nil per os encodes a conserved RNA recognition motif protein required for morphogenesis and cytodifferentiation of digestive organs in zebrafish

Alan N. Mayer1,2,* and Mark C. Fishman1,†

1 Cardiovascular Research Center, Department of Medicine, Massachusetts General Hospital and Harvard Medical School, Charlestown, MA 02129, USA
2 Pediatric Gastroenterology Unit, Department of Pediatrics, Massachusetts General Hospital and Harvard Medical School, Charlestown, MA 02129, USA
1 Present address: Novartis Institutes for Biomedical Research, 400 Tech Square, 7th floor, Cambridge, MA 02139, USA
* Author for correspondence (e-mail: mayer@cvrc.mgh.harvard.edu)

Accepted 14 May 2003

SUMMARY

Digestive organ development occurs through a sequence of morphologically distinct stages, from overtly featureless endoderm, through organ primordia to, ultimately, adult form. The developmental controls that govern progression from one stage to the next are not well understood. To identify genes required for the formation of vertebrate digestive organs we performed a genetic screen in zebrafish. We isolated the nil per os (npo) mutation, which arrests morphogenesis and cytodifferentiation of the gut and exocrine pancreas in a primordial state. We identified the npo gene by positional cloning. It encodes a conserved protein, with multiple RNA recognition motifs, that is related to the yeast protein Mrd1p. During development npo is expressed in a dynamic fashion, functioning cell autonomously to promote organ cytodifferentiation. Antisense-mediated knockdown of npo results in organ hypoplasia, and overexpression of npo causes an overgrowth of gastrointestinal organs. Thus, npo is a gene essential for a key step in the gut morphogenetic sequence.

Key words: Zebrafish, Genetics, Intestine, Digestive system, Embryology, RNA-binding proteins

INTRODUCTION

All vertebrates undergo similar morphogenetic steps in forming the digestive organs (Grapin-Botton and Melton, 2000). After specification of the endoderm, the primitive gut tube represents the first morphologically recognizable precursor of the alimentary tract. The undifferentiated endoderm that lines the gut tube ultimately gives rise to the parenchyma of the digestive organs and other derivatives, such as the lungs and thyroid. How overtly featureless tissue becomes specified to particular organ fates – adopting a genetically determined size, shape and cytoarchitecture – is not known. The genetic programs that guide the formation of organs during embryonic life may also be utilized later for repair and homeostasis, and, in some cases, may become unregulated and promote carcinogenesis. Therefore, identifying the crucial genetic components that guide organogenesis, and ultimately assembling these elements into coherent pathways, has relevance to a broad array of medical problems.

Organogenesis is conventionally framed by morphogenetic events, and as molecular insight accrues, the morphogenetic framework is annotated with details of expression patterns and gene activities. For the intestine, morphogenesis of the adult form begins with aggregations of mesenchyme beneath the epithelium to create the beginnings of intestinal villi. These changes are accompanied by epithelial cytodifferentiation, marked by the acquisition of apical-basal cell polarity and the initiation of lineage-specific gene expression programs (Montgomery et al., 1999; Roberts, 1999). Individual aspects of the anlage-to-organ transition have been linked to single genes. For example, genetic control has been demonstrated for villus number (Karlsson et al., 2000) or form (Kaestner et al., 1997), goblet cell differentiation (Katz et al., 2002) or secretory cell specification (Yang et al., 2001). Yet to our knowledge, there are no reports of mutations that arrest development after primitive gut tube morphogenesis but before the initiation of villi formation. Thus it is not known whether global regulation of this step exists, or whether such regulation might be genetically dissectible.

A similar question can be formulated for the pancreas and liver. These anlage bud from the primitive gut tube, expressing both endoderm-specific and, progressively, organ-specific genes. The pancreatic anlage expresses Pdx1, then matures through cell fate decisions that lead to islet cells and exocrine cells (Edlund, 1999). The exocrine pancreas then grows and differentiates under the influence of factors produced by the adjacent mesenchyme (Wessells and Cohen, 1967). The logic of pancreas development has become clearer in recent years, as genetic and embryologic studies have related specific signaling pathways to discrete steps of the developmental sequence (Kim and Hebrok, 2001). The liver is distinguished
by expression of organ-specific genes even before the anlage becomes morphologically detectable, but its subsequent outgrowth is also controlled by interactions with surrounding tissues (Zaret, 2000).

Classic genetic studies of development have proven their utility in creating a molecular underpinning for the metazoan body plan, but the model organisms exploited to create that framework, *Drosophila* and *C. elegans*, lack many of the organs found in vertebrates. Taking our cue from this powerful approach, we sought to discover whether there are genes that, when mutated, would freeze the developing vertebrate digestive tract in an undifferentiated state. We therefore conducted a genetic screen in zebrafish. Here, we describe the positional cloning and characterization of *npo* (nil per os, Latin for ‘nothing by mouth’). We show that *npo* encodes a conserved RNA recognition motif protein that is dynamically expressed in the embryonic digestive tract, the requirement for which defines a novel control point during organogenesis.

### MATERIALS AND METHODS

#### Zebrafish strains and studies

Care and breeding of zebrafish *Danio rerio* was performed as described (Westerfield, 1995). Developmental staging was carried out using standard morphological features (Kimmel et al., 1995) of fish raised at 28.5°C.

#### Mutagenesis and screening

Males of the TL line were treated with ENU as described previously (Haffter et al., 1996), bred with wild-type females for at least two generations, then in-crossed to drive recessive mutations to homozygosity. Live inbred progeny were examined at 4 days postfertilization (dpf) using a Wild M10 dissecting microscope.

#### Histologic methods

Fixation of embryos for histology, embedding in JB-4 (Polysciences) and plastic sectioning was performed as described previously (Pack et al., 1996). Embryos for electron microscopy were fixed in 2% glutaraldehyde in 0.1 M sodium cacodylate buffer (pH 7.4) overnight at 4°C. Embryos were rinsed in buffer, post-fixed in 1% osmium tetroxide in cacodylate buffer for 1 hour at room temperature, rinsed again in buffer, then in distilled water and stained, en bloc, in an aqueous solution of 2% uranyl acetate for 1 hour at room temperature. They were rinsed in distilled water and dehydrated through a graded series of ethanol to 100%. They were further dehydrated in 100% propylene oxide and then infiltrated with Epon resin (Electron Microscopy Sciences, Fort Washington, PA) in a 1:1 solution of Epon:propylene oxide. The following day they were placed in fresh Epon for several hours and then embedded in Epon overnight at 60°C. Thin sections were cut on a Reichert Ultracut E ultramicrotome, collected on formvar-coated slot grids, stained with uranyl acetate and lead citrate, and examined using a Philips CM 10 transmission electron microscope at 80 kV.

#### Cartilage staining

Jaw and brachial arch structures were visualized using Alcian Blue as described (Schilling et al., 1996).

#### Immunofluorescence

Embryos for Zo1 and ATPase antibody staining were fixed in Dent’s solution [80% methanol, 20% DMSO (v/v)] overnight at 4°C, and then stored in methanol at −20°C. Whole embryos were stained as described previously (Westerfield, 1995) and embedded in JB-4 for sectioning. Slides were mounted with Gel-mount (Fisher) and photographed using a Zeiss Axiophot. For Npo immunostaining of embryos, paraffin sections were permeabilized by digesting with 10 mg/ml proteinase K for 20 minutes, then post-fixed with 4% paraformaldehyde for 20 minutes at room temperature. After washing several times with phosphate buffered saline containing 0.1% Tween-20 (PBT), the tissue was blocked with PBT containing 1% bovine serum albumin (BSA) and 10% sheep serum (Sigma). Blocking solution was replaced with anti-Npo at a concentration of 1 μg/ml in blocking solution. The sections were incubated for 2 hours at room temperature, then washed six times in PBT-1% BSA before incubation with secondary antibody (Cy-3-conjugated sheep anti-rabbit; Rockland). Controls containing no primary antibody were included with all experiments. Antibodies were obtained as follows: mouse monoclonal anti-zo1 (S. Tsukita); mouse monoclonal anti-ATPase-α5f subunit (Developmental Studies Hybridoma Bank). Polyclonal antipeptide antibodies to the Zebrafish Npo protein were generated by immunizing rabbits with a peptide of amino acids 122-137 (CLNLVGLDEKDESQEF) (antibody 4151), followed by affinity purification (QCBI/Biosource International). Conjugated secondary antibodies were from Sigma or Rockland Immunochemicals.

#### Positional cloning

The *npo*<sup>W07;g</sup> (TL background) mutation was mapped by out-crossing into the polymorphic wild-type strain WIK, followed by inbreeding of heterozygous progeny. We scanned the genome for linkage by bulked-segregant analysis (Shimoda et al., 1999), which placed the *npo* mutation on linkage group 6. Fine mapping identified marker z8532 to be 0.03 cm (1/2971) from the *npo* locus. A chromosome walk was performed from z8532, and the genetic interval covered with 2 BACs, 37b12 and 90p3 from the BAC library distributed by Incyte Genomics (Amemiya et al., 1999). These were subjected to shotgun sequencing, and the assembled sequence encoded a single contig 129 kb in length, which contained four open reading frames predicted by both homology to GenBank sequences (blasts) and by the exon prediction program GENSCAN from the MIT website (http://genes.mit.edu/GENSCAN.html). Internal genetic markers were generated from simple-sequence repeats found within the contig and used to narrow the genetic interval further. The two remaining candidates were analyzed by complete sequencing of cDNAs isolated by RT-PCR from mutant and wild-type embryos. The candidate *epha2* cDNA did not contain any detectable mutations, whereas the RRM-encoding cDNA was found to have a nonsense mutation at codon 221 of the 926 codon reading frame. This result was substantiated by sequencing PCR products from genomic DNA derived from 12 mutants, 12 phenotypically wild-type siblings and 12 wild types. The GenBank Accession Number for zebrfish *npo* is AY299514.

#### In vitro transcription/translation

Total RNA was isolated from ~50 *npo*-mutant and 50 wild-type embryos at 4 dpf using Trizol reagent (Life Technologies) according to manufacturer’s instructions. We used a combination of DT and randomly primed cDNA as a template for two rounds of nested PCR to amplify the full-length cDNAs. The DNA polymerase used was Pfu-Turbo (Stratagene), and Taq polymerase was used to add a 3’ adenyne for cloning into pCRII (Topo-TA kit, Invitrogen). We isolated 12 independent clones and sequenced these completely. The in vitro coupled transcription/translation was performed using the T7 TNT system (Promega). [35S]-methionine-labeled protein was electrophoresed on a 10% SDS-polyacrylamide gel, followed by autoradiography.

#### RNA binding assays

Npo protein synthesized as above was assayed for RNA homopolymer binding activity essentially as described previously (Swanson and Dreyfuss, 1988). Briefly, homopolymeric RNA bound to solid agarose support was purchased from commercial sources (poly C and poly U from Sigma; poly G and poly A from Pharmacia). The beads were
suspended and washed extensively in binding buffer [10 mM Tris HCl (pH 7.3), 50 mM NaCl, 2.5 mM MgCl₂, 0.1% Tween 20]. In vitro translation products of Npo wild-type, mutant and luciferase control (20 µl, about 100,000 cpm of acid insoluble radioactivity) were added to ~100 µg of beads in 1 ml of binding buffer, and incubated with rocking at room temperature for 10 minutes. The beads were washed six times with binding buffer, then boiled in 25 ml SDS-PAGE sample buffer (Chantry and Glynn, 1986) for 5 minutes and loaded onto a 10% SDS-polyacrylamide gel. After electrophoresis and autoradiography the resulting bands were quantitated by using the program NIH Image 1.62. Percent bound was calculated from the ratio of bound to input radioactivity migrating at the expected molecular weight. The embryos were first dechorionated in pronase followed by an additional phenol/chloroform extraction and ethanol precipitation. BAC DNA was diluted into Danieu's medium/0.1% Phenol Red (as a tracer) to a final concentration of 100 ng/µl. The embryos were then fixed and processed for in situ hybridization to detect ifabp expression. To enhance detection of the lineage tracer, the embryos were incubated with Cy-3 streptavidin before embedding and sectioning.

**RESULTS**

**npo mutant isolation**

In zebrafish, the key events of organogenesis in the digestive tract are spread over a 3 day period, from about 24 to 84 hours postfertilization (hpf) (Pack et al., 1996). We screened a pool of ENU-mutagenized zebrafish for recessive mutations that interfere with differentiation and growth of the digestive organs, examining live embryos by dissecting microscopy after 96 hpf, a time when the differentiated digestive organs (gut, pancreas, liver) are visible. We identified a mutant allele (npo<sup>07;5</sup>) in which the gut, liver and pancreas could not be detected using a dissecting microscope, yet other organs and structures appeared relatively normal (Fig. 1A–B). The mutation is recessive lethal and 100% penetrant in all backgrounds tested (WIK, TL, Tubingen). Because the mutant larvae do not eat we named the locus *nir per os*. The mutant also has an underdeveloped jaw and branchial arch structures (Fig. 1C,D). Although live mutants appear normal until about 84 hpf, histological sectioning of mutant embryos identified by genotyping reveals developmental defects are first noticeable at about 60–72 hpf. It is at this stage that the gut begins a phase of rapid growth and cytokidifferentiation. At 96 hpf, mutant embryos exhibit overall digestive organ hypoplasia, and the absence of differentiated intestinal and exocrine pancreatic epithelium (Fig. 1G,H). Unaffected structures and organs include the notocord, somites, heart, kidney and nervous system.

**npo is required for the endoderm-intestine transition**

To determine the developmental step at which the *npo* is essential, we assessed mutant embryos for achievement of various developmental milestones. By using whole-mount in situ hybridization, we monitored expression of the *foxa3* and *sonic hedgehog* (*shh*) genes at various time points in *npo*-mutant and wild-type embryos, which allowed us to follow the morphogenesis of endoderm-derived structures through organogenesis (Chen et al., 2001; Odenthal and Nusslein-Volhard, 1998). As shown in Fig. 2A-D, the expression patterns of *foxa3* and *shh* in wild-type and mutant embryos are not discernably different before 48 hpf. *shh* expressed in the foregut is excluded at the expected site of pancreatic budding, and *foxa3* staining shows the liver and pancreas primordia budding at the same location in wild-type and mutant embryos. We also evaluated the expression of the mesenchymal targets of *shh*,
Fig. 1. *npo*-mutant phenotype. (A,B) Live larvae at 4.5 dpf, showing that the jaw, branchial arches and gut tube are markedly underdeveloped at 96 hpf, but that dorsal structures (somites, notocord) appear unaffected by the mutation. (C,D) Alcian Blue staining of wild-type and mutant larvae at 4.5 dpf demonstrates failure of branchial arch growth beyond the initial primordium. (E-G) Cross sections of embryos stained with Hematoxylin and Eosin at the level of the pancreatic islet. (E,F) 72 hpf embryos (genotyped prior to embedding) showing the first morphologically detectable differences between mutant and wild type, with hypoplastic gut and liver in the mutant. (G,H) 96 hpf embryos show a stark contrast between wild type and mutant. The mutant gut tube is substantially smaller and the epithelial architecture is less organized, with no villi formation. The exocrine pancreas is not recognizable in the mutant, yet the islet appears relatively normal. The liver is not seen because it is much smaller in the AP dimension and does not extend to this level. g, gut; p, pancreas; l, liver; i, pancreatic islet; ep, exocrine pancreas; gb, gall bladder; sb, swim bladder. Scale bars: E,F, 20 μm; G,H, 30 μm.

Fig. 2. *npo* is required for endoderm-intestine transition. (A,B) *foxA3* expression pattern at 48 hpf showing formation of liver, gut and pancreatic anlage in both wild-type and *npo* mutant embryos. (C,D) *shh* expression at 48 hpf reveals normal foregut patterning, with label exclusion at the prepancreatic endoderm. (E,F) *ifabp* expression detected in the wild-type intestine but not in the mutant. (G,H) Histochemical staining for alkaline phosphatase. Robust staining of apical aspect of epithelium in the wild type, but staining of mutant epithelial cells appears basal, suggesting mislocalization. (I,J) Na/K ATPase immunofluorescence demonstrates basolateral localization of fluorescence in wild type, but no clear localization in the mutant. (K,L) Zo1 immunofluorescence demonstrates formation of zona occludens in both wild-type and mutant embryos. (M,N) Transmission electron micrograph of intestine. Junctional complexes are present in both mutant and wild-type epithelia. Microvilli in the wild type are smooth and uniform, but in the mutant they are fewer and pleomorphic. +/-, wild type; +/-, mutant; g, gut; L, liver; p, pancreas; mv, microvilli; TJ, tight junction. Scale bars: A-F, 150 μm; G,H, 20 μm; I-L, 10 μm; M,N, 1 μm; insets, 30 μm.
ptc1 and ptc2 (Lewis et al., 1999), and \( \text{bmp4} \) (Chen et al., 1997), as well as endodermal markers \( \text{foxa2} \) (axial) (Odenthal and Nusslein-Volhard, 1998), \( \text{tcf4} \) (Dorsky et al., 1999), \( \text{gata5} \) (Pack et al., 1996) and \( \text{pescadillo} \) (Allende et al., 1996). We noted no differences in expression patterns by in situ hybridization at 48 hpf (data not shown).

At about 48 hpf, gut tube morphogenesis occurs by canalization of the endoderm and formation of tight junctions between the epithelial cells (Horne-Badovinac et al., 2001). Electron microscopy and Zo1 immunofluorescence staining of 96 hpf embryos shows that tight junctions do form between the gut epithelial cells (Fig. 2I,J). Brush border microvilli also are present in the mutant, but they are fewer in number and misshapen (Fig. 2M,N).

After the gut tube forms, the endodermal cells re-organize into a simple columnar epithelium and begin to express organ-specific genes. For the gut, this is the key distinguishing step that marks the transition to mature organ, and it has been previously termed the 'endoderm-intestine transition' (Traber and Wu, 1995). In the zebrafish, this transition occurs between 60 and 72 hpf, when the intestinal epithelial cells begin to express alkaline phosphatase. Histochemical localization to the apical aspect of the epithelial cell reflects establishment of apical-basal polarity (Pack et al., 1996). Alkaline phosphatase staining is absent from the apical aspect of the gut epithelium at 96 hpf, and appears to be basally localized (Fig. 2G,H). Immunofluorescence detection of the Na/K ATPase-\( \alpha 6f \) subunit, which is normally localized to the basolateral surface of wild-type epithelial cells, reveals no clear localization in the mutant. Expression of the enterocyte-specific gene encoding intestinal fatty acid binding protein (\( \text{ifabp} \)) becomes detectable in the foregut of the wild-type embryo between 72 and 84 hpf, and expression expands caudally (Andre et al., 2000); however, no expression is detected in the mutant intestine by 96 hpf (Fig. 2E,F). Taken together, these data point to a step early in gut cytoidifferentiation for which \( \text{npo} \) is essential.

**npo is required for liver and exocrine pancreas development**

In wild-type and mutant embryos, the pancreatic bud forms from the primitive gut tube at the proper location, as shown in Figs 2, 3. But histological sectioning of the mutant embryos at 96 hpf shows a pancreatic islet surrounded by only a rim of flat cells, rather than distinct acinar cells of the exocrine pancreas (Fig. 1G,H). \( \text{trypsin} \) gene expression and immunoreactive carboxypeptidase are not detected in the mutant, which is consistent with a failure to form the exocrine pancreas (Fig. 3). By contrast, the pancreatic islet does form in the mutant, as seen by histological examination (Fig. 1G,H), and based on presence of insulin expression (Fig. 3E-H).

The liver bud is morphologically detectable at about 40 hpf in both wild type and \( \text{npo} \) mutants, but in the mutant it never grows larger than that of a normal 72 hpf embryo. Bile synthesis and secretion does occur in the mutant based on the appearance of bright yellow material in the intestinal lumen. Staining for carbohydrate with periodic acid-Schiff reagent reveals glycogen in the hepatocytes in both mutant and wild-type embryos (data not shown). Despite these signs of hepatocyte differentiation, the mutant hepatocytes fail to express immunoreactive cytokeratin (Fig. 3). Thus, the \( \text{npo} \) requirement in liver development appears to occur toward the later phases of hepatogenesis.

In summary, the unifying feature of the organ-specific defects we observe in the \( \text{npo} \) mutant is the arrest of development just after the appearance of the endodermal organ primordia, the ‘anlage’, but prior to growth and specific cellular distinction into mature epithelial cells of the gut, liver and

---

**Fig. 3.** \( \text{npo} \mediates exocrine pancreas and liver cytoidifferentiation.** (A-F) Whole-mount in situ hybridizations show formation of pancreatic primordia in both mutant and wild-type embryos at 48 hpf (A,B), and subsequent failure to form differentiated exocrine pancreas in mutant embryos by 96 hpf (C,D). By contrast, islet formation is independent of \( \text{npo} \). (G,H). Double immunofluorescence staining for insulin (green) and carboxypeptidase (red) shows selective failure of exocrine pancreas formation in the mutant, with sparing of the pancreatic islet. (I,J) Immunofluorescence detection of cytokeratin (monoclonals AE1/AE3), demonstrating staining of wild-type liver and gut epithelia, but absent specific staining of mutant epithelia. While outline defines organ boundaries identified by phase contrast. g, gut; p, pancreas; l, liver. Scale bars: A,B, 80 \( \mu \text{m} \); C-E, 150 \( \mu \text{m} \); G-I, 25 \( \mu \text{m} \).
exocrine pancreas. This suggests that npo is crucial in traversing a key epithelial maturation step in these endodermal derivatives.

**Positional cloning of npo**

We identified the npo gene by positional cloning (Fig. 4). We mapped npo to a 0.06 cM genetic interval, within which we identified two genes. One of these encodes Epha2, in which we did not identify any coding mutations, and the overexpression of which by cDNA and BAC injection does not rescue the phenotype. The other gene, npo, encodes a hypothetical RNA-recognition motif (RRM) protein. The mutant allele has a T to A mutation, which results in a premature termination codon at position 221 of the predicted 926 amino acid sequence. In vitro coupled transcription/translation of npo cDNA obtained from wild-type and mutant embryonic RNA conforms to this size prediction (104 kDa and 25 kDa, respectively), which is consistent with truncation of the protein in the mutant.

We designed several morpholino antisense oligonucleotides to the candidate npo gene. All four npo-antisense oligonucleotides abrogate the formation of mature intestinal or exocrine pancreatic epithelium. The expression of insulin, which is present in the npo mutant, is also present in the morpholino-injected embryos (Fig. 5). Branchial arches, as monitored by Alcian Blue staining, are completely absent in the morpholino-injected embryos (data not shown).

**Rescue and overexpression**

Injection of cDNA encoding npo under the control of a CMV promoter resulted in a high frequency of gastrulation defects, which precluded our using this tactic for rescue of the npo phenotype. The BAC containing the candidate npo gene (BAC 37b12) rescues the npo phenotype when injected into 1- to 4-cell-stage embryos (Fig. 5), and the effect is blocked by co-injection of a npo-specific morpholino antisense oligonucleotide. 70 out of 82 genotypically mutant embryos injected with 37b12 were rendered ifabp positive, giving a rescue efficiency of 85%. Using trypsin as the probe, we obtained a similar result with rescue of 32 out of 47 genotypically mutant embryos (68% efficiency). Rescue of the branchial arch phenotype appears to occur less reliably, with marginally increased but disorganized cartilage detected in the BAC-injected embryos. Control injections included BAC 90p3 (which contains the entire coding and promoter sequence for the adjacent epha2 gene), and BAC 37b12 treated with the endonuclease SsaBI. The latter specifically disrupts the npo gene between exons 1 and 2. These controls both failed to show any rescue activity (ifabp or trypsin expression) in the mutant embryos.

In the course of the rescue experiments, we noted that the expression domain for ifabp and trypsin in many of the BAC 37b12-injected embryos seemed expanded relative to uninjected wild type and the other controls (Fig. 5). Indeed, in many cases the BAC 37b12-injected embryos contain an exuberant overproduction of differentiated intestinal or exocrine pancreatic epithelium. The individual epithelial cells do not appear abnormal, but the overall size of the gut tube, the number of epithelial infoldings and the size of the exocrine pancreas is dramatically increased. Thus it appears that the increased copy number resulting from BAC injection can overwhelm the normal control of npo gene expression, and this leads to increased amounts of mature organ tissue.

**npo encodes a conserved RRM protein**

Conceptual translation of the cDNA indicates that Npo is related to a protein conserved through evolution (Fig. 6). In all metazoans, the gene for this protein encodes six consensus RNA recognition motifs (RRMs). In yeast and plants, the orthologous gene encodes five RRMs (without domain 2, which is the least conserved among metazoans). As shown in Fig. 6, domain order and spacing are generally conserved. The highest amino acid homology between species occurs within the RRM domains, ranging from 30% to 75% identity. The biochemical function of the related yeast...
protein Mrd1p has recently been reported to mediate processing of pre-ribosomal RNA (Jin et al., 2002). Although the specific targets of Npo are not known, RRM domains in other proteins confer binding to homopolymeric RNA in vitro (Varani and Nagai, 1998). We found that Npo protein, when translated in vitro, does bind homopolymeric RNA with a marked preference for guanine (G) and uracil (U), as opposed to adenosine and cytosine. The truncated-mutant Npo protein also shows a similar nucleotide binding preference, but its binding affinity for polyribonucleotides is reduced (Fig. 6C).

**npo is expressed transiently in the digestive tract epithelium**

npo is expressed ubiquitously in the early embryo. At about 24 hpf, expression becomes restricted to the brain and anterior digestive tract (Fig. 7E). Expression then increases in an anterior to posterior wave, first in the branchial arches and liver, then spreading posteriorly, until by 72 hpf it is expressed in a uniform manner throughout the digestive organs (Fig. 7). Between 72 and 84 hpf, npo expression declines rapidly, from anterior to posterior, leaving a residual stippled pattern of expression in the intestine. Expression of npo in the pancreas is excluded from the islet (Fig. 7C), consistent with a lack of effect on this structure in the mutant.

Histological sectioning reveals npo expression in the gut epithelium (Fig. 8A-C). The in situ labeling pattern is heterogeneous, suggesting cell-to-cell variation in steady state levels of npo mRNA. Also, the labeling pattern appears punctate, which is suggestive of subcellular localization of the message. The focality of npo localization is illustrated by double in situ hybridization to foxa3 and npo (Fig. 8B). The former is expressed in all the gut epithelial cells and the labeling pattern is more diffuse. By contrast, the npo-specific signal is seen in a subset of the foxa3-positive cells and is highly localized.

To detect Npo protein, we developed polyclonal antibodies directed against synthetic peptides. In embryos, we found staining primarily in the gut epithelium (Fig. 8C). The degree of cell-to-cell variation in antibody staining is not as dramatic as that seen in the in situ hybridizations, but it is still present. Npo appears to be localized to the cytoplasm, mostly towards the apical aspect of the cell. We also noted label within in a heterogeneous, suggesting cell-to-cell variation in steady state levels of npo mRNA. Also, the labeling pattern appears punctate, which is suggestive of subcellular localization of the message. The focality of npo localization is illustrated by double in situ hybridization to foxa3 and npo (Fig. 8B). The former is expressed in all the gut epithelial cells and the labeling pattern is more diffuse. By contrast, the npo-specific signal is seen in a subset of the foxa3-positive cells and is highly localized.

To detect Npo protein, we developed polyclonal antibodies directed against synthetic peptides. In embryos, we found staining primarily in the gut epithelium (Fig. 8C). The degree of cell-to-cell variation in antibody staining is not as dramatic as that seen in the in situ hybridizations, but it is still present. Npo appears to be localized to the cytoplasm, mostly towards the apical aspect of the cell. We also noted label within in a heterogeneous, suggesting cell-to-cell variation in steady state levels of npo mRNA. Also, the labeling pattern appears punctate, which is suggestive of subcellular localization of the message. The focality of npo localization is illustrated by double in situ hybridization to foxa3 and npo (Fig. 8B). The former is expressed in all the gut epithelial cells and the labeling pattern is more diffuse. By contrast, the npo-specific signal is seen in a subset of the foxa3-positive cells and is highly localized.

**npo functions cell autonomously during gastrointestinal development**

The data suggesting that npo is expressed in both the mesenchyme and in the epithelium raises the question of what cell type requires npo function for epithelial cytodifferentiation. To address this we performed mosaic analysis, transplanting wild-type blastomere cells into an npo-
mutant host (Fig. 8D). Out of the 11 single wild-type cells incorporated into the mutant gut epithelium, eight were found to express ifabp, indicating that enterocyte-specific transcription had been activated in these cells. Wild-type mesenchymal cells did not appear to rescue subjacent mutant epithelium (0/28). The converse experiment, transplanting mutant cells into wild-type host could not be scored because of a lack of mosaic generation, suggesting a selection against mutant epithelial cells in the wild-type host. These data, taken together with the expression pattern, are consistent with a cell-autonomous requirement for npo during gut development.

DISCUSSION

We report the identification of the npo gene as an essential mediator of intestinal organogenesis in the zebrafish. Early endoderm development and budding of organ primordia proceed independently of the presence of npo, but there is arrest at the stage of cytodifferentiation and growth. The
freezing of maturation at this particular juncture indicates that the endoderm-intestine transition is subject to unitary genetic control, and npo appears to be one crucial element of this switch. npo encodes a conserved RRM protein, which suggests that organogenesis may be controlled in part by modulating the activity of putative target RNAs.

The requirement for npo reveals a control point during organogenesis

There are many component steps in the formation of the digestive organs, including endoderm formation, primitive gut tube patterning, organ primordium formation, organ cytodifferentiation and organotypic growth (Grapin-Botton and Melton, 2000; Montgomery et al., 1999). The formation of the endoderm depends on the Gata, forkhead and Sox transcription factors (Kikuchi et al., 2001; Reiter et al., 2001), as well as mediators and targets of the TGFβ and WNT signaling pathways (Feldman et al., 2000). Germline mutation of these genes typically leads to early embryonic lethality, precluding the assessment of their function at later stages. As the npo mutation does not significantly perturb early endoderm development, and endodermal markers are expressed normally in the mutant, npo probably functions subsequent to activity of the endodermal and early organ patterning genes.

After the specification and budding of the anlage, the intestine normally grows and differentiates (Roberts, 1999). This phase is marked by a concerted cell differentiation and rearrangement of the epithelia. Organ-specific programs are then activated to form basic functional units, such as villi or pancreatic acini. Very little is known about the molecular control of the individual processes, or whether their concerted activation reflects a unitary step. In fact, evidence suggests that the patterns of growth unique to each region arise from previous specification events and permissive external cues from the local surrounding mesenchymal tissues (Roberts, 1999). In the npo-mutant intestine, the histological appearance of the epithelia remains that of the organ primordium, apical-basal cell polarity is not well established and villi do not form. To our knowledge, there are no genetic mutations in vertebrates displaying this combined phenotype, with both arrested growth and differentiation. For example, the mutation in mice of TCF4 disrupts epithelial stem cell renewal, yet TCF4 is not required for initial villus morphogenesis (Korinek et al., 1998). Disruption of genes required for mesenchymal function, such as forkhead6 (Kaestner et al., 1997) and Pdgfa (Karlsson et al., 2000), lead to derangement of villus architecture, but enterocyte differentiation still occurs. The timing of the npo phenotype thus implicates the essential role of npo in initiating organ-specific morphogenetic and cytodifferentiation programs.

npo expression in the gastrointestinal tract is dynamic, foreshadowing the anterior to posterior wave of rapid organ growth and cytodifferentiation. Overexpression of npo causes formation of hyperplastic intestinal and pancreatic epithelium. This result complements the hypoplastic organs seen when npo activity is reduced, either by 'knockdown' or germline mutation. Taken together, these data suggest that organ growth and maturation is controlled by npo expression in a dose-dependent manner. One possible mechanism by which this could occur is by controlling a specification step common to endoderm-derived epithelia. According to this model, npo would promote the adoption of a progenitor phenotype among a subset of organ anlage cells. These cells would then possess the capacity to respond to organ-specific signals that direct their morphogenetic movements and differentiation programs. Perhaps the cell-to-cell variability of npo expression in the developing gut (Fig. 8A) reflects the possibility that only a subset of cells are capacitated to form the mature organ. Npo overexpression could thus lead to organ hyperplasia by increasing the number of organ progenitors responding to local signals. In the absence of npo function, progenitor cell capacitation would be blocked, leaving the incipient organ arrested as a primordium. That npo is needed to specify a gut progenitor cell type is also suggested by its expression in the crypts of Lieberkuhn of adult mouse intestine (A.N.M. and R. Palmer, unpublished).

Npo is an RRM protein

The npo gene encodes a conserved, 926-amino acid protein with six RRM domains. The mutant allele encodes a truncated protein containing only the N-terminal domain, indicating that the remainder of the molecule is necessary for its function in
organogenesis. Immunoreactive Npo is localized to the cell cytoplasm. Although we do not yet know a specific RNA target, it binds RNA with base sequence preference, as do other RRM proteins (Varani and Nagai, 1998).

The role of the Npo protein is not known in metazoans. In yeast, the npo ortholog Mrd1p was recently shown to be involved in pre-ribosomal RNA processing (Jin et al., 2002). Mrd1p is detected in complexes containing other proteins known to participate in RNA processing (Gavin et al., 2002). RNA binding proteins have been implicated in numerous developmental processes governed at the RNA level (Curtis et al., 1995). For example, RNA binding may offer a means to rapidly coordinate expression of a diverse subset of target genes that may be functionally related (Keene, 2001; Keene and Tenenbaum, 2002). Accordingly, npo might regulate and coordinate the activity of target RNAs important for digestive organ development and homeostasis. For example, some gene products required for epithelial morphogenesis or organ homeostasis are known to occur in multiple splice isoforms. Examples include fibronectin (Huerta et al., 2001; Inoue et al., 2001), epimorphin (Hirai, 2001; Lehnert et al., 2001) and TCF4 (Cho and Dressler, 1998; Young et al., 2002). Given that the Npo-related protein in yeast functions in splicing, it is plausible that, in metazoans, Npo could function by modulating isoform expression of developmentally important targets.

We wish to thank Jau-Nian Chen and the ‘Screen Team’ for mutagenized zebrafish. We thank Amy Ronco and Mary Mckee for invaluable technical assistance. We are grateful to Daniel Haber and Dan Podolsky for insightful comments and advice. We thank S. Tsukita for anti-ATPase antibody, and P. Ingham and R. Dorsky for probes. Supported by NIH grants S-R01DK55383-03, 5R01HL63206-02 and 2R01HL49579-08, and a sponsored research agreement with Genentech (M.C.F.); and a Howard Hughes Postdoctoral Fellowship for Physicians and NIH grant K08DK02968 (A.N.M.). The microscopy core facility used in this work was partially supported by a center grant for the study of inflammatory bowel disease (DK43351) and a Boston Area Diabetes Endocrinology Research Center grant (DK57521).

REFERENCES


