Xenopus Distal-less related homeobox genes are expressed in the developing forebrain and are induced by planar signals

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SUMMARY

The polymerase chain reaction (PCR) was used to isolated five Xenopus homeobox clones (X-dll1 to 5) that are related to the Drosophila Distal-less (Dll) gene and we propose a subdivision of the vertebrate distal-less gene family according to sequence similarities. cDNA clones were isolated for X-dll2, 3 and 4, and their expression was studied by RNase protection and in situ hybridization. X-dll2, which belongs to a separate subfamily than X-dll3 and 4, is not expressed in the neural ectoderm. X-dll3 and X-dll4, which belong to the same subfamily, have a similar but not identical pattern of expression that is restricted to anterior ectodermal derivatives, namely the ventral forebrain, the cranial neural crest and the cement gland. X-dll3 is also expressed in the olfactory and otic placodes while X-dll4 is expressed in the developing eye. X-dll3 differs from the other Xenopus genes and the previously isolated Dll-related mouse genes, in that localized expression can be detected by in situ hybridization very early in development, in the anterior-transverse ridge of the open neural plate. Based on that early expression pattern, we suggest that X-dll3 marks the rostral-most part of the neural plate, which gives rise to the ventral forebrain. Finally, we have used these Xenopus distal-less genes to show that the anterior neural plate can be induced by signals that spread within the plane of neural ectoderm, indicating that at least the initial steps of forebrain development do not require signals from underlying mesoderm.

Key words: Xenopus, distal-less, homeobox, forebrain, sense organs, neural crest, planar induction

INTRODUCTION

The development of the vertebrate nervous system begins with the induction of the neural plate on the dorsal surface of the embryo near the completion of gastrulation. A process closely linked to neural induction is the regionalization of the neural ectoderm along the anteroposterior (A-P) axis, into prospective forebrain, midbrain, hindbrain and spinal cord. The neural plate can also be divided along the A-P axis according to the character of the underlying mesoderm (reviewed in Bergquist and Källén, 1954; Saxén, 1989). The part of the nervous system posterior to, and including, the midbrain overlies the chordal mesoderm (notochord), while the forebrain is derived from the portion of the neural plate that overlies the prechordal mesoderm. There are several differences in the development of the chordal and prechordal mesoderm and the respective overlying parts of the nervous system. For example, neither the prechordal mesoderm nor the overlying forebrain undergo the powerful convergent-extension movements during gastrulation and neurulation that are characteristic of more posterior regions of the axis (Keller et al., 1992a, b). Later differences include the induction of a floor plate by the notochord in the epichordal neural ectoderm, which does not take place in the prechordal forebrain (van Straaten et al., 1989; Yamada et al., 1991; Placzek et al., 1991).

The mechanisms that establish A-P pattern within the neural ectoderm have been studied using molecular markers, most of which are homeobox-containing genes. Homeobox genes encode putative transcription factors characterized by the presence of a highly conserved 60 aminoacid (aa) DNA-binding motif. Based on sequence similarity, homeobox genes have been classified into several families that include genes from various vertebrates and from Drosophila (Scott et al., 1989). A family of vertebrate genes that show similarity to the Drosophila genes of the ANT-C and BX-C complexes, the Hox genes, have been strongly implicated in the A-P patterning of the axial skeleton and the CNS, based on the strong evolutionary conservation of sequence and gene structure, their expression pattern, and the outcome of overexpression and loss-of-function experiments (reviewed in Kessel and Gruss, 1990; McGinnis and Krumlauf, 1992). In the hindbrain, which is their rostral-most area of expression, Hox genes display sharp boundaries of expression along rhombomere boundaries and may be involved in specifying segmental fate (Wilkinson et al., 1989a; Hunt et al., 1991a). En-2, one of the vertebrate homebox genes that shows sequence similarity to the Drosophila engrailed gene, is expressed more anteriorly, in
a narrow band of cells that spans the midbrain/hindbrain boundary (i.e. Joyner and Martin, 1987; Hemmati-Brivanlou et al., 1991).

Homeobox genes of the families discussed above have been used in *Xenopus* embryos as regional markers to show that anterior chordal mesoderm can induce anterior neural tissue while posterior chordal mesoderm induces neural tissue of more posterior character (Hemmati-Brivanlou et al., 1990a; Sharpe and Gurdon, 1990; Saha and Grainger, 1992). In addition, mesoderm-inducing factors and retinoic acid have been implicated in the regionalization of the epicordial nervous system, possibly indirectly by altering the A-P character of the underlying mesoderm (reviewed in Slack and Tannahill, 1992; Papalopulu and Kintner, 1992). These results support the classical view that the regionalization of neural tissue depends on instructions from the underlying mesoderm (reviewed in Säxen, 1989). Recent studies, however, have shown that large amounts of neural tissue are also formed under experimental conditions, such as those that occur in exogastrulae or Keller sandwiches, where the mesoderm does not involute and therefore never lies in apposition with the ectoderm (Kintner and Melton, 1987; Keller and Danilchik, 1988; Dixon and Kintner, 1989; Ruiz i Altaba, 1990, 1992). Moreover, the neural tissue formed under these conditions expresses epicordial regional markers in the correct spatial order (Doniach et al., 1992; Ruiz i Altaba, 1992). These results indicate that the induction and patterning of neural tissue may depend both on signals that pass within the plane of ectoderm as well as signals from underlying mesoderm.

In contrast to posterior regions of the nervous system, relatively little is known about the contribution of vertical and planar signals to the induction of the forebrain. On one hand, head mesoderm has been shown to be a very poor inducer of neural tissue, suggesting that forebrain induction cannot occur by vertical signals alone (Dixon and Kintner, 1989; Sive et al., 1989; Sharpe and Gurdon, 1990; Ruiz i Altaba, 1992). On the other hand, Keller sandwiches or exogastrulae rarely form eyes unless combined with head mesoderm, suggesting that formation of forebrain requires the co-operation of two signals (Dixon and Kintner, 1989; Ruiz i Altaba, 1992). Further analysis of forebrain induction has been hampered by the lack of early, forebrain-specific, molecular markers. Several genes distinct from the *Hox* genes and *en-2*, such as the *POU*-genes, *Wnt* genes (Roelfink and Nusse, 1991) and *PAX* genes (Goulding, 1992), are expressed in the forebrain but these are also expressed in more posterior regions and therefore are of limited practical value as anterior-specific markers.

Recently, a number of genes have been characterized in the mouse that show restricted expression in the forebrain (Price et al., 1991; Porteus et al., 1991; Robinson et al., 1991; Price et al., 1992; Simeone et al., 1992a, b). Here we report the isolation by PCR of a family of *Xenopus* genes (*X-dll1* to *5*) that contain a homeobox most related to that of the *Drosophila Dll* gene. cDNA clones were isolated for *X-dll2, 3 and 4*, and their expression patterns were studied by RNase protection and in situ hybridization. This analysis has shown that, within the neural ectoderm, expression of *X-dll3* and *4* is restricted to the ventral forebrain and moreover, that *X-dll3* is a very early marker of this part of the nervous system, which is ontogenetically the most anterior part of the neural plate (Eagleson and Harris, 1989). Finally, we have shown that these anterior neural plate markers can be induced by signals that spread within the plane of the neural ectoderm. Thus, the initial steps of forebrain formation do not require signals from the underlying mesoderm, as is also the case for the epicordial neural ectoderm (Doniach et al., 1992; Ruiz i Altaba, 1990, 1992).

**MATERIALS AND METHODS**

**Cloning by PCR**

The degenerate primers that were used to amplify *Dll*-related sequences are underlined in Fig. 1A and were as follows: upstream primer (corresponding to aa RKRPTLY): 5′ AG(GA) AA(GA) CC(CAT) CG(CAT) AC(CAT) AT(CAT) TA 3′; downstream primer (corresponding to QVKKFQON): 5′ CA(GA) GT(AGCT) AA(GA) AT(TC) TGG TTC CAG AA 3′. PCR amplifications were in a 50 µl reaction containing 1 µl of crude phage lysate of a Jgt10 stage 17 cDNA library (titre: 5x10⁸ pfu/ml) as a DNA substrate, approximately 10 µg of each degenerate primer and Vent® DNA polymerase (New England Biolabs) according to the manufacturer’s instructions. Samples were denatured for 3 minutes at 94°C and amplified forty (40) times, each amplification cycle consisting of 1 minute at 94°C, 3 minutes at 37°C and 1 minute at 72°C. Samples were finally extended for 5 minutes at 72°C. The unusually low annealing temperature was based on Lal and Lemke, (1991). Amplified DNA sequences were resolved on a 5% non-denaturing polyacrylamide gel and fragments of the appropriate size were excised, eluted, blunt-ended with T4 DNA polymerase, phosphorylated with T4 polynucleotide kinase, subcloned into the plasmid vector pKS+ (Stratagene) and sequenced.

**Isolation of distal-less cDNAs**

PCR cDNA fragments were excised from the plasmid vector, 32P-labelled and used to screen a Jgt.10 cDNA library (10¹⁰ pfu/ml) under conditions of high stringency. The cDNA library was constructed from RNA isolated from the anterior half of stage 17 neurulae. The filters were hybridised in 50% formamide, 6x SSPE, 1x Denhardt’s, 0.1% SDS and 100 µg/ml salmon sperm DNA at 42°C overnight (O/N) and then were washed in 0.1% SDS, 0.5x SSPE at 68°C for approximately 4 hours. Positive clones were plaque purified and the largest phage cDNA clones were subcloned as EcoRI fragments into the plasmid vector pKS+(Stratagene).

**Sequencing**

Subcloned PCR products and cDNA clones were sequenced with the dyeideo chain termination method (T7 sequenase kit by United States Biochemical Corporation) and oligonucleotide primers.

**In situ hybridisation**

Embryos were fixed and processed as described in the in situ hybridization protocol of Hemmati-Brivanlou et al. (1990b). RNA probes were prepared by in vitro transcription of the linearized DNA templates shown in Fig. 1B, in the presence of digoxigenin-11-UTP (Boehringer Mannheim). The hybridization probes for actin and *en-2* are described in Hemmati-Brivanlou et al. (1990b) and Bolce et al. (1992), respectively. The probe for *X-nvi* spans the coding region (Hopwood et al., 1989) and was kindly donated by Dr D. Turner. The probe for *N-CAM* was made from a *Clu*
linearized plasmid containing an N-CAM cDNA clone (N1; Krieg et al., 1989) transcribed with SP6 polymerase. In vitro transcription was also performed as in Hemmati-Brivanlou et al. (1990b). Hybridization was detected using an alkaline phosphatase-coupled, anti-digoxigenin antibody (Boehringer Mannheim) diluted to 1:1000. Alkaline phosphatase staining was developed with NBT/BCIP (Sigma; see Hemmati-Brivanlou et al., 1990b) and the reaction was allowed to proceed from 2 hours to O/N, depending on the probe. Stained embryos were fixed O/N in MEMFA (0.1 M MOPS pH 7.4, 2 mM EGTA, 1 mM MgSO$_4$, 3.7% formaldehyde), dehydrated in methanol for 1-2 hours, cleared, mounted in 2:1 benzyl benzoate: benzyl alcohol and photographed. Some specimens were sectioned after staining, and these were fixed O/N in MEMFA, then dehydrated in methanol, permeabilised briefly (2x10 minutes in Xylene), followed by 2x20 minutes changes in 1:1 xylene: paraffin wax at 60°C, and embedded in Paraffin wax. Sections (10 µm) were cut, dried, dewaxed according to standard histological procedures, mounted in Permount and photographed with Nomarski optics.

RNA analysis

_Xenopus_ embryos were fixed and dissected in ethanol: glacial acetic acid (95:5). Dissected tissue was collected into 1 ml hyde), dehydrated in methanol for 1-2 hours, cleared, mounted in 1 ml hyde), dehydrated for 1-2 hours, cleared, mounted in 2:1 benzyl benzoate: benzyl alcohol and photographed. Some specimens were sectioned after staining, and these were fixed O/N in MEMFA, then dehydrated in methanol, permeabilised briefly (2x10 minutes in Xylene), followed by 2x20 minutes changes in 1:1 xylene: paraffin wax at 60°C, and embedded in Paraffin wax. Sections (10 µm) were cut, dried, dewaxed according to standard histological procedures, mounted in Permount and photographed with Nomarski optics.

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Embryos and Keller explants

Embryos were obtained from _Xenopus laevis_ adult frogs by hormone-induced egg laying and in vitro fertilization using standard methods. Embryos were staged according to Nieuwkoop and Faber (1967). _Xenopus_ embryo explants (Keller sandwiches), designed to test the effect of planar signals, were prepared as previously described in Keller and Danilchik (1988). Briefly, square pieces of tissue were dissected from the dorsal side of an early gastrula (blastopore lip of approximately 30°). Each piece included the prospective dorsal mesoderm (dorsal involuting marginal zone, DIMZ), the prospective neural ectoderm (dorsal noninvoluting marginal zone, DNIMZ) and part of the animal cap. Care was taken to exclude the lip itself and to scrape off any already involuted head mesoderm. Two such pieces were sandwiched together with their deep surfaces apposed and were cultured under glass coverslips in Sater’s Modified Danilchik’s medium as previously described (Doniach et al., 1992). We feel that our explants were free of underlying mesoderm because they showed two regions of convergent extension, one in the DIMZ and one in the DNIMZ, as previously described (Keller et al., 1992a,b and references therein). Keller sandwiches that contain head mesoderm fail to undergo convergent extension in their DNIMZ part (Keller et al., 1992a).

![Fig. 1](image-url) (A) Diagram of the _Xenopus distal-less_ homeodomain sequences reported in this paper (X-dll1 to 5); in bold, the homeodomain related genes from other organisms, as indicated on the right. The aa residues that are highly conserved in all eukaryotic homeodomains are shaded and the consensus (conc.) is shown on top. All genes are compared to the _Drosophila Dll_ gene (top) and identities are indicated by dashes. The vertebrate genes have been classified according to type and position of the aa differences with the _Drosophila Dll_ sequence as exemplified by the sequence of mouse _Dlx-1, 2, 3_ and _4_ (see text for details). Only part of the homeodomain sequence of _Xenopus X-dll1_ and _X-dll5_ and the mouse _Dlx-3_ and _Dlx-4_ is shown because only PCR fragments of these genes have been isolated. The aa sequence of the PCR primers used in this work is underlined. The sources of the sequences shown are: _X-dll1_ to _X-dll5_, this work; _Dlx_, Cohen et al. (1989); _Dlx-1_, Price et al. (1991); _Dlx-2_, Robinson et al. (1991); _Dlx-3_ and _Dlx-4_, Robinson et al. (1991); _Dlx-5_, Asano et al. (1992); _zebrafish dlx-3_, Ekk et al. (1992). (B) Schematic diagram of the _Xenopus distal-less_ cDNA clones. Unfilled boxes represent the coding region, filled boxes the homeodomain and lines the 3′ and 5′ untranslated regions. _X-dll3_ and _X-dll4_ are full length clones but _X-dll2_ lacks sequences from the 5′ end (box open at the left end). The subcloned fragments that were used as probes for the expression analysis are shown underneath. Probes A, C and D were used for in situ hybridization and probes A, B and D for RNase protection.
RESULTS

PCR amplification of fiveDll related genes from a Xenopus cDNA library

Distal-less related sequences were amplified from a stage 17 Xenopus cDNA library using degenerate primers that correspond to the N-terminal (RKPRTIY) and the third helical (QVKIWFQN) portions of the homeodomain in the Drosophila Dll gene (Fig. 1A). PCR products with the appropriate size were cloned and sequenced, yielding five clones, X-dll1 to X-dll5, which encode homeodomain sequences related to that of the Drosophila Dll gene. With few exceptions, the amino acid (aa) residues that are highly conserved in all higher eukaryotic homeodomains (Scott et al., 1989; shaded residues in Fig. 1A) are also conserved in the Xenopus proteins while aa variability is clustered around the region of helix 1 and in the ‘turn’ region between helix 2 and helix 3.

Fig. 1A shows the aa sequence of the homeodomains encoded by the Xenopus PCR fragments, aligned to the aa sequence of Dll related homeodomains that have been isolated from various organisms (Cohen et al., 1989; Price et al., 1991; Porteus et al., 1991; Robinson et al., 1991; Asano et al., 1992; Ekker et al., 1992). From this comparison, we have divided the vertebrate distal-less genes into four subfamilies exemplified by the mouse genes Dlx-1, -2, -3 and -4, based on the position and type of aa changes within each homeodomain (Fig. 1A). Four Xenopus genes (X-dll1, 3, 4 and 5, this report) belong in the Dlx-2 subfamily (Robinson et al., 1991; Porteus et al., 1991). These genes do not represent alleles, and the inferred aa differences are not artifacts generated by PCR, since the nucleotide difference ranges from 32 (between X-dll1 and X-dll4) to 6 (between X-dll1 and X-dll4) nucleotides over the homeobox region (105 nucleotides; data not shown). The fifth Xenopus clone that has been amplified in our PCR reaction, X-dll2, has been placed in the same subfamily as the mouse Dlx-3 (Robinson et al., 1991), because they differ in only one aa over the part of the Dlx-3 homeodomain shown in Fig. 1A.

Isolation of X-dll4, 2 and 3 cDNA clones

PCR-generated fragments were used as probes to screen for cDNA clones. This approach identified complete cDNA clones for X-dll3 (1.3 kb) and X-dll4 (2.7 kb), and a partial cDNA for X-dll2 (1.5 kb; Fig. 1B). The predicted proteins encoded by two cDNAs (X-dll3 and 4) and the mouse Dlx-2 gene are aligned in Fig. 2A. This comparison indicates that X-dll4 is the most closely related to Dlx-2 (64% identity) although whether or not these two genes are homologs is not yet certain, since other members of this

homeodomains (Krumlauf, 1992) is not present in the distal-less proteins. Although X-dll3 is slightly more similar to X-dll2 than to X-dll4 (54% and 52% at the aa level, respectively) we have placed it together with X-dll4 in the Dlx-2 subfamily, as the homeodomain comparison suggests (Fig. 1A), because it is more related to X-dll4 than X-dll2 at the nucleotide level, or at the aa level when conservative changes are taken into account. We suspect that the uncertainty regarding the placement of X-dll3 arises from the fact that the N terminus of X-dll2 is not included in the comparison. This issue may be clarified when the sequence of this region becomes available.
subfamily may be more related to Dlx-2 (Fig. 1A). Similarly, X-dll2 which was placed in the Dlx-3 subfamily on the basis of the homeobox sequence, shows only 44% overall identity with Dlx-2 but 63% aa identity with the zebrafish dlx-3 gene. Thus, the sequence comparison of proteins encoded by these cDNAs supports the notion that X-dll4 and 3 belong to one subfamily (Dlx-2) while X-dll2 belongs to another (Dlx-3). Consistent with this interpretation is the observation that the other published distal-less gene from Xenopus, xdl1, (Asano et al., 1992) contains a homeobox sequence that places it into the Dlx-1 family and an overall aa sequence that is only 40% identical with the other Xenopus distal-less proteins, with most of the identity concentrated in the homeodomain (not shown).

The sequence similarity between Dlx-2, X-dll4 and X-dll3 shows a pattern in which regions of high sequence similarity at the N terminus and the homeodomain are separated by a more variable central region (see Fig. 2A). Also, regions of highest identity between the subfamily members X-dll2 and zebrafish dlx-3 are at the N terminus and the homeodomain (Fig. 2B). This pattern of sequence similarity is reminiscent of that of Hox subfamily genes (reviewed in Krumlauf, 1992), suggesting that the vertebrate distal-less genes may have also arisen by a combination of gene and locus duplication, which created related clusters of genes. In support of clustered organisation, the mouse Dlx-1 and Dlx-2 have been shown recently to be linked (McGuinness et al., 1992).

**Spatial expression by RNase protection**

We have analyzed the developmental expression of the Xenopus distal-less genes in order to determine whether any of these genes could be used as forebrain markers. Different regions of the tadpole brain were assayed for expression of the Xenopus distal-less genes by RNase protection assays. The sequences used as probes for each gene are indicated in Fig. 1B. Tadpole brains were dissected free of epidermis and underlying mesoderm and were subdivided into forebrain, midbrain and hindbrain (fragments 1, 2 and 3, respectively), as shown in Fig. 3. In addition, RNA was prepared from the trunk (fragment 4), tail (fragment 5) and the remainder of the tadpole, which included the eyes, branchial arches and the cement gland (fragment 6). RNA from the same number of embryos was then assayed for the presence of X-dll2, 3 and 4 RNA as well as for N-CAM RNA, a neural-specific transcript, (Kintner and Melton, 1987) or for eF1-a RNA, a transcript found equally in all tissues (Krieg et al., 1989). The results of this analysis (Fig. 3) indicate that X-dll4 and 3 are expressed in the forebrain but not in the midbrain or in the hindbrain. In contrast, X-dll2 RNA does not appear to be expressed in the forebrain or in any of the more posterior brain samples. The X-dll3 and 4 signal in the forebrain appears low because very little tissue is present in the dissected brain regions as shown by the levels of eF1-a RNA. The integrity of the RNA isolated from the dissected brain regions was confirmed by probing for N-CAM RNA, which showed equal amounts of neural tissue present in all samples (Fig. 3).

The RNase protection analysis shown in Fig. 3 also indicated that each distal-less gene is also expressed at low levels in fragments 4 and 5 and at a high level in fragment 6. The very low levels of X-dll3 in fragment 5 could be attributed by in situ hybridization to a ring of cells around the closed blastopore lip that express X-dll3 RNA weakly and the expression of both X-dll3 and 4 in fragment 6 could be similarly attributed to expression in the branchial arches, cement gland and the retina as discussed further below.

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**Fig. 3.** RNase protection showing the spatial distribution of transcripts of X-dll4, -3 and -2. Xenopus tadpoles were dissected as shown diagramatically on the right and RNA from the same number of tissue pieces were analyzed by RNase protection as shown on the left. Fragments 1, 2 and 3 (lanes 1, 2 and 3) represent the forebrain (telencephalon and diencephalon), midbrain and hindbrain, respectively. These samples were dissected free of associated structures such as eyes, epidermis and underlying mesoderm. Fragments 4 and 5 (lanes 4 and 5) represent the trunk and tail respectively including the skin, while fragment 6 (lane 6) represents the remaining of the embryo, including the eyes, branchial arches and cement gland. Since the same embryo equivalents were loaded for each lane (8 embryos/lane), the lanes corresponding to fragments 1, 2 and 3 appear underloaded when hybridized to eF1-a. To ensure the integrity of the RNA in these lanes, we have simultaneously analyzed the expression of the neural-specific marker N-CAM. The N-CAM signal in fragment 6 is presumably due to expression in the retina. Note that X-dll2 is not expressed in any part of the brain (lanes 1, 2 and 3) while X-dll4 and X-dll3 are specifically expressed in the forebrain (lane 1). The tadpole diagram was based on Nieuwkoop and Faber (1967).
Fig. 4
Fig. 4. Developmental expression of X-dll4. A and B by whole-mount in situ hybridization. In all panels apart from these on the top row, anterior is to the left and dorsal to the top. A, C, E, G, H, K and M show the ontogenesis of X-dll3 while F, I, J, L and N show the ontogenesis of X-dll4. (A) Frontal view of X-dll3 expression at the open neural plate stage (stage 16). Staining is observed in the cement gland and the anterior transverse rim of the neural plate. (B) Frontal view of X-twi expression in the premigratory cranial neural crest at the same stage (stage 16). In A and B, arrows indicate the lateral limits of expression. Note that X-twi and X-dll3 expression is not overlapping and if superimposed would label most of the anterior and anterolateral rim of the neural plate. (C) Frontal view of a non-cleared embryo showing the external expression of X-dll3 a few stages later, after neural tube closure. Expression externally is detected in a band of cells, probably representing the olfactory placode (arrow) and the cement gland (cg). (D) Rear view of the same embryo as in C, showing expression of X-dll3 around the closed blastopore lip, the prospective proctodeum (arrowhead). (E,F) Side views of cleared tailbud stage (stage 25) Xenopus, showing expression of X-dll3 (E) and X-dll4 (F). (G,H) Higher magnification of E and F. X-dll3 is expressed in the prosencephalon, olfactory placode, otic vesicle and cement gland (E,G) and X-dll4 is expressed in what appears to be the same region of the prosencephalon and, in addition, in the branchial arches and cement gland (F,I). The A-P limits of expression in the prosencephalon are delimited by arrows. The contour of the brain has been traced by a dashed line in G but is also visible in I. (H) Expression of X-dll3 in the brain of a cleared stage 33 embryo. (J) expression of X-dll4 at the same stage. Note that, in addition to the sites of expression at stage 25, X-dll3 is now also expressed in the branchial arches (H) and X-dll4 is also expressed in the eye (J). (K,L) Whole cleared tadpoles showing that X-dll3 (K) and X-dll4 (L) are expressed in the forebrain and all of the branchial arches. (M,N) Higher magnifications of X-dll3 and X-dll4 expression respectively at the same stage as in K and L. In M, small arrows point to the telencephalic-diencephalic boundary. In M and N, arrowheads point to the dorsal limit of expression in the telencephalon and diencephalon. Note that expression in the tadpole brain appears more extensive relative to expression at the tailbud stage (compare M and N with G and I; see text for details). The asterisk in N indicates a staining artifact. Abbreviations: ba, branchial arches; bl, blastopore; cg, cement gland; di, diencephalon; dt, dorsal telencephalon; e, eye; fb, forebrain; op, olfactory placode; os, optic stalk; ov, otic vesicle; vt, ventral telencephalon.

Expression of the distal-less genes analyzed by in situ hybridization

The RNase protection data suggested that the neural expression of X-dll3 and 4 is restricted to the forebrain, while X-dll2 is not expressed in any part of the brain. In order to examine expression in greater detail, we have used whole-mount, in situ hybridization. Consistent with the results obtained by RNase protection (Fig. 3), X-dll2 is not expressed in the brain or in any other part of the neural ectoderm (data not shown) while X-dll3 and X-dll4 are strongly expressed in the forebrain (Fig. 4K,L). By sectioning stage37 embryos after whole-mount in situ hybridization (Fig. 5), we have found that expression of X-dll3 and 4 is detected on either side of the tel-diencephalic boundary, but the cells of this boundary are negative (Fig. 5O and data not shown). Expression in the diencephalon is confined to a band of cells that appears continuous between the anterior part of the ventral thalamus and the hypothalamus (Fig. 5B,C,D; Fig. 5G,H,I; see Fig. 6 for diagrammatic summary of expression and for definition of the A-P and D-V axes). The optic stalks are negative but the chiasmatic ridge is positive (Fig. 5C,H). Other negative structures include the dorsal telencephalon, dorsal diencephalon (dorsal thalamus and epithalamus) and the bulk of the posterior part of the ventral diencephalon (posterior hypothalamus (Figs 5O, 6). However, two narrow areas of expression are detected in the posterior hypothalamus (Fig. 5E,J). In a parasagittal plane of section (Fig. 5O) these areas correspond to a punctate band of expression, (also Fig. 5N,S) that runs from the level of the ventral thalamus to the infundibular recess and terminates in the vicinity of the hypophysis (Figs 5T,O, 6), which is itself negative (Fig. 5I,M,N,S). Along the dorsoventral (D-V) axis, both genes show a sharp boundary of expression between the ventral and dorsal thalamus, the sulcus medius (Figs 5B,G, 6). Within the limits of our resolution, X-dll3 and 4 appear to have very similar, if not identical, expression boundaries along the A-P or D-V axis. Interestingly, a difference is found along the mediolateral axis, in that X-dll4 is expressed closer to the ventricular surface than X-dll3 (compare X-dll3 staining in Fig. 5B,C with X-dll4 staining in Fig. 5G,H).

Outside the brain these two genes are expressed in complementary patterns. X-dll3 and X-dll4 are expressed in the branchial arches (Fig. 4H,J,K,L) but curiously X-dll3 is restricted to the distal part of the branchial arches while X-dll4 is expressed more uniformly and at a lower level (Fig. 5M,R). The branchial arches are populated by cranial neural crest cells, which migrate into the arches and envelope a core of muscle plate cells derived from paraxial mesoderm (Sadaghiani and Thiébaut, 1987; Noden, 1988). The pattern of staining of X-dll3 and 4 (Fig. 5M,R) suggests that expression is restricted to the cranial neural crest, rather than the paraxial mesoderm, component of the branchial arches. X-dll3 and 4 differ from other cranial neural-crest expressed homeobox genes (e.g. Hunt et al., 1991a,b), in that they are not expressed in premigratory neural crest (which is marked by X-twi expression, Fig. 4B) and are not expressed in the neural tube at the A-P level where the cranial neural crest originates, i.e. at the midbrain and hindbrain (Sadaghiani and Thiébaut, 1987; Lumsden et al., 1991 and references therein). X-dll3 and 4 are also expressed in the sense organs of the head. X-dll3 is highly expressed in sensory structures derived from placodes (olfactory placodes and the otic vesicle; Figs 4G,H, 5A,B,K) while X-dll4 is expressed in the retina, a sensory structure derived from the neural tube (Figs 4J, 5Q). It is therefore striking that the expression of these distal-less genes, while different, share a propensity for ectodermal derivatives of the head (forebrain, neural crest, anterior sense organs), which are exclusively vertebrate in character (Gans and Northcutt, 1983; Nothcutt and Gans, 1983). The mouse Dlx-1 and Dlx-2 genes are also expressed in the ventral forebrain and at a number of sites outside the neural ectoderm (Price et al., 1991, 1992; Robinson et al., 1991; Porteus et al., 1991; Dollé et al., 1992).

Ontogeny of distal-less expression

The results described above indicate that, within the CNS,
Fig. 5
Fig. 5. Expression pattern of X-dll3 and 4 in sections of Xenopus tadpoles, after whole-mount in situ hybridization. Serial sections through the brain of a stage 37 tadpole after in situ hybridization with a X-dll3 probe (A-E) or an X-dll4 probe (F-G). The plane of sectioning and the A-P level of the sections shown is approximately the same between A-E and F-G and is indicated by arrowheads in T, superimposed on whole-mount in situ hybridization of a stage 37 brain with X-dll3. For definition of the A-P and D-V axis see Fig. 6. In A and F, an arrowhead points to the dorsal limit of expression in the telencephalon. In B and C, arrowheads point to the ‘segment-like’ expression of x-dll3 in the ventral thalamus. The upper arrowhead marks the sulcus medius (unlabelled) that separates the dorsal from the ventral thalamus. Note however, that expression continues ventrally in more posterior sections, into the anterior hypothalamus (B,C and D for X-dll3, and G, H and I for X-dll4). In E and J, arrowheads point to restricted punctate expression in the posterior hypothalamus. (N,S) Sections that also show the restricted expression of X-dll3 (N) and X-dll4 (S) in the posterior hypothalamus at a level more posterior to that shown in E and J, and at slightly older embryos (stage 39). The sections shown in E, J, N and S, pass though the punctate ‘line’ of expression that is indicated by an arrow in T and by arrowheads in O. (O) Parasagittal section though a stage 37 brain hybridized with x-dll3 (the same result was obtained with X-dll4; data not shown) In O also note that there is non-expressing ‘band’ of tissue between the telencephalon and diencephalon (unlabelled), which is presumably the tel-diencephalic boundary. Although X-dll3 and X-dll4 appear to have the same A-P and D-V limits of expression within the neural ectoderm, they differ in that X-dll3 is expressed more medially than X-dll4, as can be seen by comparing the mediolateral limit of expression (arrow) between B (X-dll3) and G (X-dll4), or between C (X-dll3) and H (X-dll4). They also differ in their expression in the sense organs in that X-dll3 is expressed in the olfactory placode (A and B), the otic vesicle (K) but not in the eye (L), while X-dll4 is not expressed in the olfactory placode (F,G), and the otic vesicle (P), but is expressed in the eye (arrowhead in Q). Both genes are expressed in the branchial arch neural crest, shown in M for X-dll3 and R for X-dll4, but X-dll3 is expressed strongly only in the distal part and shows a sharp proximodistal boundary (indicated by arrows in M). Note that the neural crest envelopes a core of non-expressing mesodermally derived muscle cells.

Abbreviations: ch, optic chiasma; cg, cement gland; ddi, dorsal diencephalon; di, diencephalon; dt, dorsal telencephalon; Et, epithalamus; e, eye; Ht, hypothalamus; hy, hypophysis; Tv, ventral thalamus; Td, dorsal thalamus; me, mesencephalon; m, muscle; nc, neural crest; on, optic nerve; op, olfactory placode; os, optic stalk; ov, otic vesicle; ph, pharynx; vdi, ventral diencephalon; vt, ventral telencephalon.
expression of $X$-dll3 and 4 genes is localized to the forebrain. Since we were interested in using the expression of $X$-dll3 and 4 to follow the development of the forebrain, the expression of these two genes was examined by in situ hybridization at the tailbud and neural plate stages of development.

The earliest stage at which we have been able to detect expression by in situ hybridization is the open neural plate stage (stage 16), for $X$-dll3 (Fig. 4A). This early expression sets $X$-dll3 apart from the other mouse distal-less genes that have been isolated thus far, in that these are expressed after closure of the neural tube (Price et al., 1991; Robinson et al., 1991). $X$-dll3 is expressed in a rim of cells along the anterior-transverse ridge of the neural ectoderm (Fig. 4A), not overlapping with premigratory cranial neural crest, which stains intensely with $X$-twi, an early neural crest marker (Hopwood et al., 1989; Fig. 5B). The fate of this region is to give rise to ventral telencephalic and diencephalic structures and the olfactory placodes (Eagleson and Harris, 1989; Eagleson, personal communication), and we suggest that $X$-dll3 is a very early marker for these structures. As the neural plate rolls into a tube and sinks into the embryo, cells in the anterior neural ridge are thought to sequester into the forebrain and into the olfactory placode proper (Eagleson, personal communication). $X$dll-3 staining appears to follow this sequester event upon neural tube closure in that staining is found internally in a few clusters of cells in the prosencephalon (data not shown) and externally in a mediolateral ‘line’ that may correspond to the olfactory placodes (Fig. 4C, and data not shown). Following neural tube closure, $x$-dll4 is also detected in clusters of cells in the prosencephalon but not in presumptive olfactory placode.

In the tailbud embryo (stage 25), both genes are expressed in a restricted region of the prosencephalon (Fig. 4E,F,G,I), which lies adjacent to the anterior end of the notochord at this stage (Figs 4G, 6). Expression occurs in the region of the developing tract of post-optic commissure (TPOC; Taylor, 1991; Cornel and Holt, 1992) and it would be interesting to test whether these genes play a role in axonal guidance. Comparing the neural expression at the tailbud and tadpole stage (e.g. Fig. 4G and M; also Fig. 6), suggests that the area of distal-less expression expands as the forebrain enlarges. This expansion could be due to the new expression of distal-less genes in the forebrain tissue, or to the growth and/or migration of the cells in the distalless-expressing area. Outside the brain, $X$-dll3 expression is found in a restricted area of the cement gland, the olfactory placodes and very weakly in a rim of cells around the proctodeum and the otocyst (Fig. 4E). $X$-dll4 is also expressed in the cement gland, albeit weakly, but the placodes are negative (Fig. 4F). Instead, $X$-dll4 is already expressed in the branchial arches (Fig. 4E,I). Expression of $X$-dll4 in the developing eye is not detected until later, at stage 33 (Fig. 4J).

Expression in Keller sandwiches
In order to gain insight into the signals involved in forebrain induction, we have examined expression of $X$-dll3 in Keller sandwiches (Fig. 7). To prepare these explants, two
square sheets of tissue are dissected from the dorsal side of the early gastrula and are combined with their deep surfaces apposed (see Materials and Methods). Such explants were cultured until stage 25, at which point we analyzed expression of various markers by whole-mount in situ hybridization. In these sandwich explants, the dorsal mesoderm moves away rather than underneath the ectoderm, thus allowing the study of signals propagating within the plane of the ectoderm (Fig. 7D, J; Keller et al., 1992a, b).

In these explants, X-distal-less is expressed in two, nearly par-
allel, stripes (Fig. 7B). One stripe (arrowhead in Fig. 7B) appears to correspond to the cement gland based on the cellular morphology, the secretion of mucus and the fact that it occurs well outside the neural ectoderm (as shown by double label N-CAM staining; data not shown). The neural ectoderm of the Keller sandwiches, consists of a elongated region (posterior) and a rounded, distal region (anterior) (N-CAM staining in Fig. 7D). The second stripe of X-dll3 staining occurs around the rim of the rounded distal region of the neural ectoderm (arrow in Fig. 7B) and is therefore more anterior than en-2, which is expressed closer to the elongated neural region (Fig. 7F). One might argue that this stripe of X-dll3 expression can be attributed to expression in the cranial neural ridge. This is unlikely, first because X-dll3 is not expressed in cranial neural crest at the stage of analysis (control stage 25; Fig. 7A), and second because a neural crest marker, X-twii, (Fig. 7G; Hopwood et al., 1989) is not expressed in this region. In contrast, as shown in Fig. 7H and F, X-twii is expressed more posteriorly, around the same level as en-2, which is consistent with the A-P level of origin of the cranial neural crest (Lumsden et al., 1991, and references therein). One might also argue that this X-dll3 staining solely represents expression in the sense organ anlage such as the olfactory placode or the otic vesicle. However, the same pattern of hybridization in a Keller sandwich was obtained with X-dll4, which is not expressed in these sensory anlage (data not shown). Because the same result was obtained with both markers, we conclude that the rim-staining in a Keller sandwich includes part of the forebrain anlage. Thus, these results suggest that in addition to epichordal neural plate markers, planar interactions are responsible for inducing markers of the rostral-most part of the neural plate.

**DISCUSSION**

*Xenopus distal-less* genes are expressed in forebrain, cranial neural crest and sensory organs

In contrast to *Drosophila* where only one *Dll* gene has been reported (Cohen et al., 1989), the analysis of *distal-less* genes in the mouse, *Xenopus* and zebrafish (Price et al., 1991; Porteus et al., 1991; Robinson et al., 1991; Asano et al., 1992; Ekker et al., 1992), suggests that vertebrates contain a number of *distal-less* genes, which we have subdivided into 4 subfamilies. Sequence similarity places four of our five PCR clones into one subfamily (the *Dlx-2* subfamily) and the fifth PCR clone into another (the *Dlx-3* subfamily).

RNA corresponding to *X-dll2*, a member of the *Dlx-3* subfamily, did not appear to be localized in neural tissue either when assayed by RNase protection or by in situ hybridization. *X-dll2* and the recently described related zebrafish gene, *dlx-3* (Ekker et al., 1992), together with the mouse *Dlx-3*, define a distinct subfamily which may not be expressed in the nervous system. *X-dll3* and 4, members of the *Dlx-2* subfamily, are expressed in the tadpole nervous tissue and their expression is restricted to the forebrain as measured by both RNase protection and in situ hybridization. Expression in the forebrain is confined to the ventral telencephalon and anterior ventral diencephalon (see Fig. 6 for diagrammatic representation of expression and for definition of A-P and D-V axis). Although ventral in position, areas of the tadpole brain that express *X-dll3* and *X-dll4* are likely to be derivatives of the alar and not the basal plate, as has been previously suggested for the mouse Dlx-2 gene (Robinson et al., 1991). In most of the nerve cord, ventral and dorsal neural tissue corresponds to basal and alar plate, respectively. This distinction is less clear in the forebrain because of the bending of the neural axis during neurulation and because of the uncertainty in the course of the sulcus limits, which separates basal and alar plate in the posterior nervous system. Recent studies suggest, however, that the rostral limit of the basal plate stops in the middle of the chiasmatic ridge (Puelles et al., 1987, and see Fig. 6), in agreement with the course of the sulcus limits suggested by others (see discussions in Kappers et al., 1936 vol. 3, pp 1240-1242; Bergquist and Källén, 1954; Kuhlenbeck, 1973; vol. 3, pp 289-304). Therefore, in this view, most of the *X-dll3* and 4 expression lies in alar forebrain, while only the limited area of expression that occurs in the posterior (infundibular) hypothalamus would fall into the basal plate.

*X-dll3* expression marks the anterior extent of the neural plate, which gives rise to the ventral forebrain

Our results show that expression of *X-dll3* can be detected in embryos by in situ hybridization as early as the open neural plate stage of development where staining is localized to a thin transverse crescent along the rim of the anterior neural plate (Figs 4A, 6). We propose that the region of the anterior transverse ridge stained with *X-dll3* is likely to be the anlage for the ventral telencephalic and diencephalic brain structures and for the olfactory placodes that express *X-dll3* at tadpole stages. First, a recent fate map of the *Xenopus* neural plate shows that the anterior neural ridge gives rise to ventral telencephalic and diencephalic brain structures that express *X-dll3* (Eagleson and Harris, 1989). Second, in a number of vertebrate species, the anterior neural ridge includes the prospective olfactory placodes, derived from the nervous layer of the ectoderm which is topographically located at the anterior boundary of, and is continuous with, the neural plate (Klein and Graziaidei, 1983; Knouff, 1935; Jacobson, 1959; Couly and LeDourain, 1988; van Oostrom and Verwoerd, 1972). In addition, recent tracing studies have shown that the *Xenopus* neural ridge give rise to cells in both the olfactory placode and the ventral forebrain (Eagleson, pers. comm). Later on, the olfactory placode continues to contribute cells to the forebrain (reviewed in Schwanzel-Fukuda and Pfaff, 1990). Finally, the telencephalon fails to develop following an early removal of the olfactory placode anlage (Graziaidei and Monti-Graziaidei, 1992). Thus, the early expression of *X-dll3* in the anterior transverse ridge of the open neural plate supports the notion that there is a close topographical and functional association between cells of the olfactory placode and the forebrain. During neurulation, cells that are located in the anterior transverse ridge segregate into the brain while others give rise to the olfactory placode proper (Eagleson, personal communication), and both structures express *X-dll3* after neurulation is completed. In
contrast, X-dll4, which is not expressed in the olfactory placode, is not expressed in the forebrain until after the segregation of forebrain from olfactory placode cells, that is after closure of the neural tube. Finally, the punctate expression of X-dll3 and X-dll4 in parts of the posterior hypothalamus may be due to the extensive migrations that occur in the hypothalamic-hypophyseal area (Eagleson and Harris, 1989).

In conclusion, we suggest that X-dll3 expression marks the rostral-most part of the neural ectoderm at the open neural plate stage (Fig. 6). In addition, the expression of *Xenopus distal-less* in the forebrain may be ontogenetically related to expression in the neural crest in that the anlage of both are located along the rim of the neural plate, at an anterior and anterolateral position, respectively (Sadaghiani and Thiébaut, 1987; Couly and LeDouarin, 1988; also seen by juxtaposing the X-dll3 and X-twi staining in Fig. 4A,B).

**Expression of X-dll genes and segmentation in the forebrain**

Neuromeric segmentation has been shown to play an important role in the development of the hindbrain, where cell lineage (Fraser et al., 1990) and the early expression of molecular markers (e.g. Hox genes, Wilkinson et al., 1989a; Krox-20, Wilkinson et al., 1989b) appear to respect segment boundaries. Since several authors have proposed that neuromeric segmentation might also play a role in the development of the forebrain (see Puelles et al., 1987, and refs. therein), it is of interest to know whether the restricted expression of the *Xenopus distal-less* genes in the forebrain corresponds to the morphological boundaries that occur at neuromeric segments, as suggested for the mouse genes (Price et al., 1991, 1992; Robinson et al., 1991).

Although the exact number and location of neuromeres in the anterior end of the nervous system is not universally agreed upon (see discussion in Puelles et al., 1987), we have roughly diagrammed these boundaries onto the tadpole brain as shown in Fig. 6, and placed the distribution of X-dll3 and 4 RNA in the forebrain on this diagram, using data from whole-mount in situ hybridization and coronal sections. This comparison shows that the expression of these two distal-less genes does observe some segment boundaries. First, the expression of X-dll 3 and 4 respects a boundary that occurs between the dorsal and ventral telencephalon (Fig. 6), which supports Berquist and Källén’s model of subdividing the brain (see summary of models of segmentation in Puelles et al. (1987)). A second boundary that appears to be respected in the diencephalon is the sulcus medius, which separates the dorsal from the ventral thalamus (Herrick, 1910; reviewed in Kuhlenbeck, 1973) and is apparently topographically close to the zona limitans intrathalamica of Puelles et al. (1987). Expression of both genes is continuous ventrally until the region of the optic chiasm, and therefore spans at least one segment. The correlation with morphological segmentation is complicated by the fact that the expression of X-dll3 and 4 is restricted to a narrow portion of the diencephalic segments along the A-P axis of the tadpole (see Fig. 6), giving the impression that expression runs perpendicular to the transverse boundaries in the diencephalon. In this respect, expression of X-dll3 and X-dll4 may support the segmentation model of Berquist and Källén (1954) that subdivides the brain into longitudinal columns and transverse bands.

In sum, the X-dll3 and 4 expression in the forebrain does respect some segment boundaries but is not specific for any one segment and it does not follow neuromeric segmentation in a simple way. As an alternative model, we propose that complex pattern of distal-less expression at the tadpole brain is derived from a rather simple pattern of expression at the neural plate stage (see above). Thus, we suggest another level of regionalisation where the forebrain is subdivided into different regions at the neural plate stage, as marked by the expression of X-dll3. This model can be tested by tracing the neuromeric boundaries back to the neural stage in order to examine their correlation with early X-dll3 expression.

**Planar signals induce anterior neural plate**

At the tailbud stage, the anterior notochord is in close vicinity with the site of X-dll3 and 4 expression in the brain (see Figs. 4G, 6), offering the possibility that the expression of X-dll3 and X-dll4 in the forebrain could be established by ‘vertical’ signals emanating from the underlying chordal mesoderm. To address the role of the notochord in the induction of the forebrain anlage, we have analyzed distal-less expression in Keller sandwiches, where inducing signals pass within the plane of ectoderm rather than vertically between ectoderm and underlying mesoderm. We have shown that X-dll3 is expressed in a Keller sandwich around the anterior rim of the neural ectoderm, which would give rise to the ventral forebrain and the olfactory placodes. This staining can be identified unambiguously as including the anlage of the ventral forebrain based on comparison with other markers (see results). These results demonstrate that midline/notochord signals are not necessary, and that planar signals are sufficient to induce anterior neural plate markers such as X-dll3. These results are consistent with, and extend, previous studies that have shown that large amounts of neural tissue can form via planar signals (Kintner and Melton, 1987; Keller and Danilchik, 1988; Dixon and Kintner, 1989) and that this neural tissue is patterned along the A-P axis as measured by the correct spatial expression of genes that mark the different A-P levels within the epichordal nervous system (Doniaich, 1992; Ruiz i Altaba, 1992). Thus, the induction of the anterior neural plate is brought in line with that of more posterior, epichordal, parts of the nervous system, in that they both rely on signals propagating within the plane of the ectoderm rather than signals from underlying notochord/head mesoderm.

Dixon and Kintner (1989) and Ruiz i Altaba (1992) showed using morphological markers that planar signals need to act synergistically with vertical signals from the underlying head mesoderm in order to obtain structures characteristic of the head of a normal embryo (e.g. eyes). Our findings have shown that, although head structures may not differentiate in a Keller sandwich, planar signals are sufficient to induce anterior neural plate-expressed genes such as X-dll3, in the correct A-P spatial order in relation to epichordal gene markers (Fig. 7 and Doniaich et al., 1992). Vertical signals from the prechordal mesoderm or from the anterior notochord are presumably needed in order
for the anterior neural ectoderm to differentiate further and to give rise to a morphologically recognizable head. Keller sandwiches also lack pigment cells (Keller, 1992a), consistent with the notion that an interaction with underlying dorsal lateral mesoderm is necessary for neural crest formation (Mitani and Okamoto, 1991). However, by using a neural crest-specific marker, we have shown that cranial neural crest does form in these explants, at an A-P level that corresponds to its origin in vivo (Sadaghiani and Thiébaud, 1987). Perhaps, as in the case of forebrain, vertical signals are essential for further differentiation of neural crest derivatives.

Vertical signals are also needed for morphogenetic events such as the rolling of neural plate into a tube, a process that is not thought to take place in a Keller sandwich (Keller, 1992a). Indeed, we have noted that, in a Keller sandwich at the control tailbud stage, X-dll3 is still expressed in a transverse, slightly curved, stripe, resembling the normal expression of the gene at the open neural plate stage (compare Figs 4A and 7B). Failure of the neural tube to close may account for the observation that in a Keller sandwich the separation of X-dll3 staining in the olfactory placodes from ventral forebrain does not take place.

In conclusion, the results from Keller sandwiches indicate that forebrain induction and patterning may occur by planar signals, although the nature and source of these signals remain unknown. It is intriguing that, at the neural plate stage, the shape of the forebrain and cranial neural crest anlage, which both stain with X-dll3 (albeit at different developmental stages), is semi-circular, perhaps suggesting that planar signalling at the anterior neural plate is radial in orientation.

We would like to thank Drs Oliver Bögler, Gerry Eagleson, Anthony Graham, Bill Harris, Christine Holt, Greg Lemke, Luis Puelles and Claudio Stern for comments and discussions on this crest derivatives. Drs Tabitha Doniach and Amy Sater for helpful advise on how to prepare Keller sandwiches, Dr Cary Lai for valuable advise on the PCR technique, Dr Milan Jamrich for communicating results prior to publication, Dr Dave Turner for providing the X-tw1 probe and Dama Morales for technical assistance during part of this work. N. P. is grateful to Oliver Bögler for his excellent help with computer graphics. N. P. is supported by a long-term fellowship from the Human Frontier Science Program Organization.

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Xenopus distal-less in forebrain development


(Accepted 18 December 1992)

Note added in proof

The nucleotide sequences of the genes reported in this paper have been submitted to GenBank database under the following accession numbers: L09730 for X-dll2; L09729 for X-dll3 and L09728 for X-dll4.