was detected. (C) In vivo interaction between Celf1 with dmrt2a (upper left panel), myod (upper right panel), rbpja (middle left panel), rbpjb (middle right panel), β-actin (lower left panel) or cyclinA1 (lower right panel) mRNAs. Column 1: RIP control sample using normal serum from uninjected embryos; column 2: RIP sample using Celf1 antiserum (Celf1 AS) from uninjected embryos; column 3: RIP sample using Celf1 AS from embryos injected with dmrt2a-TP-MO. Celf1 interacted with dmrt2a, myod, rbpja and rbpjb mRNAs. dmrt2a-TP-MO specifically blocked the interaction of Celf1 with dmrt2a mRNA.
Somite and LR patterning by Celf1

Vilhais-Neto et al., 2010). Because celf1 overexpression led to unbiased somite asymmetry (Fig. 1B-D), we reasoned that celf1 overexpression resulted in a failure of LR axis determination, leading to asymmetric somitogenesis. To test this, we investigated laterality in either celf1- or celf1Δ linker-overexpressing embryos. Left-sided expression of pitx2a in the lateral plate mesoderm was randomized in celf1-overexpressing embryos but not in celf1Δ linker-overexpressing embryos (Fig. 2B,C). Consistent with this phenotype, cardiac laterality evaluated by expression of myosin light chain 2a (mlc2a) was also randomized only in celf1-overexpressing embryos (Fig. 2E,F). These results suggest that celf1 overexpression fails to determine proper LR axis, eventually leading to unbiased somite asymmetry as well as laterality defects.

To investigate the endogenous role of celf1, we knocked down celf1 in zebrafish embryos using antisense morpholino oligonucleotides (MOs). Because two forms of Celf1 (long and short) are expressed in zebrafish (Hashimoto et al., 2006), MOs for long and short forms of celf1 (celf1_long-MO and celf1_short-MO) were used in this study (for details, see Materials and methods and supplementary material Fig. S1A,B). Almost all celf1 morphants showed somite segmentation defects (94%, n=88; supplementary material Fig. S1,C,D) similar to the phenotype induced by knockdown of EDEEN-BP in frog (Gautier-Courteille et al., 2004). In addition, 22-28% of celf1 morphants displayed defects in somite symmetry and LR asymmetric patterning (Fig. 3B,D,F,H). These results indicate that Celf1 is essential for generating proper somite symmetry and LR asymmetric body plan.

Celf1 binds to dmrt2a mRNA in vitro and in vivo

Celf1 acts as a negative regulator of gene expression by binding to specific mRNAs (Lee et al., 2010; Marquis et al., 2006; Mori et al., 2008; Rattenbacher et al., 2010; Suzuki et al., 2002; Takahashi et al., 2000), which harbor the putative Celf1-binding sites within the 3′UTR of target mRNAs (Lee et al., 2010; Marquis et al., 2006; Mori et al., 2008; Rattenbacher et al., 2010; Suzuki et al., 2002; Takahashi et al., 2000). Based on our data and these findings, we anticipated that knockdown of target genes would yield similar defects to those seen in celf1-overexpressing embryos. To identify such a target(s), we undertook a search for genes involved in both somite symmetry and LR asymmetric patterning. We found putative Celf1-binding sites in several genes, including wnt11, duboraya, one-eyed pinhead, no tail and dmrt2a, that are involved in LR patterning. However, the knockdown phenotypes of wnt11, duboraya, one-eyed pinhead or no tail are different from those of celf1 overexpression, suggesting that these genes are unlikely to be the target of Celf1 in the context of somite symmetry and LR patterning. As a candidate, we selected dmrt2a for the following three reasons: (1) knockdown of dmrt2a in zebrafish embryos results in laterality defects as well as an uneven number of somites without bias (Saude et al., 2005) (supplementary material Fig. S2); (2) expression of dmrt2a is detected in the somites, the presomitic mesoderm and the tailbud, where celf1 is also expressed (Meng et al., 1999) (supplementary material Fig. S3A); and (3) a putative Celf1-binding site containing four UGU repeats and U- and A-rich sequences within 35 nucleotides is present in the 3′UTR of dmrt2a mRNA (supplementary material Fig. S3C).

Because in situ hybridization confirmed that celf1 and dmrt2a expression overlap in the tailbud and the somites at 12-14 hpf (supplementary material Fig. S3A,B), we performed further experiments to elucidate the relationship between Celf1 and dmrt2a mRNA. In vitro binding assays using biotinylated RNA probes revealed that Celf1 associated with the putative binding site in the 3′UTR of dmrt2a mRNA (Fig. 4B, lane 1), but not with mutated sequences in which all or three UGU repeats were disrupted (Fig. 4B, lanes 2 and 3), indicating that Celf1 binds to the UGU repeats in the 3′UTR of dmrt2a mRNA. To examine whether endogenous Celf1 also binds to dmrt2a mRNA in zebrafish embryos, we performed RNA immunoprecipitation (RIP) of Celf1-mRNA complexes in embryos at 12-14 hpf. RIP using Celf1 antiserum led to a 3.3-fold enrichment of dmrt2a mRNA relative to negative control using normal serum (Fig. 4C). The integrity of the RIP assay was ensured by testing whether Celf1 interacts with either its known targets including myod or rbpg (rbpja or rbpgb) (Cosson et al., 2006; Takahashi et al., 2000), which harbor the putative Celf1-binding sites within the 3′UTR (supplementary material Fig. S3D,E), or non-targets such as β-actin and cyclin A1 (Fig. 4C).

Celf1 controls dmrt2a mRNA decay in vivo

To test whether the interaction between Celf1 and dmrt2a mRNA affects dmrt2a expression, we examined the amounts of dmrt2a mRNA in either celf1 morphants or celf1-overexpressing embryos by qPCR. celf1 knockdown resulted in a 57% increase of the amount of dmrt2a mRNA relative to embryos injected with control-MO (Fig. 5A). Conversely, celf1 overexpression led to a 50% reduction of dmrt2a mRNA relative to control mRFP overexpression (Fig. 5A). In addition, qPCR analyses in celf1 morphants treated with a transcription inhibitor (Actinomycin D) revealed that dmrt2a mRNA is stabilized in celf1 morphants (Fig. 5B), meaning that Celf1 promotes dmrt2a mRNA decay in zebrafish embryos. These results therefore suggest that Celf1 is
required to maintain \( dmrt2a \) mRNA at an appropriate level, and that Celf1 regulation of \( dmrt2a \) might contribute to proper symmetric somitogenesis and LR asymmetric patterning.

**Celf1 regulation of \( dmrt2a \) is required to generate proper somite symmetry and LR asymmetric patterning**

Target protector MOs (TP-MOs) have been developed to disrupt the interaction of specific microRNA-mRNA or protein-mRNA pairs (Choi et al., 2007; Cibois et al., 2010; Staton et al., 2011). To investigate the role of specific pairing between Celf1 and \( dmrt2a \) mRNA, we used \( dmrt2a \)-TP-MO, the sequence of which is complementary to the UGU repeats in the 3'UTR of \( dmrt2a \) mRNA. Injection of \( dmrt2a \)-TP-MO in zebrafish embryos interfered with the specific interaction between Celf1 and \( dmrt2a \) mRNA (Fig. 4C) and led to a 53% increase of \( dmrt2a \) mRNA (Fig. 5A), showing that \( dmrt2a \)-TP-MO protects \( dmrt2a \) mRNA from Celf1 in vivo. Notably, injection of \( dmrt2a \)-TP-MO only resulted in failures of somite symmetry and LR asymmetric patterning, whereas co-injection of \( dmrt2a \)-TP-MO and \( dmrt2a \) mRNA restored the failures caused by \( dmrt2a \)-TP-MO in a dose-dependent manner (Fig. 3C,D,G,H). These results indicate that Celf1-mediated regulation of \( dmrt2a \) is essential for somite symmetry and LR asymmetry during zebrafish development.

Based on these results, we hypothesized that celf1 overexpression intensifies \( dmrt2a \) mRNA decay, eventually leading to LR asymmetric somitogenesis as well as a failure of LR patterning. If this is the case, either blocking the interaction between Celf1 and \( dmrt2a \) mRNA or increasing the amount of \( dmrt2a \) should cancel the effects of celf1 overexpression on somite symmetry and LR patterning. To test this, we co-injected celf1 mRNA and either \( dmrt2a \)-TP-MO or the Celf1-resistant \( dmrt2a \) mRNA into zebrafish embryos and found substantial alleviation of the disruption of both symmetric somitogenesis (Fig. 6A-D,I) and cardiac laterality (Fig. 6E-H,J), relative to the effects of co-injection of celf1 mRNA and either control-MO or mRFP mRNA. Hence, our results demonstrate that Celf1-mediated post-transcriptional regulation of \( dmrt2a \) is required to

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**Fig. 6. Disruption of Celf1-\( dmrt2a \) mRNA interaction cancels the effects of celf1 overexpression on somite symmetry and LR asymmetric patterning.** (A-D) Representative images of uncx4.1 expression showing left-biased (celf1 mRNA plus control-MO; A), right-biased (celf1 mRNA plus control-MO; B) or symmetric (celf1 mRNA plus dmrt2a-TP-MO; C,D) somitogenesis in zebrafish embryos at 12-14 hpf. Dorsal view, anterior to the top. Asterisks mark the last-formed somite. (E-H) Representative images of mlc2a expression showing R-jog (celf1 mRNA plus control-MO; E), no-jog (celf1 mRNA plus control-MO; F) or L-jog (celf1 mRNA plus dmrt2a-TP-MO; G,H) of the heart in embryos at 24-28 hpf. Dorsal view, anterior to the top. Arrows indicate the direction of heart jogging. (I,J) Percentages of symmetric (L=R), left-biased (L>R) or right-biased (L<R) asymmetric somitogenesis in embryos injected with 50 pg celf1 mRNA and either 5 ng control-MO and either 5 pg celf1 mRNA and either 5 ng control-MO and different doses of \( dmrt2a \)-TP-MO. Scale bars: 200 \( \mu \)m.
control two key processes that generate a properly organized body during vertebrate development: symmetric somitogenesis and LR asymmetric patterning.

**DISCUSSION**

The vertebrate body displays invariant LR asymmetry, which is determined by symmetry-breaking events during early embryonic development. The other and contrasting feature of vertebrate body is the bilaterally symmetric arrangement of skeletal structures, including vertebrae and skeletal muscles, which arises from the metameric structures of the somites during early embryonic development. In this study, we characterize an RBP named Celf1 in zebrafish and show a previously unidentified role of Celf1 in coordinating symmetric somitogenesis and LR asymmetric patterning, which are essential processes for generating a properly organized body during embryonic development.

Phenotypes in embryos injected with 50 pg celf1 mRNA point to crucial roles of Celf1 in the control of somite symmetry and LR patterning. However, it is noteworthy that Celf1 function is not exclusive for these processes. Injection of higher amounts of celf1 mRNA (150 pg) led to additional defects including failures of epiboly and gastrulation at early stages and multiple defects, such as short body axis, abnormal segmentation, small head and small eyes at later stages (supplementary material Fig. S4). Such broad phenotypes suggest that Celf1 is involved in the regulation of multiple developmental processes in zebrafish. This is consistent with the fact that hundreds of Celf1’s targets have been identified in various types of cells (Lee et al., 2010; Marquis et al., 2006; Mori et al., 2008; Rattenbacher et al., 2010; Suzuki et al., 2002; Takahashi et al., 2000). The observation that specific phenotypes could be segregated by lowering the amount of celf1 mRNA might be a result of different thresholds of Celf1 activity.

In our model, Celf1 maintains dmrt2a mRNA at an appropriate level, and Celf1 regulation of dmrt2a is required to generate proper symmetric somitogenesis and LR asymmetric patterning. However, even in the presence of dmrt2a-TP-MO, 20-30% of celf1-overexpressing embryos display defects in symmetric somitogenesis and LR asymmetric patterning (Fig. 6J), suggesting that either efficacy or specificity of dmrt2a-TP-MO is low and/or that other targets of Celf1 contribute to regulation of these processes. Two lines of evidence argue against the first possibility: (1) the amount of dmrt2a mRNA in embryos injected with dmrt2a-TP-MO is similar to that of celf1 morphants (Fig. 5A), showing high efficacy of dmrt2a-TP-MO; and (2) dmrt2a-TP-MO does not hamper the interaction of Celf1 with mRNA encoding either myod or suppressor of hairless (rbpja or rbpjb) (Fig. 4C), which are known targets of Celf1 in C2C12 cells (Lee et al., 2010) and in frog (Cibois et al., 2010; Gautier-Courteille et al., 2004), respectively, meaning that specificity of dmrt2a-TP-MO is also high. Importantly, frequencies of somite symmetric and LR patterning defects in embryos co-injected with 50 pg celf1 mRNA and 5 ng dmrt2a-TP-MO (Fig. 6J) are similar to those of embryos injected with 5 ng dmrt2a-TP-MO alone (Fig. 3D,H). This similarity suggests that phenotypes seen in embryos co-injected with celf1 mRNA and dmrt2a-TP-MO are caused by the dominant effect of dmrt2a-TP-MO, and thus supports the second possibility.

The zootype hypothesis proposed by Yost (Yost, 1999) suggests that major events in determining LR asymmetry, such as left-sided gene expression, are evolutionarily conserved, whereas the expression patterns, regulation and functions of genes are not necessarily conserved among vertebrates (Hirokawa et al., 2006; Yost, 1999). This notion is further supported by our findings that the functional interaction between Celf1 and dmrt2a mRNA might not be conserved among vertebrates because no putative Celf1-binding site is present within the 3′ UTR of mouse and chick Dmrt2.

**Conclusions**

Hundreds of RBP-mRNA interactions have been predicted in vitro and in vivo, but just a few have been shown to have an in vivo function. Using an approach combining gain-of-function for RBP and protection of RBP-target interaction, we reveal the in vivo role of the specific RBP-mRNA pair in generating a properly organized body during zebrafish development. Our strategy therefore provides a powerful tool for understanding better the roles of specific RBP-mRNA pairs in vertebrate development and other experimental settings.

**Acknowledgements**

We are grateful to Thomas N. Sato, Yasukazu Nakahata, Naoyuki Inagaki and Kinichi Nakashima for advice, helpful discussions and critical reading of the manuscript. We also thank Ian Smith and Muh Chyi Chai for help in preparing the manuscript; Tomoko Murata, Maiko Yokouchi and Hiroko Shigesato for technical assistance; and Kunio Inoue for sharing anti-Celf1 antiserum.

**Funding**

This work was supported by Grants-in-Aid for Scientific Research [23111517 and 24681043 to T.M., 17017027 to Y.B. and T.M.] from the Ministry of Education, Culture, Sports, Science and Technology (MEXT), Japan and by the Global COE Program in Nara Institute of Science and Technology, MEXT, Japan.

**Competing interests statement**

The authors declare no competing financial interests.

**Supplementary material**

Supplementary material available online at http://dev.biologists.org/lookup/suppl/doi:10.1242/dev.077263/-/DC1

**References**


