EGL-38 Pax regulates the ovo-related gene lin-48 during Caenorhabditis elegans organ development

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SUMMARY

The Pax gene egl-38 plays an important role in the development of several organs in C. elegans. To understand how a Pax transcription factor influences distinct developmental choices in different cells and tissue types, we have characterized a second gene, lin-48. lin-48 functions with egl-38 in the development of one structure, the hindgut, but not in other tissues such as the egg-laying system. We show that lin-48 encodes a C2H2 zinc-finger protein that is similar to the product of the Drosophila gene ovo and is expressed in the hindgut cells that develop abnormally in lin-48 mutants. We present evidence that lin-48 is a target for EGL-38 in hindgut cells. We show that lin-48 requires egl-38 for its expression in the hindgut.

Using deletion analysis, we have identified two elements in the lin-48 promoter that are necessary for lin-48 expression. We demonstrate that EGL-38 binds with high affinity to one of these elements. In addition, we have observed genetic interactions between mutations in the lin-48 promoter and specific alleles of egl-38. These experiments demonstrate a functional link between Pax and Ovo transcription factors, and provide a model for how Pax transcription factors can regulate different target genes in different cells.

Key words: Organogenesis, Pax2, Paired domain, C. elegans

INTRODUCTION

Pax transcription factors play an important role in organogenesis during animal development. In mammals, genes of the Pax2, Pax5 and Pax8 (Pax2/5/8) subclass play a role in the development of cell types and organs including B lymphocytes, the kidney, the thyroid, the eye and the brain (Urbánek et al., 1994; Torres et al., 1995; Schwartz et al., 1997; Mansouri et al., 1998). Pax factors influence development by binding DNA in a sequence-specific manner and affecting the expression of target genes. The DNA-binding domain of Pax transcription factors (the paired domain) is composed of two helix-turn-helix domains that can interact with DNA across 20 base pairs (Czerny et al., 1993; Xu et al., 1999). Pax proteins can bind DNA as a monomer, but they can also act in combination with other transcription factors (Fitzsimmons et al., 1996). Owing to the relatively large size of the DNA-binding domain and the possibility for altered binding properties when complexed with other proteins, the consensus DNA sequence for Pax-responsive elements is notably degenerate (Czerny et al., 1993). This suggests that a wide range of sites within a genome are capable of binding Pax proteins, but that cellular context may influence Pax DNA binding and activity in vivo. Differences in cellular context may include other proteins that interact with Pax proteins to restrict or enhance their DNA binding, or which modulate their functional properties when bound to DNA (Eberhard et al., 2000). To better understand how a single factor recognizes different targets in different cells, it is essential first to identify tissue-specific targets and then to characterize the regulation of these target genes.

The C. elegans gene egl-38 encodes a Pax transcription factor that is most similar to the mammalian Pax2/5/8 subclass of factors (Chamberlin et al., 1997; Czerny et al., 1997). egl-38 is an essential gene, and mutants that bear a strong reduction-of-function allele die as embryos or soon after hatching (Chamberlin et al., 1997). Analysis of three non-null alleles has permitted characterization of additional egl-38 functions in patterning of cell types during development of the hindgut (rectal epithelium), the egg-laying system and the spicules of the male tail. Genetically, these three alleles preferentially disrupt different functions of egl-38. Each allele corresponds to a different missense mutation that affects the DNA binding domain of EGL-38. The localization of these tissue-preferential mutations to the DNA binding domain suggests a model in which alterations of the DNA-binding properties of EGL-38 have different consequences in different tissues, i.e. these mutations preferentially affect the ability of EGL-38 to bind to and regulate certain targets and not others.

To better understand how a Pax transcription factor might affect the expression of different genes in different tissues, we have characterized a second gene that functions with egl-38 in
the development of the hindgut: *lin-48*. Genetic analysis has shown that *egl-38* and *lin-48* affect the development of the same subset of hindgut cells, and act to make those cells different from other hindgut cells (Fig. 1). However, *egl-38* and *lin-48* are functionally distinct (Table 1). This analysis suggests *lin-48* function is associated with *egl-38* in the development of the hindgut, but not in other cell types. To investigate the functional relationship between *egl-38* and *lin-48*, we initiated a molecular analysis of *lin-48*. We report that *lin-48* encodes a C2H2 zinc-finger protein similar to the product of the *Drosophila ovo* gene. Our results indicate *LIN-48* is localized to nuclei, and required for the specification of specific cell types as are *Drosophila* and mammalian OVO. We show that there are at least two important regulatory elements in the *lin-48* promoter, and that *EGL-38* can bind specifically to one of these elements in vitro. In addition, the different mutant alleles of *egl-38* exhibit allele-preferential sensitivity to mutations in the *lin-48* promoter. Taken together, these results identify *lin-48* as a tissue-restricted target for EGL-38, and provide the first evidence for a direct relationship between Pax factors and ovo genes.

**MATERIALS AND METHODS**

**Nematode strains**

Nematode strains were cultured according to standard techniques (Sulston and Hodgkin, 1988). Mutations used are described by Hodgkin (Hodgkin, 1997), and are noted as such.

Linkage group (LG) III: *egl-5*(*sy279*); *lin-48*(*sa469*), *lin-48*(*sy234*), *lin-48*(*sy348*) (Chamberlin et al., 1999; Jiang and Sternberg, 1999); *unc-119*(*e2498*).  
LG IV: *egl-38*(*n578*), *egl-38*(*sy287*), *egl-38*(*sy294*), *egl-38*(*s1775*) (Chamberlin et al., 1999).  
LG V: *him-5*(*e1490*).

**Molecular cloning of *lin-48***

*lin-48* was mapped to LG III between *unc-93* and *dpy-17* (Chamberlin et al., 1999). Cosmids and DNA sequence from this genomic region were provided by Alan Coulson and the *C. elegans* sequencing consortium. DNA was microinjected into the mitotic germline of hermaphrodites according to the method of Mello et al. (Mello et al., 1991). 100 ng/µl of plasmid containing the rol-6(*su1006*) allele (pRF4) was co-injected as a marker with 1-10 ng/µl of test DNA into *lin-48*(*sa469*); *him-5*(*e1490*) animals. Heritable lines were tested by assaying Rol males for rescue to wild-type tail morphology. Transgenes containing the cosmid F34D10 rescued *lin-48* in two out of two heritable lines. Subclones of the cosmid were used for restriction mapping using standard methods (Ausubel et al., 2000). pTF972 (Fig. 2A) is a 10.5 kb BamHI subclone from F34D10 into pHBluescript (Stratagene) that rescued *lin-48*(*sa469*) in three out of three heritable lines. We sequenced the DNA of *lin-48* mutants as described previously (Chamberlin et al., 1997). We used BLAST 2.0 (http://www.ncbi.nlm.nih.gov/BLAST/) to identify and evaluate the molecular homologs of *LIN-48* and ClustalW 1.7 (http://dot.imgen.bcm.tmc.edu:9331/) and Boxshade 3.21 (http://www.isrec.isb-sib.ch:8080/software/BOX_form.html) to align and display the zinc-finger domain in Fig. 2B. We used RT-PCR to characterize *lin-48* CDNA. Our cDNA sequence results match those of Schonbaum, Fantes and Mahowald (GenBank Accession Number, AF134806), and indicate that *lin-48* is trans-spliced to SL1.

**Construction and analysis of *lin-48::gfp* transgenes**

We made GFP reporter constructs for *lin-48* expression using GFP (pPD) vectors provided by Andy Fire. Upstream deletions were generated by designing forward PCR primers corresponding to different positions in the *lin-48* promoter region. Point mutations were generated using a two-step, PCR-based method (Ausubel et al., 2000). The cloned PCR fragments were sequenced to verify. Transgenes for all GFP reporter constructs were produced by microinjection of plasmid DNA into animals, as described above. For all experiments that test expression of *lin-48* promoter constructs, 40-50 ng/µl reporter clone was co-injected with 15 ng/µl pP84M016 (*unc-119*+) plasmid; Maduro and Pilgrim, 1995) into *unc-119*(*e2498*); *him-5*(*e1490*) animals.

The activity of each transgene was assessed in animals from heritable transgenic lines. Larvae were anesthetized on pads of 5% agar containing 5 mM sodium azide, and scored for sex, larval stage and GFP expression at 1000x. For almost all experimental conditions, the expression of at least two independently derived transgenes was tested. For critical transgenes, two independently isolated DNA clones were also tested. For the data in Figs 4 and 6, L1 and L2 animals of both sexes were scored. Each hindgut cell was scored for expression, resulting in four hindgut cells scored for each animal. Transgenic animals were verified by confirming expression of GFP in at least one cell in the animal before scoring.

**EGL-38 protein expression and EMSA**

For production of recombinant EGL-38 DNA-binding domain (EGL-38 DBD) in *Escherichia coli*, nucleotide sequences comprising amino acids 22-156 (Chamberlin et al., 1997) were amplified using PCR and cloned into pET11a vector. Expression of EGL-38 DBD was induced in *E. coli* strain BL21lysSDE3 cells. Bacterial lysate proteins were prepared as described previously for Pax5 (Wheat et al., 1999). The integrity of the EGL-38 protein was confirmed with SDS-PAGE.

EMSA was performed essentially as described in Wheat et al. (Wheat et al., 1999). For DNA probes, oligonucleotides (Integrated DNA Technologies, Coralville, IA) 5’TCGAGCTGTCATTTATGGA-GCGTGACGATTACGG and 5’TCGAGCTGGAGGGCACTCAACC-GCGCCTTTC (lre1), 5’TCGAGCAGACACCCA TGGTTGA-TCGACCTGGAGGGCACTCAACC-GCGCCTTTC (lre2) were annealed to make the lre2 or CD19 probes, respectively.

Labeling of double stranded oligonucleotide probes with 32 P, probe purification and preparation of competitor oligonucleotides were done as described previously (Fitzsimmons et al., 1996). Oligonucleotide probes included 5’TCGAGAAAAGCGCAAGTTTGCG-GTGCGAGATTG and 5’TCGACATCCGCGACCCGCAAATCTT-GCCCTTTC (lre1).

**Table 1. egl-38 shares a subset of egl-38 functions**

<table>
<thead>
<tr>
<th>Gene function</th>
<th>egl-38</th>
<th>lin-48</th>
<th>Refs</th>
</tr>
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<tbody>
<tr>
<td>Hindgut development</td>
<td>U. F. K’ specification</td>
<td>U. F. K’ specification</td>
<td>Chamberlin et al., 1997; 1999</td>
</tr>
<tr>
<td>Egg-laying system</td>
<td>Vulval expression of lin-3 (and uv1 specification)</td>
<td>None</td>
<td>Chamberlin et al., 1997; Chang et al., 1999</td>
</tr>
<tr>
<td>Viability</td>
<td>Essential</td>
<td>Not essential</td>
<td>Chamberlin et al., 1997; 1999</td>
</tr>
<tr>
<td>Male spicule development</td>
<td>Yes*</td>
<td>Yes*</td>
<td>Chamberlin et al., 1999; Jiang and Sternberg, 1999; H. M. C., unpublished</td>
</tr>
</tbody>
</table>

*egl-38* has additional functions in male spicule development not shared with *lin-48*.
TAAG and 5’CTACGTCACGCTTCAAAATGCACCG (lre2), and 5’TAGATCCCTTCTGGGAATTTCCTAGATC and 5’TGCAGA-

GATCCTAAGAACCTCCAGAGGATC (STAT3). CD19 competitor was identical to CD19 probe oligonucleotides.

RESULTS

Summary of egl-38 and lin-48 function in C. elegans hindgut development

We identified alleles of both lin-48 and egl-38 in a genetic screen for genes important in the development of the C. elegans hindgut (Chamberlin et al., 1999). The C. elegans hindgut can serve as a simple model for animal organ development. It is composed of only 11 cells, representing eight distinct cell types (Fig. 1A; Sulston et al., 1983). Development of the C. elegans digestive system and differentiation of hindgut cell types occurs during embryogenesis. However, the hindgut cells also contribute to larval development as one (in hermaphrodite animals) or five (in male animals) of the cells undergo further stereotypic postembryonic cell divisions (Sulston and Horvitz, 1977; Sulston et al., 1980). We have used a combination of postembryonic cell lineage analysis and analysis of the production of differentiated cell types to interpret the patterning defects in the hindgut of egl-38 and lin-48 mutant animals (Chamberlin et al., 1997; Chamberlin et al., 1999). This analysis shows that egl-38 and lin-48 are each required for the normal specification of cell type for three cells in the middle of the hindgut (U, F and K), and to make these cells different from other cells in the hindgut (Fig. 1B, C).

lin-48 encodes a zinc finger protein similar to Drosophila OVO

We used DNA transformation rescue and the sequence of DNA from mutant animals to identify the gene F34D10.5 as lin-48 (see Materials and Methods). lin-48 encodes a protein that contains four C2H2 zinc-finger repeats (Fig. 2B). Within the 130 amino acids of the zinc-finger domain, LIN-48 is 73% identical to Drosophila OVO and 66% identical to mouse mOVO1 (Mevel-Ninio et al., 1991; Dai et al., 1998). OVO proteins in Drosophila and mouse act as transcription factors and play an important role in the development of several distinct cell types (Oliver et al., 1987; Payre et al., 1999; Dai et al., 1998). Drosophila OVO binds DNA in a sequence-specific manner, and can act as a transcriptional activator and as a repressor, depending on the isoform (Lu et al., 1998; Lee and Garfinkel, 2000; Andrews et al., 2000). We characterized the lesions associated with three lin-48 mutations. Although all are

Fig. 2. (A) Genomic clones of lin-48. Rectangles indicate exons of lin-48, with black bars corresponding to the sequences that code for the zinc-finger domain in B. Ovals indicate the position of regulatory elements lre1 and lre2 from Fig. 5. (B) lin-48 encodes an OVO zinc-finger protein. Alignment of the C2H2 zinc-finger domain from C. elegans LIN-48, Drosophila OVO and mouse OVO1 (mOVO1). Identical amino acids are highlighted in black, conserved amino acids in gray. The cysteines and histidines predicted to coordinate zinc ions are indicated with an asterisk. The amino acids affected by lin-48 mutations are indicated. sy234 is a GAC-to-TAC transition. sy469 is a CAT-to-CGT transition. sy548 is a CCC-to-TCC transition.
missense mutations, each mutation is recessive and the mutant
phenotypes are not enhanced when the alleles are tested in trans
to a deficiency (Chamberlin et al., 1999). Thus, we believe these
mutations are reduction- or loss-of-function alleles.

lin-48 is expressed in hindgut cells

To investigate the expression pattern of lin-48, we created a
reporter in which the last two codons of lin-48 were replaced
with sequences encoding the green fluorescent protein (GFP; pTJ1038; Fig. 2A). When expressed in mutant animals, these
transgenes are capable of rescuing lin-48. In the hindgut, these
transgenes are expressed in U, F, K and K’ cells (Fig. 3A-B).
As the development of U, F and K’ is affected in lin-48
mutants, this expression pattern is consistent with lin-48 acting
directly within the cells that express the gene. The significance
of lin-48::gfp expression in K is not clear, although this
expression is affected in the same manner as the other hindgut
expression in our experimental analysis (see below). In addition
to hindgut cells, lin-48::gfp is expressed in the excretory duct cell, neuronal support cells of the phasmid and
labial sensory structures and a small number of additional
unidentified cells in the head. Male animals exhibit additional
expression in the developing tail structures (data not shown).
lin-48::gfp expression is initiated in late embryogenesis and
persists into adulthood. The chimeric LIN-48::GFP protein is
localized to the nuclei of expressing cells, consistent with the
idea that OVO-related proteins like LIN-48 function as
transcription factors. A second reporter construct that includes
only the lin-48 upstream regions (pTJ1157; Fig. 2A) expresses
in the same pattern as the full-length transgene, but is
expressed at much higher levels (Fig. 3C, D).

The lin-48 promoter contains DNA elements
necessary for its expression

To investigate the regulation of lin-48, we performed a deletion
analysis of the lin-48 promoter. We generated a series of clones
that progressively deleted more upstream regions of the lin-48
promoter between positions 0 and 5205 (Fig. 4B-F; we defined
the BamHI site upstream of lin-48 as 0 following the standard
of Okkema et al. (Okkema et al., 1993)). When tested for
expression in transgenic animals, these transcriptional
reporters identified a domain between 4697 and 4892 required
for normal expression of lin-48 in all four hindgut cells and the
excretory duct cell. Reporters that included sequences 4697
and upstream were expressed in hindgut cells, the excretory
duct and other cells (head and phasmid), whereas clones
including 4892 or less were expressed only in head and
phasmid. These experiments also identified a region upstream
of 2846 necessary for expression in many of the head cells, as
the full-length reporter is expressed in up to ten head cells,
whereas the truncated reporters generally express in only two
cells. As no mutant reporter transgenes in either wild-type or
mutant animals failed to express lin-48::gfp in hindgut cells. Scale bars: in A, 20 µm for A,B; in C, 20 µm for C-H.
and identified a domain with similarity to mammalian DNA elements that bind Pax proteins. As our genetic results indicated lin-48 requires the Pax gene egl-38 for its expression in hindgut cells (see below), we mutated this site in a reporter that included sequences to 4697, and found that the mutant transgenes fail to express in hindgut and excretory duct cells (Fig. 4G). We define this site as lre2 (lin-48 regulatory element 2; Fig. 5B), as we ultimately identified two elements in the lin-48 promoter. Although truncated reporters are sensitive to mutations in lre2, we found that expression is restored when the site is mutated in a full-length reporter (Fig. 4M). This result suggests an additional element(s) is present upstream of this site in a reporter including sequences to 4697, and found that the mutant transgenes fail to express in hindgut cells (Fig. 4L). As recombinant EGL-38 does not bind this site with high affinity (see below), it is possible that the similarity of this element to Pax-binding sites is coincidental. Nevertheless, the mutation analysis identifies it as an important regulatory element. To confirm the importance of the two sites, we created full-length reporter transgenes bearing mutations in both lre2 and lre1, and found that these two mutations effectively eliminated expression of lin-48::gfp in hindgut cells (Figs 3E,F, 4O).

**lin-48 requires egl-38 for its expression in hindgut cells**

To investigate the relationship between lin-48 and egl-38, we characterized lin-48 expression in egl-38 mutant backgrounds. Expression of lin-48::gfp in the hindgut cells of egl-38(s1775) and egl-38(sy294) mutants is eliminated, although expression in other cell types is maintained (Figs 3G,H, 6B,C). This result indicates that lin-48 requires egl-38 for its expression in the hindgut. However, hindgut expression of lin-48::gfp is still observed in egl-38(sy287) and egl-38(n578) mutants (Fig. 6D,E). Taken together, these results provide a link between the activity associated with different egl-38 alleles in different developmental processes and their ability to activate lin-48 expression, as genetic tests indicate s1775 and sy294 strongly disrupt egl-38 activity in hindgut development, whereas sy287 and n578 disrupt this function to a lesser extent (Table 2; Chamberlin et al., 1997).

To further investigate the relationship between egl-38 genotype and lin-48 expression, we tested the expression of transgenes bearing mutations in lre1 or lre2 in egl-38(sy287) and egl-38(n578) mutants (Fig. 6F-K). egl-38(sy287) mutants exhibit moderate defects in hindgut development, these animals exhibit reduced expression of lin-48::gfp in hindgut cells, and this expression is sensitive to a single mutation in lre1 or lre2. In contrast, egl-38(n578) mutants exhibit only minor defects in hindgut development, and they still express mutant transgenes, although at reduced levels. This sensitivity of mutant lin-48 transgenes to different egl-38 genotypes provides further support for an in vivo relationship between EGL-38 and the promoter of lin-48.

To investigate the specificity of the relationship between egl-38 and lin-48, we characterized lin-48::gfp expression in egl-5 mutants (Fig. 6L). egl-5 is the C. elegans posterior HOM-C gene required for regional specification of cells in the hindgut (Chisholm, 1991). We find that lin-48::gfp expression is normal in egl-5 mutants. This indicates that not all genes required for normal development of hindgut cells affect lin-48 expression. Finally, we tested lin-48::gfp expression in lin-48 mutants, and found it to be unaltered (Fig. 6M). This result indicates there is no positive autoregulation of lin-48, and

<table>
<thead>
<tr>
<th>lin-48 sequences in transgene</th>
<th>Expression in hindgut (percent of cells)</th>
<th>Expression in excretory duct (percent of cells)</th>
<th>head cell expression (average no.)</th>
<th>n</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>0</td>
<td>0</td>
<td>100</td>
<td>5.8</td>
</tr>
<tr>
<td>B</td>
<td>284</td>
<td>100</td>
<td>0</td>
<td>1.5</td>
</tr>
<tr>
<td>C</td>
<td>487</td>
<td>100</td>
<td>0</td>
<td>1.6</td>
</tr>
<tr>
<td>D</td>
<td>4892</td>
<td>100</td>
<td>0</td>
<td>1.8</td>
</tr>
<tr>
<td>E</td>
<td>5205</td>
<td>100</td>
<td>0</td>
<td>1.4</td>
</tr>
<tr>
<td>F</td>
<td>4697</td>
<td>100</td>
<td>0</td>
<td>1.8</td>
</tr>
<tr>
<td>G</td>
<td>3985</td>
<td>100</td>
<td>0</td>
<td>1.8</td>
</tr>
<tr>
<td>H</td>
<td>418</td>
<td>100</td>
<td>0</td>
<td>1.6</td>
</tr>
<tr>
<td>I</td>
<td>4191</td>
<td>100</td>
<td>0</td>
<td>1.8</td>
</tr>
<tr>
<td>J</td>
<td>4240</td>
<td>100</td>
<td>0</td>
<td>1.6</td>
</tr>
<tr>
<td>K</td>
<td>3985</td>
<td>100</td>
<td>0</td>
<td>1.6</td>
</tr>
<tr>
<td>L</td>
<td>3985</td>
<td>100</td>
<td>0</td>
<td>5.3</td>
</tr>
<tr>
<td>M</td>
<td>4128</td>
<td>100</td>
<td>0</td>
<td>5.6</td>
</tr>
<tr>
<td>N</td>
<td>3985</td>
<td>100</td>
<td>0</td>
<td>5.3</td>
</tr>
</tbody>
</table>

**Fig. 4.** The lin-48 promoter contains two redundant elements important for lin-48 expression in hindgut cells. lin-48 sequences were tested for their ability to drive expression of GFP, and are diagrammed using the conventions of Fig. 2A. Transgenes containing the mutant sequences illustrated in Fig. 5 are indicated with X. The percentages of cells expressing GFP (black bar), expressing very low but detectable levels of GFP (gray bar) or not expressing GFP (white bar) are indicated for each construct. n, number of animals scored for expression.
provides indirect evidence that LIN-48 does not reciprocally affect the expression of egl-38.

**EGL-38 binds to the lin-48 promoter**

Our genetic studies suggest that EGL-38 may regulate lin-48 transcription directly by binding to regulatory elements that may include lre1 and/or lre2. To assess whether these sites include recognition sequences for EGL-38, we expressed the DNA-binding domain (DBD) of the protein in *E. coli* and tested its DNA-binding abilities in vitro in an electrophoretic mobility shift assay (EMSA; see Materials and Methods). It was shown previously that promoter sequences of the murine CD19 gene include a site that binds proteins of the Pax2/5/8 family, including EGL-38, with high affinity (Czerny et al., 1997). In initial experiments, EGL-38 DBD binding was evidenced by detection of a single band with CD19 control or lre2 probe DNAs at very great (up to 100,000-fold) dilutions of bacterial lysate, but was detected only weakly using the lre1 probe (undetectable at greater than 1:15 dilution; data not shown). Binding was not detected using control lysate from *E. coli*.

### Table 2. Summary of the functions associated with different egl-38 alleles

<table>
<thead>
<tr>
<th>Function</th>
<th>Allele*</th>
</tr>
</thead>
<tbody>
<tr>
<td>Hindgut development</td>
<td>++ + n578 sy287 sy294 s7775</td>
</tr>
<tr>
<td>Eg-g-lying</td>
<td>++ - ++ ++ -</td>
</tr>
<tr>
<td>Viability</td>
<td>+++ ++ + +</td>
</tr>
<tr>
<td>Male spicule development</td>
<td>++ ++ - -</td>
</tr>
<tr>
<td>Activation of lin-48::gfp</td>
<td>+++ +++ + -</td>
</tr>
<tr>
<td>Activation of lre1 mutant lin-48::gfp</td>
<td>++ + - n.d. n.d.</td>
</tr>
<tr>
<td>Activation of lre2 mutant lin-48::gfp</td>
<td>++ + - n.d. n.d.</td>
</tr>
</tbody>
</table>

*s775 is a lethal allele that behaves as a genetic null. n578, sy287, and sy294 are all non-null, reduction of function alleles that preferentially disrupt different functions of egl-38.

†Data for developmental functions of egl-38 alleles are summarized (Chamberlin et al., 1997; Chamberlin et al., 1999; H. M. C., unpublished). In these experiments each allele was tested for each function in trans to the other alleles and in trans to a deficiency that deletes the gene. n.d., not determined.

Fig. 6. Mutations in egl-38 affect the expression of lin-48 in hindgut cells. Data presented as in Fig. 4.
Fig. 7. The DNA-binding domain of EGL-38 specifically binds the lin-48 lre2 site with high affinity. E. coli containing EGL-38 DBD was incubated with the lre2 probe at a final dilution of 1:51,200 (top), or with the CD19 control probe at 1:6400 (bottom). Competitor sequences are described in Materials and Methods. The CD19 probe corresponds to the CD19-1 element of Fig. 5.

coli containing empty expression vector. To demonstrate the specificity of these interactions, we incubated binding reactions in the absence or presence of excess double-stranded competitor oligonucleotides (Fig. 7). EGL-38 DBD binds the lre2 probe with high affinity, as evidenced by the efficient competition of binding to the lre2 by low levels of unlabeled competitor oligonucleotides (Fig. 7, lanes 3-6, top). Similarly, binding of EGL-38 DBD to the CD19 probe (lower panel) was efficiently competed by low levels of lre2 competitor (Fig. 7, lanes 3-6, bottom). As expected, binding to each probe was competed, although less efficiently, by excess CD19 competitor (Fig. 7, lanes 7-10). Competition was not detected using lre1 DNA, or by control STAT3-binding sites, even when added at 1000-fold molar excess (Fig. 7, lanes 11-14). Together, these data show that EGL-38 specifically binds the lre2 site in vitro with relatively high affinity.

**DISCUSSION**

**The role of lin-48 ovo in C. elegans development**

In this paper, we report the characterization of the C. elegans ovo-related gene lin-48 and provide evidence that it is a direct target for the EGL-38 Pax transcription factor in hindgut cells. lin-48 and egl-38 are functionally similar in that they affect the development of the same subset of hindgut cells (Fig. 1). However, their specific hindgut functions differ. For example, the presumptive U cell behaves like its posterior neighbor Y in egl-38 mutants, whereas it behaves like its right side lineal homolog B in lin-48 mutants. Anterior/posterior, dorsal/ventral, and left/right patterning information plays a role in hindgut development (Chamberlin et al., 1999; Wollard and Hodgkin, 2000). Our experiments provide a link between genes important in anterior/posterior (egl-38) and left/right (lin-48) patterning. Furthermore, these experiments suggest that egl-38 and lin-48 are not part of a strictly linear pathway, as the function(s) of egl-38 and lin-48 in the hindgut are not identical. We speculate that lin-48 is only one of the hindgut targets of EGL-38, and it mediates a subset of functions.

lin-48 is expressed in a small number of cells in addition to the hindgut cells. Further work will be necessary to clarify the function of lin-48 in these cells. In particular, it will be interesting to investigate the potential role of lin-48 in the development of the excretory system. The excretory system is proposed to mediate osmotic regulation, and the excretory duct cell is essential for viability (Nelson and Riddle, 1984). As lin-48 mutants are viable, lin-48 can not be essential for excretory duct cell development or differentiation. However, lin-48 mutant stocks exhibit a low but reproducible level of lethality, and the inviable animals die around hatching with the characteristics of animals that lack a functional excretory system (Chamberlin et al., 1999). Thus lin-48 may play a role in excretory duct development, but its function may be compensated by another gene in most animals. Work with ovo genes in Drosophila and mouse has focused on their roles in fertility and epidermal development (Oliver et al., 1987; Payre et al., 1999; Dai et al., 1998). Although lin-48 plays no apparent role in fertility or development of epidermis, ovo genes in mouse, Drosophila and C. elegans exhibit parallels in that they all play a role in the differentiation and maintenance of specific cell types. In addition, C. elegans and mouse ovo genes are similar in that they play a role in urogenital development. Mouse Ovo1 is important in development of the genitral tract and kidney, and lin-48 plays a role in development of the hindgut (which develops into the adult male cloaca) and potentially the excretory system.

**The functional relationship between Pax factors and ovo genes**

Our experiments indicate lin-48 is a direct target for EGL-38 in C. elegans. A direct link between Pax factors and ovo genes has not been previously reported. However, genetic parallels in mammals indicate the potential for a conserved functional relationship between these classes of genes. In vertebrates, the Pax2 gene is essential for development of kidney, brain and ear (Torres et al., 1995; Torres et al., 1996; Schwartz et al., 1997), and the Pax8 gene plays a role in thyroid and kidney development (Mansouri et al., 1998; Carroll and Vize, 1999). Mouse Ovo1 is expressed abundantly in the kidney, and is required for its normal differentiation (Dai et al., 1998). Thus, as in C. elegans, Ovo1 acts in a subset of the cells that require Pax2/5/8 factors. Future experiments will be required to test whether Ovo1 is a target for Pax2 or Pax8 during kidney development. As all of the functions of the Drosophila
Pax2/5/8 gene sparkling (shaven) have not been characterized (Fu et al., 1998), it is not known whether there are developmental functions shared by ovo and sparkling.

**Tissue-restricted activity of EGL-38**

An interesting feature of the genetics of egl-38 is that mutations that preferentially affect a subset of egl-38 functions correspond to mutations in the DNA-binding domain. This contrasts with the tissue-preferential alleles of the Drosophila Pax gene sparkling, which affect non-coding regulatory parts of the gene (Fu et al., 1998). We have shown the tissue-preferential activity of each allele also correlates with ability to promote lin-48 gene expression in hindgut cells. For example, the sy294 allele preferentially disrupts development of hindgut cells and mutants fail to express lin-48. In contrast, the n578 allele preferentially disrupts development of the egg-laying system, and disrupts hindgut development to a minimal extent. Correspondingly, egl-38(n578) mutants can express lin-48 even when the lin-48 promoter is compromised by mutations. These results suggest the tissue-preferential alleles affect the ability of EGL-38 to regulate certain target genes and not others. The mutations may affect the ability of EGL-38 protein to bind particular DNA targets (Czerny et al., 1993; Czerny and Busslinger, 1995), or to interact with protein partners (Fitzsimmons et al., 1996).

Our characterization of lin-48 indicates that EGL-38 has tissue-restricted targets that are expressed in only a subset of EGL-38-expressing cells. We have identified two promoter elements important for lin-48 expression, and one of these (Ire2) binds EGL-38 with high affinity. Genetic results indicate that both of these elements mediate the EGL-38 response. Specifically, both elements must be mutant to mimic the lin-48 expression pattern observed in egl-38 mutants, and single Ire1 or Ire2 mutant transgenes are equally sensitive to the egl-38(sy287) and egl-38(n578) mutant backgrounds. As EGL-38 does not specifically bind Ire1 in vitro, it is possible that it acts indirectly through Ire1, or that in vivo EGL-38 can bind Ire1, but it requires another protein or proteins to bind with high affinity. Alternatively, as lin-48::gfp is in multiple copies and overexpressed from the transgenes, it is possible that Ire2 alone mediates the in vivo response, but Ire1 is capable of functioning when multiple copies of the gene are present. Further experiments will be required to distinguish among these possibilities.

One way EGL-38 may have different targets in different tissues is to act in a combinatorial manner with one or more additional transcription factors. In this model, both EGL-38 and the second factor would be necessary for the hindgut expression of lin-48. Our analysis of the lin-48 promoter, however, identified only elements that mediate the response to EGL-38. Consequently, if both EGL-38 and an additional factor are required, then the second factor must meet one of the following criteria. It could act through a DNA element between Ire2 and the downstream HindIII site, as we have systematically analyzed only the region containing Ire2 and upstream. It could act through a DNA element immediately adjacent to Ire1 or Ire2, which would have been deleted at the same time as deleting these EGL-38-sensitive sites. This raises the possibility that EGL-38 and the second factor would physically interact. Alternatively, the second factor may not act through a discrete site, but act in a manner different from EGL-38. For example, it might influence accessibility of the lin-48 regulatory regions. Future work to identify additional genes important for lin-48 expression should clarify how the EGL-38 Pax protein mediates tissue-restricted gene expression.

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**REFERENCES**


EGL-38 regulates lin-48


