

Expression of *engrailed* Proteins in Arthropods, Annelids, and Chordates

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Summary

engrailed is a homeobox gene that has an important role in *Drosophila* segmentation. Genes homologous to *engrailed* have been identified in several other organisms. Here we describe a monoclonal antibody that recognizes a conserved epitope in the homeodomain of *engrailed* proteins of a number of different arthropods, annelids, and chordates; we use this antibody to isolate the grasshopper *engrailed* gene. In *Drosophila* embryos, the antibody reveals *engrailed* protein in the posterior portion of each segment during segmentation, and in a segmentally reiterated subset of neuronal cells during neurogenesis. Other arthropods, including grasshopper and two crustaceans, have similar patterns of *engrailed* expression. However, these patterns of expression are not shared by the annelids or chordates we examined. Our results provide the most comprehensive view that has been obtained of how expression patterns of a regulatory gene vary during evolution. On the basis of these patterns, we suggest that *engrailed* is a gene whose ancestral function was in neurogenesis and whose function was co-opted during the evolution of segmentation in the arthropods, but not in the annelids and chordates.

Introduction

Early pattern formation in *Drosophila* organizes the blastoderm into a series of repeated units and uniquely specifies each of these units. It is controlled by a hierarchy of maternal-effect, segmentation, and homeotic genes (reviewed by Ingham, 1988). One of these genes is *engrailed*.

In *Drosophila*, *engrailed* is essential during several developmental phases, and it has characteristics common to both segmentation and homeotic genes. For instance, *engrailed* mutant embryos do not segment normally (Kornberg, 1981; Nüsslein-Volhard and Wieschaus, 1980). Other aspects of the *engrailed* mutant phenotype are suggestive of homeotic function (Garcia-Bellido, 1975; Lawrence and Morata, 1976), of a role in organizing the preblastoderm (Karr et al., 1985), and, in imaginal posterior compart-

ments, of a role in maintaining compartment and segment borders (Morata and Lawrence, 1975; Kornberg, 1981; Lawrence and Struhl, 1982). One further aspect of *engrailed* function is its expression during neurogenesis in a segmentally reiterated subset of neuroblasts and neurons (DiNardo et al., 1985; Brower, 1986). Thus, *engrailed*, like other segmentation genes (Doe et al., 1988a, 1988b), appears to play multiple roles during development: during organization and growth of epidermal derivatives and during neurogenesis.

During segmentation, the *Drosophila engrailed* protein is produced in the cells of the posterior region of each body segment (DiNardo et al., 1985; Karr et al., 1989). Consistent with its putative regulatory role, the *engrailed* protein contains a homeodomain (Fjöse et al., 1985; Poole et al., 1985), localizes to nuclei (DiNardo et al., 1985; Karr et al., 1989), and has the capacity to bind to DNA in vitro (Desplan et al., 1988). The *Drosophila engrailed* homeobox sequence is distinctive, but it is not unique. The *invected* gene, juxtaposed to *engrailed* on the *Drosophila* chromosome and expressed in an almost identical pattern during segmentation, has a homeobox sequence that is strikingly similar (52/61 amino acids) to that of *engrailed* (Coleman et al., 1987). In addition, *invected* has regions closely related to *engrailed* upstream (23/26 identical amino acids) and downstream (26/30 amino acids) of its homeobox, and in a region near the amino terminus (8/12 amino acids). Thus *Drosophila* has a second *engrailed* gene, *invected*, the function of which is not known.

A number of *engrailed* genes have been identified in other organisms. For example, honeybee (U. Walldorf and W. Gehring, personal communication), mouse (*En-1* and *En-2*, Joyner et al., 1985; Joyner and Martin, 1987), chicken (Darnell et al., 1986), zebrafish (Fjöse et al., 1988), and human (Poole et al., 1989; Logan et al., 1989) contain two *engrailed* genes, and single *engrailed* genes have been found in sea urchin (Dolecki and Humphreys, 1988), leech (Weisblat et al., 1988), grasshopper (this report), and nematode (A. Kamb and T. B. Kornberg, unpublished data). The homeodomain sequences of these genes are similar to *Drosophila engrailed* and, where sequence analysis extends sufficiently, to regions immediately upstream and downstream of the homeodomain as well. For the mouse *En-1* gene, most of the coding sequence has been obtained, and in addition to the conserved extended homeodomain region (69/99 of the residues are conserved), it contains the region near the amino terminus conserved in *Drosophila engrailed* and *invected* (Frohman and Martin, personal communication). These two conserved regions, the small amino-terminal one and the extended homeodomain, are the only sequences conserved among these three genes. Conservation of the homeobox regions of the other vertebrate and invertebrate *engrailed* genes is comparable. Since the sequence of the *engrailed*-type homeodomains is distinctive and unlike any of the other homeodomain sequences known (Scott et al., 1989), and since it is in every known case surrounded by a con-

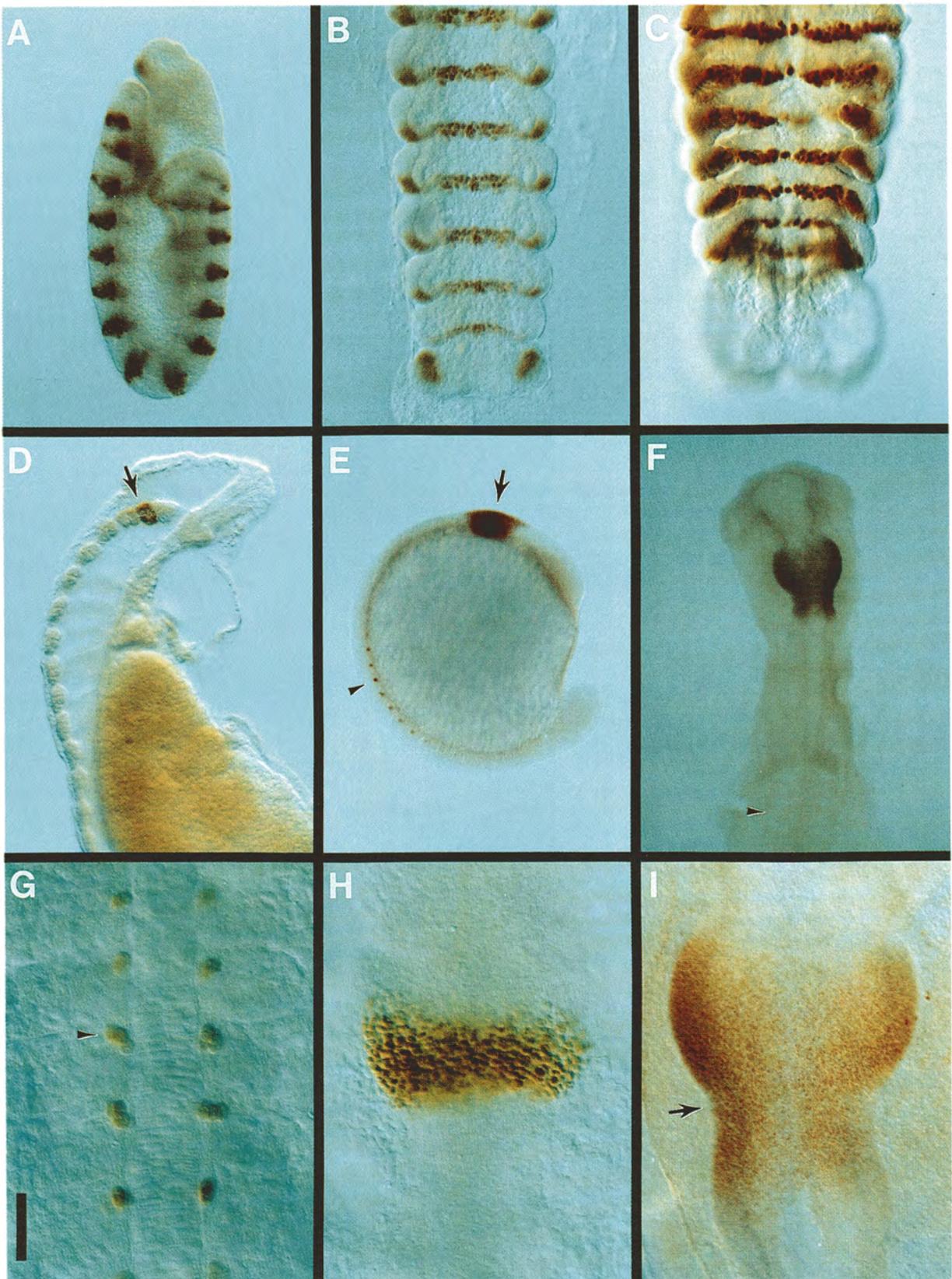


Figure 1. Expression of *engrailed* Proteins in Arthropods, Annelids, and Chordates

Staining of *Drosophila* (A), grasshopper (B), crayfish (C), leech (D), zebrafish (E, G, H), and chick (F, I) embryos with the 4D9 MAb and HRP immunocytochemistry. In all three arthropods (A, B, C), *engrailed* is expressed in the posterior region of each segment; in the other organisms examined (D-I), *engrailed* does not appear to play a role during metameric development (for example, arrowhead in F marks the developing somites in the chick

served region, we consider this extended *engrailed* homeodomain region a signature of *engrailed* genes.

Proteins that share extensive sequence similarity have structural and functional identity in their conserved regions. Since the conserved portion of the *engrailed* proteins is in the putative DNA-binding domain, we assume that the biochemical function of these proteins as transcription regulators has been conserved. Given the strong correlation between patterns of *engrailed* expression and function in the *Drosophila* epidermis and the varied developmental programs of the different animals in which *engrailed* genes have been identified, it is of interest to determine if *engrailed* has a conserved pattern of expression indicating a common, and possibly ancestral, developmental function.

In the studies described here, a monoclonal antibody reagent (MAB 4D9) was found to recognize specifically *engrailed* proteins in a variety of species. Use of the 4D9 MAb has allowed us to show that *engrailed* proteins can be found in many organisms throughout the animal kingdom, including annelids, chordates, and arthropods (and other phyla not described here). In all arthropods examined, *engrailed* is expressed during segmentation in the posterior portion of each segment, and subsequently in a subset of neuronal cells during neurogenesis. Among the members of the three phyla described here, expression of *engrailed* during neurogenesis is the only conserved feature. We conclude that an ancestral function of *engrailed* may have been in neurogenesis, and its other functions in arthropods may represent a more recent addition, not shared by the annelids and chordates.

Results

Monoclonal Antibody 4D9

Lines of myeloma cells producing monoclonal antibodies directed against *E. coli*-derived *engrailed* and *invected* proteins were generated. Among these cell lines, two (4D9 and 4F11) recognized epitopes conserved between the *invected* and *engrailed* proteins. 4D9 and 4F11 antibodies bound to nuclei of *Drosophila* cell lines that express *engrailed* or *invected*. These cell lines were derived from a Schneider 2 (S2) cell line that was transfected with plasmids carrying either *engrailed* or *invected* cDNAs under HSP-70 promoter control (Gay et al., 1988). Both monoclonals are effective histological reagents that localize *engrailed*-*invected* proteins in *Drosophila* embryos (Figure 1A), and the patterns they generate are consistent with previous studies (DiNardo et al., 1985; Karr et al., 1989). Cross-reaction of 4D9 or 4F11 with other antigens in em-

bryos is not detectable. The two MAbs also recognize both *engrailed* and *invected* proteins in Western blot assays (data not shown). Due to its ability to recognize *engrailed* in a wide variety of organisms (Figure 1), MAb 4D9 was characterized further.

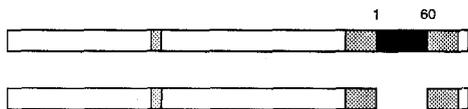
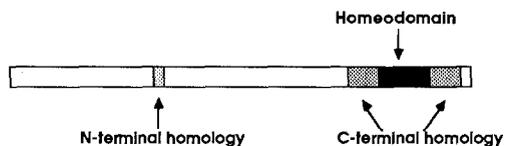
To identify the epitope recognized by the 4D9 MAb, various portions of the *engrailed* protein were produced in *E. coli*, and these were used in Western blot assays. Whereas the complete *engrailed* protein reacts with MAB 4D9, the protein deleted of the homeodomain does not (Figure 2). The *engrailed* homeodomain, produced as a fusion protein linked to the N-terminal portion of TRP-LE (see Experimental Procedures) is recognized by the MAB. Portions of the *engrailed* homeodomain were produced in the same way, and reaction of these constructs with 4D9 indicates that the epitope includes the 14 amino acids, 35–48, of the homeodomain (Figure 2). This determination was confirmed with a synthetic peptide representing residues 36–50, which reacts directly with MAB 4D9 on dot blots and which blocks binding of MAB 4D9 to *Drosophila* embryos.

Eighty-one homeobox-containing genes have been isolated from a variety of organisms (Scott et al., 1989). Comparing the sequence of the peptide recognized by 4D9 with the homologous portion of these other genes reveals that this region is highly variable and that the sequence of *engrailed* residues 36–50 is unique. Even among the known *engrailed* genes, some of the residues in this region of the homeobox vary. Amino acid 36 (serine in *Drosophila engrailed*) is alanine in the murine, human, chicken, zebrafish, and sea urchin genes. Amino acid 37 (serine) is glycine in *invected*, glutamine in the murine, human, chicken, and zebrafish, and lysine in the sea urchin and leech genes. Amino acid 40 (glycine) is serine in the murine and human, threonine in the sea urchin, and asparagine in the leech gene. With the exception of *invected*, amino acid 44 (alanine) is serine in all of the other genes. Residues 46–48 are invariant among the *engrailed*-like genes, and are also highly conserved among other homeobox genes.

This comparative sequence information further limits the size of the MAB 4D9 epitope, since 4D9 recognized some but not all of the *engrailed* genes. For instance, when expressed in *Drosophila* S2 cells, a chicken *engrailed* protein reacts with 4D9, but the mouse *En-1* protein does not. This result suggests that residues 36, 37, and 44 have little influence on antibody binding, since the murine and chicken genes have identical amino acids at these positions. This result also implicates residue 40 as critical to antibody binding, and suggests that serine at this position

embryo, which do not express *engrailed*). In leech (D), *engrailed* is expressed in most if not all nuclei in the second suboesophageal ganglion (arrow in D), in a number of nuclei in the anterior region of the third suboesophageal ganglion, and in four nuclei in the fourth suboesophageal ganglion. In zebrafish (E, H) and chick (F, I), *engrailed* is expressed in the posterior mesencephalon and anterior metencephalon of the developing neural tube (arrow in E). The arrow in (I) marks the invagination demarcating the mesencephalon/metencephalon boundary. In zebrafish, a short time after somitogenesis begins, additional staining is observed in three to four nuclei in each somite (G; also see arrowhead in E). However, it is quite likely that *engrailed* is not involved in the process of segmentation in zebrafish, because the expression of *engrailed* in the somites occurs after the delineation of the somites. These nuclei are positioned in the most ventral and anterior parts of the somite and close to the spinal cord (arrowhead in G). Staining in these nuclei lags about four or five somites behind the position of the most newly formed somite. Calibration bar: (A) 85 μ m; (B) 160 μ m; (C) 60 μ m; (D) 85 μ m; (E) 200 μ m; (F) 425 μ m; (G) 35 μ m; (H) 55 μ m; (I) 115 μ m.

A. engrailed Protein

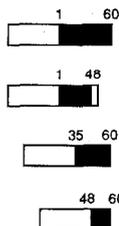


MAb 4D9

+

-

B. Fusion Proteins



+

+

+

-

C. Protein Sequences

	35	48	
Drosophila en	LSSELGLNEAQIKI		
Drosophila inv	--G-----		
Chicken	-AQ-----S---		
Leech	--K--N---S---		+
Zebra Fish	-AQ-----S---		
Grasshopper	-AR-----		
Mouse-1,2; Human	-AQ--S---S---		-
Sea Urchin	-AK--T-S-S---		

D. Peptides

	36	50	
	SSELGLNEAQIKIWF		+
	---S-----		-

Figure 2. Localization of the MAb 4D9 Epitope

The structure of the *Drosophila engrailed* protein is portrayed with the homeobox and other regions of conservation indicated (A). MAb 4D9 binds on Western blots to the intact protein (+), but not to protein lacking the homeodomain (-). MAb 4D9 also binds to fusion proteins (B) and to synthetic peptides (D) containing residues 36-48 of the homeodomain, and to *engrailed* proteins in chicken (references denote source of sequence information for residues 36-48; Darnell et al., 1986), leech (Wedeen, Price, and Weisblat, personal communication), zebrafish (Fjose et al., 1988), and grasshopper embryos (Patel et al., submitted) (C). MAb 4D9 does not bind to recombinant mouse (Joyner et al., 1985; Joyner and Martin, 1987) or human (Poole et al., 1989) *engrailed* protein, or to protein in sea urchin embryos (Dolecki and Humphreys, 1988), in which residue 40, a glycine, is instead serine or threonine. Nor does it bind to a synthetic peptide (D), in which residue 40, a glycine, is instead serine.

prevents it. Indeed, a synthetic peptide representing residues 36-50, but in which serine substitutes for glycine at position 40, fails to block MAb 4D9 binding to *Drosophila* embryos. We conclude that the MAb 4D9 epitope is in the 11 residues 38-48 (Figure 2).

It is interesting to note that residues 38-48 of the homeodomain include a region that has sequence and structural homology (Laughon and Scott, 1984; Otting et al., 1988) to the DNA-binding portion of several bacterial proteins. These comparative studies suggest that the MAb 4D9 epitope is a turn region of a helix-turn-helix structure that directly interacts with DNA. Consistent with the hypothesis that this portion of the homeodomain mediates DNA binding, MAb 4D9 blocks association of the *engrailed* homeodomain peptide with DNA (E. Martin and T. B. Kornberg, unpublished data).

In summary, the evidence that the MAb 4D9 specifically recognizes *engrailed* protein is as follows. First, the MAb

4D9 staining pattern in *Drosophila* is consistent with previous data: it is nuclear and includes only those cells known to express *engrailed*. Second, MAb 4D9 recognizes the protein product of the *Drosophila engrailed* and *invected* genes and a chicken *engrailed* gene when expressed in *E. coli*. Third, the MAb 4D9 epitope is in a variable region of the homeodomain that is unique to the known *engrailed* genes. We have obtained no evidence that it cross-reacts with homeodomain proteins other than those with sequence homology to *engrailed*.

MAb 4D9 Recognizes the Grasshopper engrailed Protein

We used MAb 4D9 to screen a grasshopper (*Schistocerca americana*) embryo λ gt11 cDNA library. Five antibody-positive plaques were isolated from a screen of 4.0×10^5 recombinants. All five phages contain inserts that hybridized at moderate stringency to a *Drosophila engrailed*

homeobox probe. The largest cDNA was 2.6 kb and consisted of two EcoRI fragments of 1.1 and 1.5 kb. Hybridization experiments using a *Drosophila engrailed* homeobox probe indicated that an *engrailed*-type homeobox was present in the 1.1 kb fragment. To confirm the identity of the cDNA, we carried out tissue in situ hybridization analysis and sequenced the homeobox region of the cDNA.

Both strands of both EcoRI fragments were used to generate RNA probes. Only one probe from each fragment hybridized to RNA in sections of grasshopper embryos, and the patterns observed for each were identical. In sections of grasshopper embryos at 35% of embryonic development (Bentley et al., 1979), striped patterns of hybridization were localized to the ectodermal cells in the posterior portion of each segment (Figure 3). The grasshopper cDNA also reveals a pattern of RNA distribution in the nervous system that matches the protein distribution revealed by MAb 4D9. Unfortunately, the in situ technique cannot resolve patterns at the level of single neurons, as is possible with immunohistochemistry (see below). However, the patterns obtained with the two techniques are in general agreement. Both antibody and in situ analyses indicate that the majority of neuronal expression is underneath the region of ectodermal expression. In addition, there is a distinct cluster of neurons positioned in the anterior part of the neuromere that is observed with both methods (Figures 3B and 3D). Thus, the grasshopper cDNA reveals a pattern of RNA distribution that closely correlates with the protein distribution as seen with MAb 4D9.

A portion of the 1.1 kb fragment was sequenced, and as suggested by its hybridization properties, this fragment contains a homeobox (Figure 4A) and encodes an *engrailed*-like homeodomain (Figure 4B). Several important features are revealed by comparing this sequence to the *Drosophila engrailed* and *invected* genes. Foremost, the amino acid sequence ELGLNEAQIKI, previously identified as the residues that make up the epitope recognized by the 4D9 MAb (see above), is present within the grasshopper homeodomain. Additionally, the nucleotide sequence of this grasshopper homeobox is much closer to that of the *Drosophila engrailed* and *invected* genes than to the homeobox sequence from any other known *Drosophila* gene. Nevertheless, the grasshopper sequence (G-en) cannot unambiguously be determined to be closer to either the *Drosophila engrailed* (D-en) or the *invected* (D-inv) sequences. Within the homeodomain, D-en and D-inv differ at nine of 61 positions; G-en also differs by nine residues from either D-en or D-inv. Comparing all three sequences, 13 positions within the homeodomains show discordance. At one of these locations, all three genes contain a different amino acid. At four positions, D-en and D-inv share the same amino acid sequence; at four other positions, G-en and D-en share the same residues; and at the remaining four residues, G-en and D-inv are identical. Thus these three sequences appear to be equidistant from one another.

The relationship of G-en to the *Drosophila* genes is not resolved by examining the 75 bp of G-en sequence upstream of that shown in Figure 4, since no way was found

to align it with the D-en or D-inv sequences at either the nucleotide or amino acid level. At the beginning of the alignment that was found, a stretch of 17 amino acids (upstream homology region) is conserved between G-en, D-en, D-inv, and the two mouse genes, En-1 and En-2 (Joyner and Martin, 1987). This is followed by the amino acids Arg-Ser in both G-en and D-inv, which, in the D-inv gene, are known to be introduced by a six-nucleotide microexon (Coleman et al., 1987). Thus we would suspect the existence of the same microexon in the G-en gene, but do not know if alternative transcripts exist without this predicted microexon. The sequence Pro-Arg-X-Arg-X-X-Lys follows in all three insect genes and in both mouse genes. After these amino acids, there is a stretch of 5–7 amino acids before the beginning of the homeodomain, except in D-inv, in which there are 28.

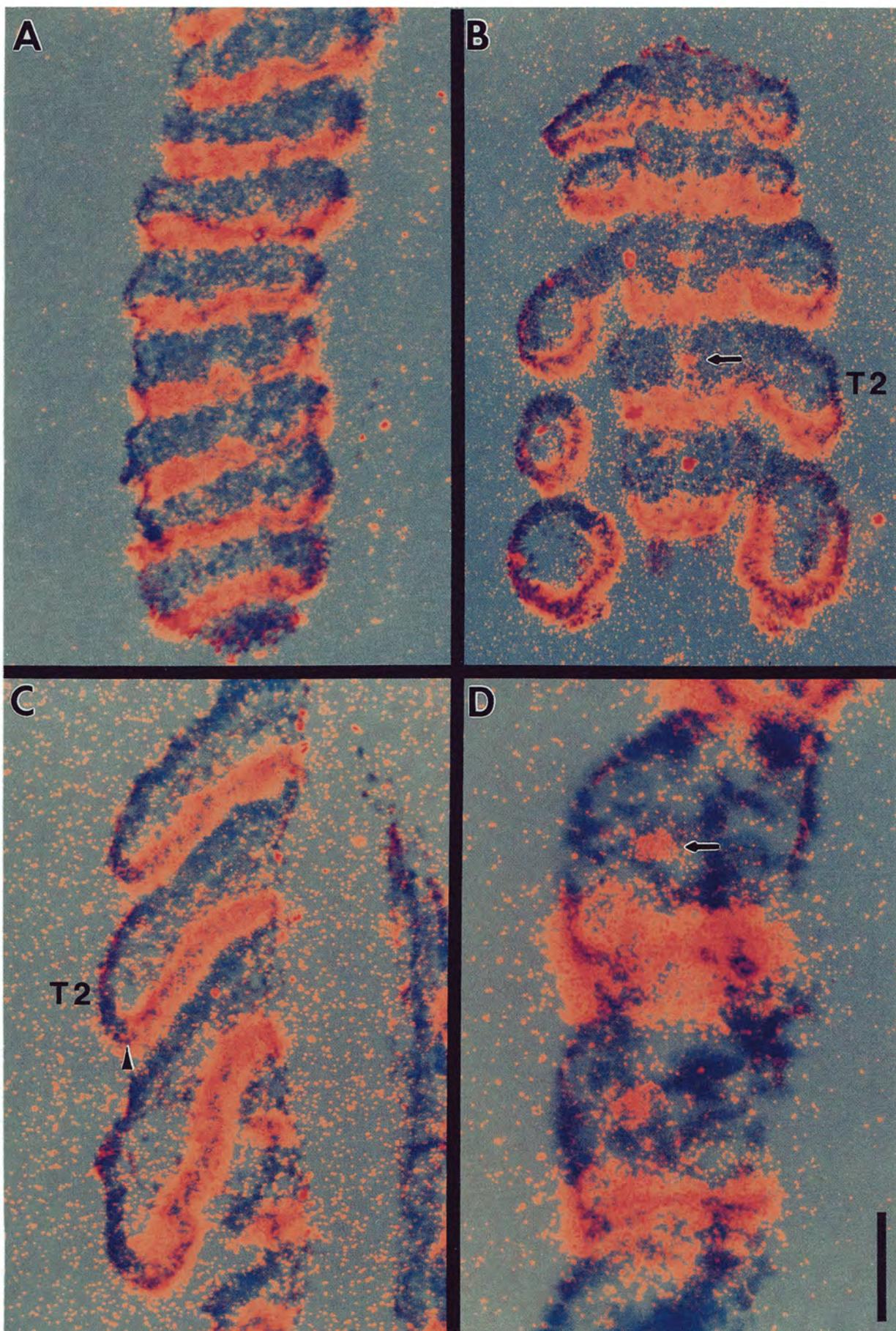
To examine more rigorously the relatedness of these three sequences, we employed the method of evolutionary parsimony analysis (Lake, 1987). We applied the analysis to the G-en sequence shown in Figure 2A and to the *Drosophila engrailed* and *invected* sequences (Poole et al., 1985; Coleman et al., 1987), disregarded regions where gaps were inserted for alignment, and used the mouse sequences (Joyner and Martin, 1987) as the out groups (Lake, 1987). This analysis (see Experimental Procedures) confirms that G-en is equidistant from both of the *Drosophila* genes.

We have also used the 1.1 kb homeobox-containing fragment of the G-en cDNA to probe genomic Southern blots (Figure 5). Under standard conditions of high stringency, this probe is able to detect both *engrailed* and *invected* in *Drosophila* genomic digests. However, only a single band of hybridization in grasshopper genomic digests is observed even under conditions of reduced stringency, suggesting that this is the sole grasshopper *engrailed* gene.

Expression of *engrailed* in Arthropods

Grasshopper (Schistocerca americana)

We examined grasshopper embryos ranging from the beginning of gastrulation to organogenesis stages (13% to 60% of development [Bentley et al., 1979]). Patterns of *engrailed* protein expression are, in most respects, remarkably similar to those of *Drosophila* embryos. Expression appears shortly after the start of gastrulation in a series of stripes in the developing thorax and then extends both anteriorly into the head and posteriorly into the abdomen; these stripes are in the posterior part of every segment (Figure 1B). During neurogenesis, a subset of neuroblasts, ganglion mother cells, and neurons also expresses *engrailed* protein (Figure 6E). Both antibody and in situ analyses indicate that the majority of neuronal expression is underneath the region of ectodermal expression. In addition, there is a distinct cluster of neurons positioned in the anterior part of the neuromere that is observed with both methods (Figures 1B and 1D). Thus, the grasshopper cDNA reveals a pattern of RNA distribution that closely correlates with the protein distribution as seen with MAb 4D9. Expression in the ectodermal stripes becomes weak-



A

G-en CTTG TTGG CCG CCG TTGG TTGG TAC TTG AGG CGA TAC TTGG GAC CGC CCG TTG TTC CGA AGA ACTT CCG CCG TTGG CCG
 CGA CTG AAG CCG AAC AAG AAG --- --- CCG GAG GAG AAG CCG CCG CCG ACG GCG TTC ACG GCG GAG CAG CTTG
 CCG CCG CTTG AAG CAG CAG TTT ACC GAG AAG AGA TTT CTTG TCT GAG CCG CCG CCG CAG CAG CTTG CCG ACG GAG
 CTTG CCG CTTG AAG CAG CCG CCG TTT AAG AAT TGG TTC CAG AAG AAG CCG GCG AAG AAT AAG AAG GCG ACC

B

D-en MET TRP PRO ALA TRP VAL TYR CYS THR ARG TYR SER ASP ARG PRO SER SER GLY --- --- PRO ARG TYR ARG
 *** **

G-en LEU TRP PRO ALA TRP VAL TYR CYS THR ARG TYR SER ASP ARG PRO SER SER GLY ARG SER PRO ARG SER ARG
 *** **

D-inv VAL TRP PRO ALA TRP VAL TYR CYS THR ARG TYR SER ASP ARG PRO SER SER GLY ARG SER PRO ARG ALA ARG
 *** **

1

D-en ARG PRO LYS GLN PRO LYS ASP LYS THR ASN ASP GLU LYS ARG PRO ARG THR ALA PHE SER SER GLU GLN LEU
 *** **

G-en ARG LEU LYS ARG ASN LYS LYS --- --- PRO GLU GLU LYS ARG PRO ARG THR ALA PHE SER GLY GLU GLN LEU
 *** **

D-inv LYS PRO LYS LYS PRO ALA THR SER [] PRO GLU ASP LYS ARG PRO ARG THR ALA PHE SER GLY THR GLN LEU
 *** **

15 30

D-en ALA ARG LEU LYS ARG GLU PHE ASN GLU ASN ARG TYR LEU THR GLU ARG ARG ARG GLN GLN LEU SER SER GLU
 *** **

G-en ALA ARG LEU LYS HIS GLU PHE THR GLU ASN ARG TYR LEU THR GLU ARG ARG ARG GLN GLU LEU ALA ARG GLU
 *** **

D-inv ALA ARG LEU LYS HIS GLU PHE ASN GLU ASN ARG TYR LEU THR GLU LYS ARG ARG GLN GLN LEU SER GLY GLU
 *** **

45 60

D-en LEU GLY LEU ASN GLU ALA GLN TLE LYS TLE TRP PHE GLN ASN LYS ARG ALA LYS TLE LYS LYS SER THR
 *** **

G-en LEU GLY LEU ASN GLU ALA GLN TLE LYS TLE TRP PHE GLN ASN LYS ARG ALA LYS TLE LYS LYS ALA SER
 *** **

D-inv LEU GLY LEU ASN GLU ALA GLN TLE LYS TLE TRP PHE GLN ASN LYS ARG ALA LYS LEU LYS LYS SER SER
 *** **

brackets in the *invected* sequence denote 22 amino acids that are not shown. The homeodomain is underlined in all three sequences. The three homeodomains differ by nine residues when analyzed in any pairwise combination. Comparing the three sequences at once, there are 13 residues that show mismatch. One of these (amino acid 37 of the homeodomain) is different in all three genes. Four (positions 22, 34, 36, and 60) are the same in D-en and D-inv, but different in G-en. Another four (positions 1, 11, 19, and 61) are the same in G-en and D-inv, but different in D-en. At the remaining four positions (2, 12, 30, and 57), G-en and D-en are the same, but D-inv is different.

Figure 4. Partial Nucleotide and Amino Acid Sequence of the Grasshopper *engrailed* Gene

The nucleotide sequence of the grasshopper *engrailed* gene (G-en) is shown in (A), and the deduced amino acid sequence is shown in (B). Dashes in the G-en nucleotide sequence introduce a gap to allow for alignment to the amino acid sequence shown in (B). The homeobox is underlined. The deduced amino acid sequence of G-en and its alignment to *Drosophila engrailed* (D-en) and *invected* (D-inv) (Poole et al., 1985; Coleman et al., 1987) is shown in (B). The alignment is based in part on the published alignment of En-1 and En-2 to *engrailed* and *invected* (Joyner and Martin, 1987). Sets of three asterisks denote positions of amino acid identity between the G-en sequence and the *Drosophila engrailed* or *invected* sequences. The dashes in the *Drosophila engrailed* sequence coincide with the amino acids introduced by the microexons of G-en and *invected*. Dashes in the G-en sequence allow for alignment of both the upstream homology region and the homeodomain. The

er after about 35% of development, but is still detectable at all stages examined.

The principal difference between the patterns of *engrailed* expression in *Drosophila* and in grasshopper is the order in which the segmental stripes appear. In *Drosophila*, the stripes appear in an order characterized by a rapid anterior-to-posterior gradient in which even-numbered stripes appear slightly before odd-numbered stripes (Figure 6A). In grasshopper, segments are added with a rostral-caudal polarity and the stripes of *engrailed* expression follow, forming one at a time. In grasshopper, no transient pair-rule patterns appear (compare Figures 6A and 6B). (For further details, see Patel et al., 1989.)

Crayfish and Lobster (*Procambarus clarki* and *Homarus americanus*)

Crayfish embryos were examined from the time of early abdominal segmentation through the period of neurogenesis (equivalent to 25% through 45% of grasshopper development). As in grasshopper, the abdominal stripes of *engrailed* protein are added one at a time (Figure 6C) and correspond to the posterior part of each segment (see Figure 1C). During neurogenesis, *engrailed* expression is almost indistinguishable from that in grasshopper (Figure 6F) and includes a similar set of neuroblasts and apparently homologous neurons.

Lobster embryos were examined at only one stage of

embryonic development (equivalent to about 75% of grasshopper development). These embryos revealed ectodermal stripes in the posterior part of each segment and a pattern of neuronal expression that was nearly identical with the pattern observed in the oldest crayfish embryos.

Expression of *engrailed* in Annelids

Leech (Helobdella triserialis)

We first observe staining with the 4D9 MAb in leech embryos during the phase of teloblast divisions (between late stage 7 and early stage 8, Stent et al., 1982). At this stage, *engrailed* expression is confined to the progeny of one of the teloblast lineages. Not all of the progeny of this particular teloblast are *engrailed*-positive, but rather only a small group of progeny in a continuous band appear transiently to express *engrailed* protein. At late stage 8, by which time the two germinal bands have come together, expression is in two rows of bilaterally symmetric cells; these rows are positioned at the dorsal edge of the germinal plate. There is one 4D9-positive cell per hemisegment, and there are about 12 segments containing these stained cells. At this stage there is also a series of large, flat nuclei positioned around the yolk sac that also stain with the 4D9 MAb.

Nervous system expression of *engrailed* in the leech begins at early stage 9 and appears first in the subset of nuclei in the second suboesophageal ganglion. By late

Figure 3. Tissue In Situ Hybridization Analysis of the Grasshopper *engrailed* Gene

Double exposure bright-field and dark-field photographs of frontal (A, B, C) and parasagittal (D) sections of 35% grasshopper embryos. Anterior is up in all panels. Sections were hybridized with an RNA probe from the 1.5 kb non-homeobox-containing EcoRI fragment of the G-en cDNA. Position of the second thoracic leg is indicated in (B) and (C). Hybridization (revealed by accumulation of silver grains that appear red in these photographs) is clearly localized to the posterior region of each segment in the abdomen (A) and extends along the posterior margin of each leg (C). Hybridization is also seen in the posterior portion of each neuromere (B, D), and a cluster of neurons in the anterior region also contains the transcript (arrows in B and D). These patterns closely match those seen with the 4D9 MAb. Scale bar: (A, B) 135 μm; (C) 110 μm; (D) 40 μm.

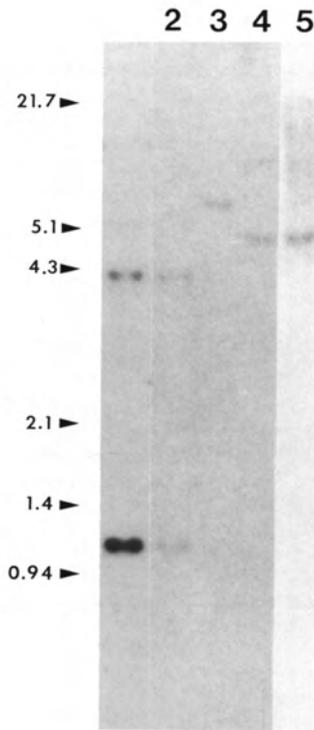


Figure 5. Grasshopper Has Only One *engrailed* Gene

Genomic southern blots of *Drosophila* (lanes 1 and 2) and grasshopper (lanes 3, 4, and 5) DNA digested with *Eco*RI (lanes 1, 2, 4, and 5) or *Hind*III (lane 3) and hybridized with a *Drosophila engrailed* homeobox probe (lane 1) or a grasshopper *engrailed* homeobox probe (lanes 2–5) at high (lanes 1–4) or reduced (lane 5) stringency. In lane 1, a *Drosophila engrailed* probe reveals *Eco*RI bands at 4.0 and 1.1 kb that correspond to the *invected* and *engrailed* genes, respectively. The grasshopper *engrailed* homeobox probe hybridizes to these same two *Drosophila* genes even under high-stringency conditions (lane 2). When grasshopper genomic DNA is probed with the grasshopper *engrailed* homeobox probe under high-stringency conditions, hybridization is seen to a single 5.9 kb band in a *Hind*III digest (lane 3), a single 4.8 kb band in an *Eco*RI digest (lane 4), and a single 5.5 kb band in a *Sall* digest (not shown). No additional bands are seen in any of the digests under reduced-stringency conditions. Lane 5 shows one such example; a single 4.8 kb band is present in a grasshopper *Eco*RI genomic digest hybridized with the grasshopper *engrailed* homeobox probe at reduced stringency. These conditions (see Experimental Procedures) are sufficiently low to allow one *Antennapedia* class homeobox to detect other *Antennapedia* class homeoboxes (McGinnis et al., 1984). Arrowheads mark positions of various DNA size standards (given in kb).

stage 9, most, if not all, nuclei in the second suboesophageal ganglion stain with MAb 4D9 and, in addition, there are also a number of positive nuclei in the anterior region of the third suboesophageal ganglion and four stained nuclei in the fourth suboesophageal ganglion (Figure 1D). There are also strongly stained nuclei extending ventrally from the second suboesophageal ganglion to the ectoderm and occasionally a 4D9-positive nucleus in the ectodermal layer. At this stage, staining at the dorsal edges of the germinal plate forms a series of arcs of weakly positive cells extending out dorsally.

Oligochaeta (*Eisenia foetida*)

We examined oligochaete embryos during the period of

neurogenesis; this period corresponds to stage 9 of leech development. In this annelid, however, the pattern of MAb 4D9 staining is quite different from that observed in the leech. Expression of *engrailed* occurs in a segmentally reiterated pattern of neuronal nuclei in the developing central nervous system (data not shown). This is in marked contrast to the regionalized pattern observed in the central nervous system of leech embryos at the same stage.

Expression of *engrailed* in Chordates

Zebrafish (*Brachydanio rerio*)

Zebrafish embryos were examined from a period before gastrulation until formation of the most posterior somites. As in the other chordates (see below), expression was first observed when the neural tube forms (Figure 1E) in the posterior mesencephalon/anterior metencephalon (Figure 1H). As development proceeds, a deep indentation separates these two regions of the central nervous system, and expression clearly extends across this morphological boundary.

A short time after somitogenesis begins, additional staining was observed in three to four nuclei in each somite (Figure 1G). These nuclei are positioned in the most ventral and anterior parts of the somite and close to the spinal cord. No expression in the somites is present prior to or during the time that the somites become delineated. Rather, as the wave of somitogenesis proceeds posteriorly, staining lags about four to five somites behind the most newly formed somite. It appears that these stained nuclei correspond to a particular set of muscle cells (C. Kimmel, personal communication). A second wave of additional somite staining follows this original somite expression, and lags behind the first by about 10 somites. These additional 10–15 nuclei are stained less intensely than the original 3–4 nuclei and are loosely packed around the developing spinal cord. These nuclei are probably a subset of the sclerotome. The nervous system staining in the posterior mesencephalon/anterior metencephalon is maintained through the oldest embryos examined.

Frog (*Xenopus laevis*)

Xenopus embryos were examined from the early gastrula period (stage 10; Nieuwkoop and Faber, 1956) to near the end of somitogenesis (stage 30). At stage 20, immediately following fusion of the neural folds, MAb 4D9 staining was observed on the dorsal surface of a region of the neural tube (data not shown). As in zebrafish, this region corresponds to the posterior mesencephalon/anterior metencephalon. As more nuclei begin to express *engrailed* protein, staining also extends ventrally around the neural tube. At stage 25 we noted a few positive nuclei far anterior in the region of the prosencephalon. Staining in the posterior mesencephalon/anterior metencephalon persisted through the oldest stages examined, and no expression was observed in the somites or spinal cord.

Chick (*Gallus domesticus*)

Chicken embryos were examined from stage 7 (one somite; Hamburger and Hamilton, 1951) to stage 15 (25 somites). We did not observe any MAb 4D9 staining until approximately stage 9. At this time, just prior to the fusion of

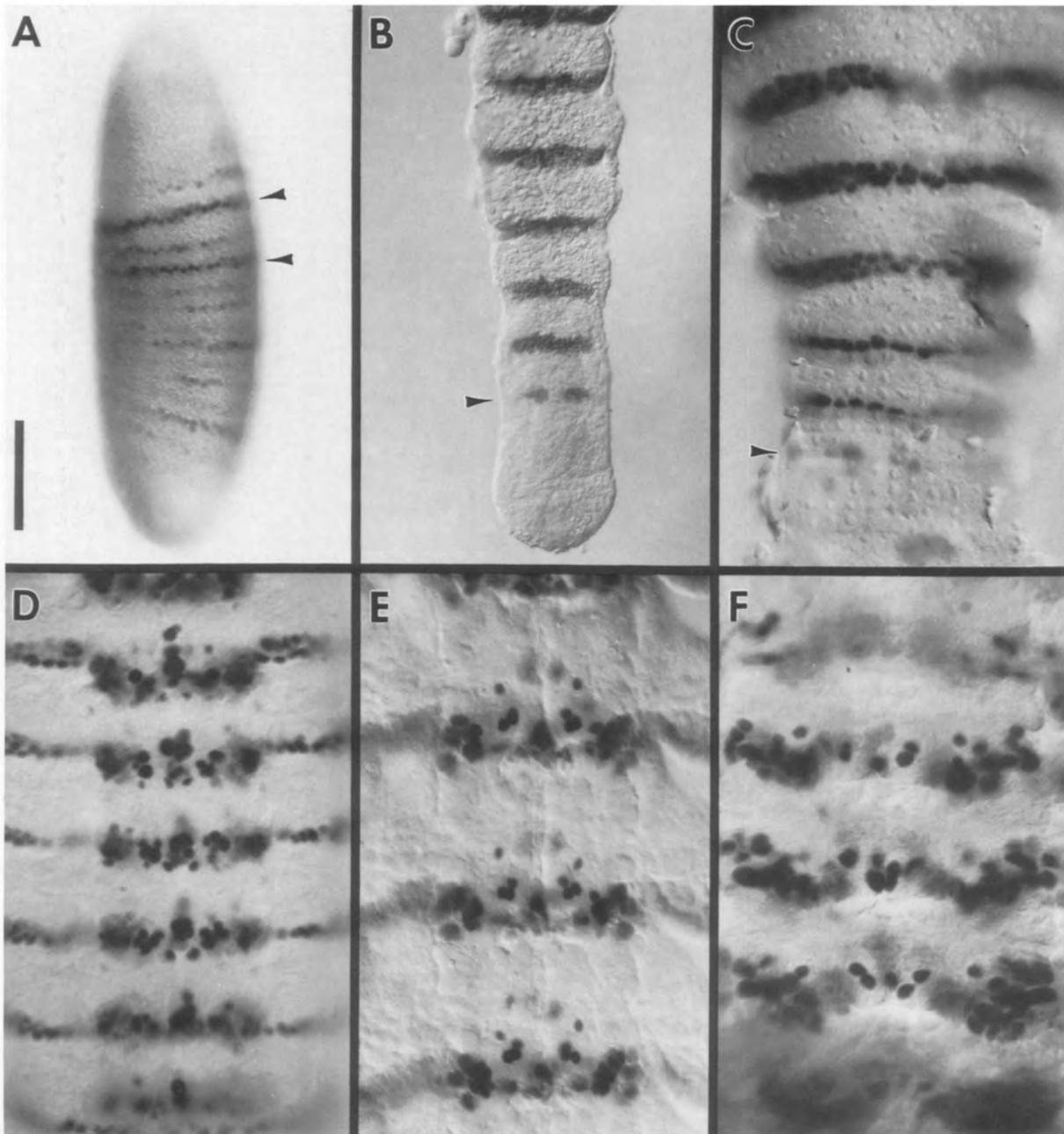


Figure 6. Expression of *engrailed* Proteins during Arthropod Segmentation and Neurogenesis

Expression of *engrailed* proteins during segmentation in *Drosophila* (A), grasshopper (B), and crayfish (C), and during neurogenesis in *Drosophila* (D), grasshopper (E), and crayfish (F), as revealed by the 4D9 MAb and HRP immunocytochemistry. (A) This cellular blastoderm has virtually completed the formation of segmentally reiterated stripes, although the formation of odd-numbered stripes lags behind the even-numbered stripes (arrowheads). (B, C) The grasshopper and crayfish embryos, however, generate *engrailed* stripes one at a time (arrowheads) as their germ bands extend caudally. In grasshopper and crayfish, the abdominal stripes form without apparent pair-rule patterning. (E, F) During the period of neurogenesis, a subset of neuroblasts, ganglion mother cells, and neurons expressed *engrailed* protein; this pattern appears quite similar in *Drosophila* (A), grasshopper (B), and crayfish (C). Calibration bar: (A) 90 μm ; (B) 200 μm ; (C) 110 μm ; (D) 40 μm ; (E) 50 μm ; (F) 40 μm .

the neural folds, *engrailed* expression appears in a scattering of nuclei on the dorsal surface of a rostral region of the neural tube. As development progresses, increasing numbers of nuclei in this region stain, and by stage 11, it is clear that the region of expression is the posterior

mesencephalon and anterior metencephalon (Figure 1F). MAb 4D9 staining begins dorsally, but moves ventrally at about the time of cranial flexure. The borders of the MAb 4D9 staining are well defined and clearly extend to both sides of the mesencephalon/metencephalon invagination

(Figure 1I). There is also a region of stained nuclei at the dorsal surface of the neural tube extending posteriorly through the metencephalon. The pattern of expression of *engrailed* proteins in the developing chick neural tube is therefore generally similar to both zebrafish and *Xenopus* although, in contrast to zebrafish, no staining was detected in the chick somites.

Discussion

Analysis of pattern formation in the *Drosophila* embryo has led to the discovery of a hierarchy of genes that controls the generation and specification of the body segments. Two aspects of these studies are relevant here. First, the regions in which these segmentation genes are expressed in the embryo correlate in most cases with the areas in which their functions are required. Therefore, in *Drosophila*, it is clear that their patterns of expression are intimately related to their functions. Second, many of these genes encode proteins that have homeodomain sequences, and similar homeobox genes have been isolated in vertebrates. The patterns of expression of some of these vertebrate proteins have been described, and the presence of a homeodomain suggests a function in transcriptional regulation. For many of these proteins, however, their developmental roles and their relationships to the *Drosophila* homeodomain proteins are unclear. Given the extraordinary sequence conservation among these regulatory proteins, it is important to determine how their functions and roles are related, and to understand how they evolved. Fortunately, the expression and evolution of one of these segmentation genes, *engrailed*, can be readily studied.

The MAb 4D9 binds to a conserved region in the homeodomain of the *engrailed* protein and recognizes this epitope in animals from many phyla (Figure 1). These include *Drosophila*, a more primitive insect (grasshopper), and two crustaceans (crayfish and lobster), annelids from two different groups (a leech and an oligochaete), and chordates from three different groups: teleost fish (zebrafish), amphibians (*Xenopus*), and birds (chick). Chordates and arthropods are thought to have diverged over 600 million years ago, yet *engrailed* genes are present in both phyla and their protein products are recognized by MAb 4D9.

Evidence that MAb 4D9 recognizes *engrailed* proteins in these organisms is strong. Its epitope is unique to *engrailed* homeodomains. It stains *Drosophila* embryos in a manner consistent with the known patterns of *engrailed* expression, indicating that it binds selectively to *Drosophila* *engrailed* proteins. Furthermore, it has been used to isolate a grasshopper *engrailed* gene and, moreover, its staining patterns in grasshopper and other arthropods are similar to *Drosophila*. The antibody recognizes the protein product of the *Drosophila* *engrailed* and *invected* genes and a chicken *engrailed* gene when expressed in *E. coli*. MAb 4D9 also stains chicken, zebrafish, and frog with patterns that have significantly greater resolution than, but are consistent with, patterns of expression previously detected by in situ hybridization of zebrafish (Njølstad and

Fjöse, 1988), chicken (Gardner et al., 1988), and mouse (Davis et al., 1988; Davidson et al., 1988; Davis and Joyner, 1988). As noted in the Introduction, conservation of a sequence of almost 100 amino acid residues in and around the homeodomain of *engrailed* genes is an indication of the functional relatedness of their protein products. This extended sequence similarity justifies their common designation as *engrailed* genes and suggests that they are true evolutionary homologs. MAb 4D9 is therefore a probe that can be used specifically to detect *engrailed* proteins in distantly related animals.

While the evolutionary conservation of the *engrailed* homeodomain indicates a conserved biochemical function as a transcriptional regulator, the patterns of expression of *engrailed* protein in different animals suggests that *engrailed* has several developmental roles, only some of which have been conserved. Within the arthropods we examined the pattern is consistent: *engrailed* is expressed in the posterior portion of each metamere during segmentation and in a segmentally reiterated subset of cells during neurogenesis. Interestingly, no other organism examined expresses *engrailed* in developing metameres. All do share one feature, namely, expression during neurogenesis. This has important implications for comparison of metameric development in different phylogenetic lineages and for determination of how, during their evolution, different developmental programs utilized regulatory genes such as *engrailed*.

In young leech embryos, transient patterns of expression in the progeny of a particular teloblast lineage are followed later by expression in the developing nervous system. Neuronal expression is regional (within only a few anterior segmental ganglia) and is not segmentally reiterated. In contrast, *engrailed* is expressed in the developing nervous system of an oligochaete in a segmentally reiterated subset of neurons. Therefore, these annelids feature *engrailed* expression in the developing nervous system in quite different patterns.

The three chordates examined in this study (zebrafish, *Xenopus*, and chick) have similar patterns: *engrailed* is expressed in a specific region of the developing neural tube (posterior midbrain and anterior hindbrain), but not in developing metameres. This pattern of expression is reminiscent of the leech patterns, and recalls the regional expression of homeotic genes in the developing *Drosophila* nervous system (reviewed by Doe and Scott, 1988).

In zebrafish, *engrailed* is expressed in a region of the developing neural tube and, a short time after somitogenesis begins, in three to four nuclei in each somite. However, it is likely that *engrailed* is not involved in the process of segmentation in zebrafish, because the expression of *engrailed* in the somites occurs after the delineation of the somites. Thus, in addition to its role in neurogenesis, *engrailed* may also be involved in specifying the fate of a segmentally reiterated subset of mesodermal cells. When comparing the patterns of expression of different animals, it is relevant that many organisms have two *engrailed* genes, and MAb 4D9 may not recognize the products of both genes. For instance, MAb 4D9-positive mesodermal cells seen in zebrafish were not seen in *Xenopus* or chick,

and this may reflect recognition by MAb 4D9 for the products of only one of the two *engrailed* genes in chick and *Xenopus* and both *engrailed* genes in zebrafish.

Clearly, different phyla have different patterns of *engrailed* expression. If we can infer function from pattern of expression, then it is only in the arthropods that *engrailed* plays a major role during the process of segmentation. It is possible, of course, that the *engrailed* function was initially involved in chordate metamerization, but that this role was lost during evolution. However, the most parsimonious hypothesis to account for these staining patterns is that *engrailed* was never involved in chordate metamerization, and that an ancestral function of *engrailed* was to specify cell fate within the nervous system. Some present groups of organisms appear to use *engrailed* to specify a region of the developing nervous system (e.g., in the leech and in chordates), whereas other organisms appear to use *engrailed* to specify a reiterated subset of neurons within the developing nervous system (e.g., in an oligochaete and in arthropods).

The differences between the patterns of *engrailed* expression in the annelids and in arthropods lead to the conclusion that arthropods are not closely related to annelids. This argues against the popular notion that metamerism in arthropods evolved from annelids (Anderson, 1973). Our data are consistent with the evolutionary analysis of the sequences of 18S rRNA (Field et al., 1988), which also suggested that arthropods and annelids are not closely related. Moreover, our data help to clarify further another evolutionary question: the relationship of crustaceans and insects. Previous work on the pattern of neuronal cells (Thomas et al., 1984), on embryology (Weygolt, 1979), and on comparative anatomy (Boudreaux, 1979) of crustaceans and insects suggested that these two groups of arthropods share a relatively recent common ancestor. The similar pattern of *engrailed* expression in these two classes is consistent with this hypothesis. This is in contrast to the arguments of others (Anderson, 1979, 1982; Manton, 1977; Schramm, 1986), who asserted that crustaceans and insects represent unrelated groups sharing convergence toward "arthropodization."

Our analysis of a grasshopper *engrailed* gene has interesting implications with respect to the evolution of the *engrailed* gene. Whereas *Drosophila* contains two *engrailed* genes, *engrailed* and *invected* (Coleman et al., 1987), only a single gene was found in grasshopper, and analysis of its sequence indicates that it is equally related to the two *Drosophila* genes. This arrangement may have been generated in either of two ways. First, the two *Drosophila* genes may have arisen by duplication some time in the insect lineage after the last ancestor common to both *Drosophila* and grasshopper. This hypothesis suggests that the two genes in mouse (En-1 and En-2; Joyner and Martin, 1987), chicken (Darnell et al., 1986), zebrafish (Fjose et al., 1988), and human (Poole et al., 1989; Logan et al., 1989) also arose as an independent duplication of an ancestral *engrailed* gene early in the chordate lineage. This is supported by the observation that the mouse genes are more similar to each other than either is to the *Drosophila* *engrailed* or *invected* genes. The same conclu-

sion has been suggested by Dolecki and Humphreys (1988), after finding a lone *engrailed* gene in sea urchin. The second possibility is that the duplication occurred before the split of the lines leading to *Drosophila* and grasshopper, and then one of the genes was later lost in the grasshopper lineage. The lone grasshopper gene may appear to be equidistant from the two *Drosophila* genes because of certain functional constraints on the G-en gene product.

Sequence analysis has also been used recently as a way of addressing some of the unresolved questions of phylogenetic relationships, and thus of supplementing previous morphological, embryological, and paleontological data (e.g., Field et al., 1988). The phylogenetic patterns of expression of regulatory genes such as *engrailed* present another way of using molecular data to examine phylogenetic relationships. Previous studies have examined slow changes in highly conserved, house-keeping molecules like 18S rRNA (Field et al., 1988). In contrast, the *engrailed* gene is a regulatory gene whose patterns of expression are conserved within groups of closely related organisms, and yet vary dramatically between more distantly related groups. The nature of these differences may reflect the evolutionary radiation of different phylogenetic lines.

In summary, our results suggest that *engrailed* is a gene that predates the divergence of arthropods, annelids, and chordates; had an ancestral function controlling cell fate during neurogenesis; and was co-opted for the process of segmentation during the evolution of the arthropods but not the annelids and chordates. Furthermore, the data support the hypothesis that metameric development evolved independently enough in these three different phyletic lines (annelids, arthropods, and chordates) that a regulatory gene that plays a crucial role during segmentation in one phylum (*engrailed* in arthropods) does not appear to play the same role in the other two.

Experimental Procedures

Generation of Monoclonal Antibodies

Full-length *engrailed* protein and the C-terminal two-thirds of the *invected* protein were generated in *E. coli* with the T7 polymerase expression system (Studier and Moffatt, 1986). BALB/c mice were immunized with either protein by intraperitoneal injections; each injection contained about 100 µg of either *engrailed* or *invected* protein. Primary injections (300 µl) consisted of protein suspended in 150 µl PBS and 150 µl complete adjuvant. Mice were given three boosts of 100 µg protein in incomplete adjuvant at approximately 2 week intervals. Three days before fusion, a final injection of 50 µg was administered. Spleen cells were fused with NS-1 myeloma cells (Kohler and Milstein, 1975; Oi and Herzenberg, 1980). Hybridoma supernatants were screened on Schneider 2 cell lines that express either *engrailed* or *invected* protein under HSP-70 promoter control (Gay et al., 1988), and hybridoma lines of interest were isolated and recloned by single-cell cloning. The MAb 4D9 was derived from a mouse injected with *invected* protein; the MAb 4F11 was derived from a mouse injected with *engrailed* protein. The 4D9-producing line has been deposited with the American Type Culture Collection and is available on request.

Fusion Proteins

The homeobox fusion protein clone (pMNRIST) was produced from the plasmid pE18 BH, which contains DNA from the BamHI site at nucleotide 1405 to the EcoRI site at nucleotide 2017 of the clone C2.1 (Poole et al., 1985). The BamHI-EcoRI fragment was sequentially mutage-

nized in two positions by site-directed mutagenesis employing two synthetic primers: first, by introducing a UGA codon after the serine at position 512, and second, by introducing an in-frame EcoRI site (Glu Phe) and a Met before the Asn at position 453 at the beginning of the homeobox. This clone, pEMRIST, was verified by the dideoxynucleotide sequencing method using single-stranded DNA. From pEMRIST, a 450 bp EcoRI fragment was cloned into the expression plasmid pMNCV1 to generate pMNRIST and to engineer the production of a protein that includes 106 amino acids of *E. coli* TrpLE protein and 60 amino acids of the *engrailed* homeodomain.

To produce a protein with only the terminal 26 amino acids of the homeodomain, a linker for EcoRI-Met (12-mer) was introduced at the PvuII site located at the middle of the homeobox (between amino acids 486 and 487) on the plasmid pEMRIST. An EcoRI band of ~330 bp was cloned into pMNCV1, and the protein induced by this plasmid (pPVST) included residues from amino acid 487 (Leu) to the end of the homeodomain.

Plasmids pRIBG and pBGST, which generate the amino-terminal 47 amino acids of the homeodomain (to amino acid 500 [Ile]) and the carboxy-terminal 14 amino acids of the homeodomain (from amino acid 500 [Ile]), respectively, were produced by introducing an EcoRI-Met linker (10-mer) at the BglII site located at amino acid 500 in pEMRIST. The EcoRI bands, of approximately 150 and 300 bp, were cloned into pMNCV1. The protein produced by pRIBG includes a tail of five carboxy-terminal amino acids (Met Asn Ser His Val STOP).

Fusion proteins were induced by adding 3- β -indolacrylic acid (20 μ g/ml) to a mid-log culture at OD₆₀₀ 0.7, and expression proceeded for 3 hr. Bacterial pellets were resuspended directly in SDS-sample buffer and protein was fractionated in a 15% SDS-polyacrylamide gel. Western analysis was according to standard protocols.

Peptides

Two different peptides were synthesized and purified (Biosearch): SSELGLNEAQIKIWF and SSELSLNEAQIKIWF. A 0.05 mg/ml solution of each of the two different peptides (in 1% DMSO, 1% Triton X-100, 0.5% deoxycholate) was made and then mixed with an equal volume of the MAb 4D9 supernatant for 1 hr (the peptides are at approximately a 100-fold molar excess to the antibody). These solutions were then placed on the embryos which were then stained normally. Control embryos received the detergent mixture without the peptides and showed normal staining.

Histochemistry

All embryos were stained and viewed as whole-mount preparations. *Drosophila* embryos were fixed for 45 min in a 1:1 mixture of heptane and PEM-FA (0.1 M PIPES [pH 6.95], 2.0 mM EGTA, 1.0 mM MgSO₄, 3.7% formaldehyde). The aqueous layer was removed and replaced with an equal volume of methanol to devitellinize the embryos (Mitchison and Sedat, 1983). The embryos were washed three times with methanol and then transferred to PBT (1x PBS, 0.2% BSA, 0.1% Triton X-100).

Chicken, crayfish, and grasshopper embryos were dissected in PBS and then transferred to the PEM-FA fixative for 45-60 min. Zebrafish, *Xenopus*, leech, and oligochaete embryos were dissected directly in PEM-FA and fixed for 45-60 min. After fixation, chick, crayfish, grasshopper, zebrafish, *Xenopus*, leech, and oligochaete embryos were washed three times in PBS for a total of 30 min and then transferred to PBT.

At this point, the protocol is identical for all organisms. Embryos were washed twice for 30 min each in PBT and then incubated in PBT plus N (PBT plus 5% normal goat serum, Gibco) for 30 min. An equal volume of MAb 4D9 supernatant was added to the PBT plus N and the embryos were incubated overnight at 4°C. Embryos were washed three times for 5 min and four times for 30 min in PBT. Embryos were again incubated in PBT plus N for 30 min and then goat anti-mouse IgG (Jackson Immunoresearch Lab) was added to a final dilution of 1:200 in PBT plus N. After 2 hr at room temperature, the embryos were washed three times for 5 min and four times for 30 min in PBT. The embryos were placed in a solution of 0.3 mg/ml DAB in PBT for 15 min and then H₂O₂ was added to a concentration of 0.03% and the reaction was allowed to proceed for 10-15 min. *Drosophila* embryos were dehydrated in EtOH and cleared in methyl salicylate. Other organisms

were cleared in glycerol. Photographs were taken using Nomarski optics on either a Zeiss Axiophot or a Nikon compound microscope.

Expression Cloning

Expression cloning was done as described previously (Patel et al., 1987), using the methods of Huynh et al. (1985). The 4D9 MAb was used at a concentration of 1:3 and the secondary antibody, peroxidase-conjugated goat anti-mouse IgG (Jackson Immunoresearch Labs), was used at a concentration of 1:200.

Genomic Southern Analysis

Molecular biology techniques followed standard methods (Maniatis et al., 1982). For genomic Southern blots, 5 μ g of *Drosophila* DNA and 40 μ g of grasshopper DNA were loaded per lane after digestion with EcoRI. Probes were made using the random priming method of Feinberg and Vogelstein (1983). The grasshopper *engrailed* homeobox probe was made from the 1.1 kb EcoRI cDNA fragment. The *Drosophila engrailed* homeobox probe was made from a 237 bp PvuII to Sall fragment kindly supplied by S. J. Poole. For high-stringency conditions, hybridization was in 5x SSC, 50% formamide at 42°C followed by washing at 65°C in 0.2x SSC. For reduced stringency conditions, hybridization was in 5x SSC, 43% formamide at 37°C followed by washing at 50°C in 2x SSC.

Tissue In Situ Hybridization

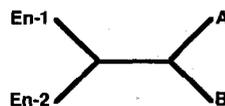
In situ analysis was done using ³⁵S RNA probes and the protocols established for *Drosophila* tissue by Akam (1983) and Hafen and Levine (1986).

Sequencing

Sequencing was done from Bluescript (Stratagene) subclones using the dideoxy method (Sanger et al., 1977).

Evolutionary Parsimony Analysis

The analysis of the phylogenetic relationships among the five *engrailed* class genes (mouse *En-1* and *En-2*, *Drosophila engrailed* and *invected*, and grasshopper *engrailed*) was performed on the alignable parts of the sequences (273 nucleotides), using evolutionary parsimony (Lake, 1987). We chose this method because (first), it is based on inherent vector algebraic properties of nucleotide sequence evolution; (second), it yields the correct phylogenetic tree under circumstances where parsimony or distance matrix analysis may fail; and (third), it offers a robust statistical test of the results.



Of all the possible four taxon tests using D-en, D-inv, G-en, En-1, and En-2, the tree shown above was the only tree supported by a significant X-invariant where A and B designate any two of the three insect genes (D-en, D-inv, and G-en). The exact branching pattern of the three insect genes relative to each other is, however, irresolvable at statistical significance.

Genes A and B	X-invariant	Chi square	P>	Y, Z-invariants
D-inv, D-en	18	12.5	0.005	not significant
D-inv, G-en	10	4.5	0.05	not significant
D-en, G-en	14	9.8	0.005	not significant

Acknowledgments

For supplying animals, we thank the members of the following labs: L. Reichardt (chick), J. Gerhart and R. Harland (*Xenopus*), J. Kuwada (zebrafish), J. Weeks (moth), J. Wine (crayfish), A. Hertz (lobster), D. Bentley (grasshopper), and D. Weisblat (leech and oligochaete). We thank W. Wood of Genentech for the pMNCV1 expression plasmid; V. Paragas, Z. Traquina, K. Jepson-Innes, G. Ghiselli, and P. Pazimino for

technical assistance; A. Sidow for performing the evolutionary parsimony analysis; C. Wedeen, D. Price, and A. Hemmati Brivanlou for help with dissections and interpretations of staining patterns; S. Smiley, A. Kolodkin, C. Kimmel, A. Joyner, and C. Lehner for helpful discussions; S. Smiley and K. Sander for thoughtful suggestions on the manuscript; and P. Njølstad, A. Fjöse, C. Wedeen, D. Price, and D. Weisblat for communication of results prior to publication. Supported by postdoctoral fellowships from the C. S. I. C. (to E. M.-B.) and the Weingart Foundation (to K. C.), by a predoctoral fellowship from the National Science Foundation (to M. C. E.), and by grants from the National Institutes of Health (to T. B. K. and C. S. G.) and the Howard Hughes Medical Institute (to C. S. G.).

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Received March 10, 1989; revised June 27, 1989.

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