Abstract. Cloned complementary DNAs representing the complete coding sequence for an embryonic gap junction protein in the frog *Xenopus laevis* have been isolated and sequenced. The cDNAs hybridize with an RNA of 1.5 kb that is first detected in gastrulating embryos and accumulates throughout gastrulation and neurulation. By the tailbud stage, the highest abundance of the transcript is found in the region containing ventroposterior endoderm and the rudiment of the liver. In the adult, transcripts are present in the lungs, alimentary tract organs, and kidneys, but are not detected in the brain, heart, body wall and skeletal muscles, spleen, or ovary. The gene encoding this embryonic gap junction protein is present in only one or a few copies in the frog genome. In vitro translation of RNA synthesized from the cDNA template produces a 30-kD protein, as predicted by the coding sequence. This product has extensive sequence similarity to mammalian gap junction proteins in its putative transmembrane and extracellular domains, but has diverged substantially in two of its intracellular domains.

Gap junctions form an aqueous pathway connecting one cytoplasm to the next in a multicellular system (Gillich et al., 1974; Loewenstein, 1981). The channels that make up a vertebrate gap junction allow passage of ions and molecules <20 Å in diameter, and show weak charge selectivity (Simpson et al., 1977; Flagg-Newton et al., 1979; Schwartzmann et al., 1981; Brink and Dewey, 1980; Neyton and Trautmann, 1985). Thus, cells coupled to each other by gap junction channels form an electrical syncytium and potentially share a host of metabolic intermediates and effectors such as cyclic nucleotides and other "second messengers" (Pitts and Sims, 1977; Lawrence et al., 1978; Murray and Fletcher, 1984).

Gap junction-mediated intercellular coupling is widespread during embryonic development and pattern formation in many organisms. Regional variations in junctional communication can be correlated in some cases with specific morphogenetic behaviors and cell fate (reviewed by Caveney, 1985). In the frog *Xenopus laevis*, the pattern of gap junctional communication in early embryos seems to be related to the plane of bilateral symmetry. Animal hemisphere blastomeres near the future dorsal midline of the 32-cell embryo transfer the dye Lucifer Yellow to their neighbors more frequently than do cells flanking the ventral midline (Guethrie, 1984). This suggests that there are consistent dorsoventral differences in the number of functional gap junctional channels very early in development.

In *Xenopus* and other amphibian embryos, changes in the pattern of junctional coupling occur during several episodes of tissue morphogenesis and embryonic induction. Blackshaw and Warner (1976) found that ionic coupling between prospective myotomal cells in *Xenopus* disappears when the somites begin to segment and rotate, but then reappears. Electrical continuity has been observed between prospective chordamesoderm and neural plate cells of the newt embryo during the period of neural plate induction and regionalization (Ito and Ikematsu, 1980). While prospective epidermal and neural epithelial cells are well coupled across the neural plate border during neurulation in the axolotl, this becomes a communication boundary at about the time the neural folds meet and fuse (Warner, 1973). Finally, junctional coupling among progenitor cells of the central nervous system in *Xenopus* embryos can be reduced by microinjection of antibodies raised against the predominant protein of rat liver gap junctions (Warner et al., 1984). In these embryos, abnormalities in development of the brain, eye, and other anterior structures are common.

Taken together, these results suggest that cell–cell interactions crucial for normal development in amphibians involve regulated diffusion of ions or small molecules via gap junctions. Modulation of gap junctional communication during embryonic development may reflect regulated conductance at existing junctions or alterations in the number of junctions in the plasma membranes. Junctional conductance is affected by intracellular events such as membrane depolarization, calcium and proton fluxes, and changes in intracellular second messenger activities (reviewed by Spray and Bennett, 1985). Gap junction number may be regulated at many levels—from the control of gene transcription to rates of protein modification and degradation. Finally, structurally distinct...
gap junction proteins may be present during embryogenesis, as they are in diverse adult organs (Hertzberg et al., 1982; Gros et al., 1983; Kumar and Gilula, 1986; Beyer et al., 1987; see also Kistler et al., 1988; Nicholson et al., 1987).

To fully understand the developmental role of gap junctions, it is essential to determine their number and distribution in the embryo, their chemical composition and structure, and the mechanisms which regulate their activity. This paper describes a first step in this direction using a system especially suited for embryological study, the *Xenopus* embryo. Complementary DNAs that contain the complete coding sequence for a gap junction protein in *Xenopus* have been cloned and sequenced. In addition, the pattern of accumulation of mRNA encoding this protein has been determined.

**Materials and Methods**

**Collection, Culture, and Staging of Embryos**

Adult *Xenopus laevis* were maintained at 22°C on a 12-h light/dark cycle and a diet of chopped beef liver and Purina Trout Chow. Ovulation was induced by injection of 400-700 IU of human chorionic gonadotropin (Sigma Chemical Co., St. Louis, MO) into the dorsal lymph sac, and stripped eggs were fertilized in vitro with minced testis. Fertilized eggs were dejellied in a solution of 0.1 M NaCl, 25% (wt/vol) l-cysteine hydrochloride (Sigma Chemical Co.), pH 7.9. Embryos were cultured at 18-22°C in 33% modified Ringers solution (33% MR; MR is 0.1 M NaCl, 0.002 M KCl, 0.001 M MgCl₂, 0.002 M CaCl₂), and staged according to the normal table of *Xenopus* development (Nieuwkoop and Faber, 1975). Oocytes were staged according to Dumont (1972). Embryos at stage 26 were dissected with watchmaker’s forceps and a hair-loop in a bath of 33% MR on an agar substratum.

**Extraction of Nucleic Acids from Embryos and Tissues**

RNA was extracted from whole embryos or microdissected embryonic parts by the method of Aviv and Leder (1972). Polyadenylated RNA was selected by chromatography on oligo-dT cellulose (Berk and Sharp, 1977). DNA fragments protected by annealing with RNA were separated by electrophoresis in 6% polyacrylamide gels containing 8 M urea and detected by autoradiography at −70°C using Kodak XAR-5 film with an intensifying screen. Absolute transcript numbers were estimated by probe excess hybridization or titration (Lev et al., 1980), with varying amounts of unfraccionated or polyadenylated RNA. The total RNA mass in each reaction was adjusted to 30 μg by addition of yeast tRNA. Hybridization and SI nuclease digestion were followed by phenol/chloroform (1:1) extraction and ethanol precipitation. Radioactive hybrids were bound to DE81 filters (Schleicher & Schuell, Inc., Keene, NH), washed in 0.5 M NaHPO₄, and quantitated by scintillation counting. Background nuclease-resistant radioactivity was determined using parallel reactions with 30 μg yeast tRNA. Transcription abundance was calculated as described by Scheller et al. (1978). The accuracy of this method was checked using control hybridizations with in vitro-synthesized RNA (see below).

**In Vitro Translation of Xenopus Gap Junction Polypeptides**

An Eco RI fragment from the stage-li embryonic gap junction cDNA clone was inserted into the vector pT7/T3-18 (Bethesda Research Laboratories). Coding RNA was transcribed in vitro using T3 bacteriophage RNA polymerase after linearizing the plasmid with Pvu II. Antisense RNA was transcribed using T7 polymerase after linearizing with Hind III. Bacteriophage RNA polymerases were purchased from Bethesda Research Laboratories, and transcription reactions were as described by Melton et al. (1984). In vitro translation was performed using 10 μl of synthetic RNA in 50 μl of rabbit reticulocyte lysate (Bethesda Research Laboratories), containing [35S]methionine (Amersham Corp.). Translation reactions were terminated by addition of SDS-containing gel loading buffer. Translation products were analyzed using SDS-PAGE, transferred to nitrocellulose filters, and exposed to X-ray film.
Figure 1. Nucleotide sequence of the *Xenopus laevis* embryonic gap junction cDNA. The complete sequence of the XE1 la cDNA is presented (lines designated X) together with the amino acid sequence deduced from its longest open reading frame (in single letter code). Numbering at right refers to the *Xenopus* sequences. The human liver gap junction coding sequence and translation product is shown for comparison (lines designated H). Dashes indicate gaps introduced into the frog sequence for optimal alignment with the human codons. Underlined sequences indicate the positions of the four putative transmembrane helices (Milks et al., 1988). Arrowheads identify the 5' and 3' ends of the *Xenopus* liver partial cDNA XL1. The three overlined cytosine residues (817-819) were missing in the XL1 cDNA, leading to the absence of proline residue 253. Both strands of each cDNA were completely sequenced as described in Materials and Methods.
Southern analysis of genomic DNA. Frog liver DNA was digested to completion with the following restriction endonucleases: (a) Barn HI, (b) Dde I, (c) Pst I, and (d) Eco RI. Separated fragments were immobilized on nylon and hybridized with an XE1la DNA probe. Blots were washed at high stringency, and exposed to x-ray film for 1 wk. Size markers (in kilobases) are lambda DNA fragments of an Eco RI, Hind III digest.

Racions of Xenopus Gap Junction cDNAs

The antigenic properties of gap junctions have been highly conserved in the evolution of deuterostomes (Hertzberg and Skibbens, 1984; Warner et al., 1984; Fraser et al., 1987). The complete primary structure of the 32-kD protein subunit of the mammalian liver gap junction has been deduced from the sequences of cloned cDNAs (Kumar and Gilula, 1986; Paul, 1986). Since embryos and adult tissues of Xenopus laevis contain proteins antigenically related to the rat liver junction protein (Warner et al., 1984; Green, C. R., unpublished results), it was anticipated that frog and mammalian liver would contain homologous gap junction mRNAs. To recover related mRNA sequences, Xenopus cDNA libraries were screened by hybridization at low stringency with the human liver gap junction cDNA.

A 997-bp restriction fragment of the human cDNA (Kumar and Gilula, 1986) containing the 5' untranslated region, the 849-bp protein coding sequence, and 85 bp of the 3' untranslated region was isolated. This fragment was labeled to high specific activity and used to screen a frog liver cDNA library in lambda gt10. In a screen of 500,000 recombinant phage, a single hybridizing plaque was obtained. After plaque purification, the phage genome was found to contain a 426-bp cDNA insert which hybridized to the human gap junction probe. The insert was purified and subcloned in M13mpl9 for DNA sequencing. It contained a 282-bp open reading frame sharing 67 of 111 codons with the sequence encoding the carboxyl-terminal portion of the human liver gap junction protein. This partial cDNA clone was designated XL1 (Fig. 1).

The XL1 insert was excised and purified from the replicative form of M13mpl9 and labeled to high specific activity for use as a hybridization probe. A screen of ~150,000 recombinants from a stage-11 gastrula cDNA library yielded a single hybridizing plaque. The 1,032-bp insert in this phage was subcloned in M13mpl9 and both strands were sequenced as described in Materials and Methods. The complete sequence of this cDNA, designated XE1la, is shown in Fig. 1.1 A 795-bp open reading frame encodes a polypeptide with striking similarity to mammalian liver gap junction protein.

1 These sequence data have been submitted to the EMBL/GenBank Data Libraries under the accession number Y00791.
Figure 4. Nuclease protection analysis. A 480 nucleotide single-stranded DNA probe synthesized from XE1la was annealed to completion with 25 μg of each RNA. A fragment of 440 nucleotides is protected by hybridization from SI nuclease digestion, a shows the accumulation of transcripts during embryogenesis. P, probe; RNA from (1) yeast, (2) Xenopus ovary, (3) fertilized eggs, (4) stage 8, (5) stage 10, (6) stage 12, (7) stage 14, (8) stage 19, and (9) stage 25. Northern analysis of these RNAs with a mitochondrial genomic DNA probe showed approximately equivalent recovery of mitochondrial ribosomal RNAs and mRNAs (data not shown). b shows hybridizations to RNA extracted from (1) Xenopus lung, (2 and 3) liver, two independent preparations, (4) intestine, (5) stomach, (6) spleen, (7) body wall muscle, (8) larynx, (9) thigh muscle, (10) kidney, (11) heart, (12) brain, and (13) yeast. Abundant intact actin mRNAs were detected in each of the Xenopus samples by Northern analysis (data not shown). Markers at 518 and 396 nucleotides are Hinf I fragments of pGEMI DNA.

proteins. When the predicted frog and human amino acid sequences are aligned for optimal fit, they show ~71% identity. Of the 272 nucleotide alterations between human liver and frog embryonic coding sequences, 115 are conservative, leaving amino acid coding unchanged.

Like the mammalian liver gap junction proteins (Kumar and Gilula, 1986; Paul, 1986), the protein encoded by the XE1la sequence contains four hydrophobic domains capable of spanning the lipid bilayer (Kyte and Doolittle, 1980). The location of putative transmembrane domains indicated in Fig. 1 is based on experimental and theoretical considerations detailed by Milks et al. (1988). Each sequence is rich in charged and polar amino acids at residues 100–130 and in the carboxy-terminal 40–60 residues. Only 45 of the first 223 amino acids differ between frog and human sequences; similarities in the carboxy-terminal region are more limited. There are 20 positions in the two sequences at which codon changes produce a change in charge at neutral pH; however, the net charge difference between the predicted frog and human proteins is 0. Based on these sequence similarities, the product of the XE1la coding sequence was tentatively identified as a Xenopus embryonic gap junction protein.

Genomic Sequences Encoding Embryonic Gap Junctions

To estimate the number of genes encoding this putative gap junction protein, chromosomal DNA was prepared from the liver of an individual frog and digested with several restriction endonucleases. The pattern of hybridization of the XE1la probe to separated restriction fragments is shown in Fig. 2. Digestion of genomic DNA with Bam HI or Eco RI, neither of which cleaves the cDNA, produced a single fragment of 16–20 kb with complementarity to the cDNA probe. The enzymes Pst I and Dde I both recognize single sites in the cDNA. Digestion with Pst I generated two fragments which hybridized with the probe. Three Dde I fragments in genomic DNA bound the XE1la probe. This could indicate the presence of an intron containing a Dde I site, or the occurrence of sequence polymorphism at this locus. Low stringency hybridization of XE1la with genomic DNA did not reveal any additional hybridizing fragments (data not shown). These results suggest that the XE1la genomic sequence is unique or exists in highly conserved copies.

Abundance of Gap Junction mRNAs in Embryos and Frog Tissues

Polyadenylated RNA was purified from adult tissues and from embryos at various developmental stages. RNA gel blots probed with the radiolabeled XE1la fragment revealed hybridizing transcripts of ~1.5 kb in polyadenylated RNA from adult liver and neurula stage embryos (Fig. 3). The transcripts were not detected in polyadenylated RNA from the heart or the ovary, nor in stage-VI oocytes or early gastrula stage embryos. These RNA samples contained abundant intact actin mRNAs, showing that they were intact.

A more detailed determination of the abundance of transcripts complementary to XE1la is provided by SI nuclease protection assays. A radiolabeled single-stranded DNA probe complementary to bases 590-1,030 of the XE1la coding sequence was annealed in solution with unfragmented RNA from adult frog tissues and embryos. After digestion with SI nuclease, protected probe fragments were resolved on sequencing gels. Transcripts which hybridize to this probe were not detected in total RNA (Fig. 4 a) or polyadenylated RNA (data not shown) from ovaries or stage VI oocytes, but accumulated between stages 10 and 12, the early to middle gastrula stages. Accumulation continued until at least stage 25, after the end of neurulation. In adults, transcripts were detected in RNA from the lungs, liver, intestine, stomach,
Table I. Titration of Excess XE1la Probe with Liver and Neurula RNAs

<table>
<thead>
<tr>
<th>RNA assayed</th>
<th>Experiment</th>
<th>Mass probe protected per µg RNA</th>
<th>Mass transcript per µg RNA</th>
</tr>
</thead>
<tbody>
<tr>
<td>Liver poly(A)‡</td>
<td>A‡</td>
<td>0.33</td>
<td></td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>0.52</td>
<td>1.35 ± 0.42</td>
</tr>
<tr>
<td>Neurula total RNA</td>
<td>A</td>
<td>0.20</td>
<td></td>
</tr>
<tr>
<td></td>
<td>B</td>
<td>0.18</td>
<td>0.60 ± 0.04</td>
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</table>

* Transcript mass was calculated as probe mass times the length ratio of transcript to protected probe (1,500:440).
‡ Probe specific activity was 5 × 10⁸ cpm/µg. Samples of 0.5, 1.0, 2.0, 3.0, or 5.0 µg polyadenylated RNA were hybridized with 5 × 10⁶ cpm, or 100 µg probe, per assay. Linear correlation coefficient >0.97.
§ Probe specific activity was 1 × 10⁹ cpm/µg. Samples of 5.0, 10.0, 20.0, or 30.0 µg of stage-19 total RNA were assayed, using 1 × 10⁵ cpm, or 100 µg probe. Linear correlation coefficient >0.96.

and mesonephric kidney, but not in spleen, body wall, thigh muscle, heart, or brain (Fig. 4 b). These results confirm and extend the results of Northern blot analysis of polyadenylated RNAs.

Transcript abundance in several of the RNA samples was quantitatively determined using probe–excess titration with varying amounts of RNA (Table I). Total RNA from the late neurula stage (stage 19) contained 2–5 × 10⁶ copies of the putative junction mRNA per embryo equivalent (i.e., per 4 µg RNA). By comparison, the abundance of α-cardiac actin mRNA was estimated to be 10⁷–10⁸ copies per embryo at this stage (Mohun et al., 1984). Titration analysis also showed that transcripts complementary to XE1la were at least 10-fold rarer in liver than in neurulae. Putative gap junction mRNA comprised <0.001% of the mass of polyadenylated RNA in liver. Assuming that 1–1.5% of the RNA mass is polyadenylated (Sagata et al., 1980), the transcripts accounted for as much as 0.01% of the poly(A)-containing RNA from the stage-19 embryo. These quantitative results also suggested that the transcript abundance in the ovary and oocytes was at most 10⁻³% of the poly(A)-containing maternal RNA, or 0.01 times the abundance found in the liver.

Regional Abundance of Gap Junction RNAs

The distribution of putative gap junction mRNAs in the embryo was also assessed by hybridization analysis. Tadpoles at stage 26 were dissected into anterior and posterior portions by cutting just caudad to the otic vesicle and heart rudiment. Dorsal and ventral subfragments were then made by cutting through the cement gland and branchial region, along the flank just ventral to the pronephric duct rudiment, and through the closed blastopore or protodaeum, as shown in Fig. 5 a. Equivalent amounts of total RNA from each region were assayed by nucleic acid digestion (Fig. 5 b). Complementary RNA was detected in several of the fragments, but was most abundant in the ventral pieces. These contain ventrolateral epidermis and mesoderm, and the rudiments of the heart and endodermal structures (Nieuwkoop and Faber, 1975). Within the ventral portion of the embryo, most of the putative gap junction mRNA was found at, or posterior to, the position of the liver diverticulum.

In Vitro Translation of the Embryonic Gap Junction cDNA

The Xenopus cDNA sequence described above potentially encodes a protein of 30,122 D. In vitro translation of synthetic RNA transcribed from the XE1la insert is shown in Fig. 6. Addition of coding strand RNA transcribed in vitro (Melton et al., 1984) to a rabbit reticulocyte lysate stimulated synthesis of a major product migrating as a 30-kD protein in polyacrylamide gels. In contrast, synthetic mRNA for the human 32-kD liver gap junction protein (Kumar and Gilula, 1986) directed synthesis of a product migrating discernably slower than the frog protein. Control translations with in vitro transcribed noncoding strand RNA from the XE1la clone produced no labeled proteins besides the endogenous...
bands at 23 kD and below are attributable to premature termination above 29 kD represent full-length translation products, while minor pattern similar to that in lane a (data not shown). The major bands XE1la sequence is capable of directing expression of the albumin (45 kD).

predicted 30-kD protein.

hibitor (20.1 kD), bovine carbonic anhydrase (29 kD), and egg al-

Discussion

The Xenopus embryonic cDNA XE1la represents the mRNA for a protein with clear structural similarity to the predominant protein in mammalian liver gap junctions. The 1.5-kb transcripts that hybridize to the XE1la probe are not detectably represented in the pool of mRNA which is synthesized and stored during oogenesis. The putative gap junction mRNA apparently begins to accumulate at the midgastrula stage (stage 12). Its abundance increases rapidly during gastrulation and neurulation, and continues to increase at least to the tailbud stage. Therefore, these transcripts may be classified as "late" embryonic mRNAs, according to the nomenclature of Davidson (1986).

In the adult frog, nuclease protection assays that use the embryonic cDNA probe reveal closely related RNAs in the lung, the mesonephric kidney, and a variety of organs of the alimentary tract, including the liver. It should be noted that full-length cDNA clones of Xenopus liver gap junction mRNA have not yet been recovered. Therefore, it is not known whether the 1.5-kb liver polyadenylated RNA detected by hybridization is a product of the same gene that gives rise to the embryonic transcript. Although the cloned embryonic and liver cDNA sequences differ by one codon, no mismatch at this position is detected by S1 nuclease protection analysis of liver RNA with the embryonic probe. Consequently, it is likely that this difference represents an artifact of the cloning process or a sequence polymorphism. The near identity of the cDNA sequences and the apparent low copy number of the gene encoding them argue that the 1.5-kb transcripts in liver and embryos are the same.

Nuclease protection assays with RNA from the early tailbud stage showed that the putative gap junction mRNA has a restricted distribution in the embryo. The highest concentration of transcripts is found in the ventral portion containing ventrolateral epidermis and mesoderm and the rudiments translation products (data not shown). Thus, the cloned XE1la sequence is capable of directing expression of the predicted 30-kD protein.

It was surprising to find that the embryonic gap junction transcript was not represented in the maternal RNA pool. Several types of data argue for the existence of functional gap junctions in the gastrula Xenopus embryo. It is clear that cell-to-cell channels exist as early as the 32-cell stage which allow diffusion of a small dye, Lucifer Yellow (Guthrie, 1984), but not of macromolecular tracers such as horseradish peroxidase and fluorescent dextrans (Hirose and Jacobson, 1979; Gimlich and Braun, 1985). Warner et al. (1984) found that microinjection of antibodies that bind to determinants on the cytoplasmic surface of mammalian gap junctions and block channel conductance (Young et al., 1987) reduced dye and ionic coupling of cells in the frog early blastula. These authors also showed that antibodies specific for the major gap junction protein of rat liver recognize Xenopus early embryonic proteins in immunoblot experiments. A simple prediction from the present data on RNA accumulation is that early embryonic gap junctions, while antigenically related to the liver type of junction, are the products of oocyte mRNAs which do not form stable hybrids with the XE1la probes. Unless such transcripts were abundant, they would be difficult to detect by low stringency hybridization on gel blots. Indeed, in more recent work (Gimlich, R. L., N. M. Kumar, and N. B. Gilula, manuscript in preparation), we have identified two maternal mRNAs that encode proteins closely related to the gap junction subunit predominant in the rat heart (Beyer et al., 1987). One of these mRNAs accumulates during oogenesis, but is absent by the neurula stage. Thus it seems that Xenopus embryonic gap junction proteins are the products of a family of related genes with distinct patterns of expression. The developmental significance of a switch in predominant gap junction subunit structure is a topic of current research in this laboratory.

Structural features believed to be determinants of protein folding and membrane association are well conserved among the predicted XE1la translation product and the known gap junction proteins of mammals (Kumar and Gilula, 1986; Paul, 1986). In particular, the number and placement of predicted transmembrane domains is similar in the frog and mammalian proteins. The amino acid sequences of these hydrophobic domains, including a putative amphipathic channel-forming helix (Milks et al., 1988), are also highly conserved. The amino terminal 220 residues show identical spacing of cysteine residues and domains rich in charged amino acids. Topological considerations based on the existence of cytoplasmic sites and four potential transmembrane helices (Unwin, 1986) predict that the gap junction protein has two extracellular domains (around residues 40-75 and 160-190 in Xenopus). The excellent sequence conservation in these regions is consistent with the capacity of phylogenetically diverse cells in culture to establish heterospecific gap

Figure 6. In vitro translation of synthetic gap junction mRNA. Xenopus or human liver gap junction cDNAs were cloned in the vector pT3/T7-18 and coding strand RNA was synthesized and translated in vitro as described in Materials and Methods. Translation products labeled with [35S]methionine were separated by PAGE and detected by fluorography. Translation products resulting from addition of (a) no exogenous RNA, (b) XE1la coding strand RNA, and (c) human liver gap junction protein coding strand are shown. Addition of noncoding strand RNAs consistently yielded a pattern similar to that in lane a (data not shown). The major bands above 29 kD represent full-length translation products, while minor bands at 23 kD and below are attributable to premature termination or proteolysis. Size markers are soybean trypsin inhibitor (201 kD), bovine carbonic anhydrase (29 kD), and egg albumin (45 kD).

of pharynx, heart, and endodermal structures. Within this region, the greatest abundance is found in a posterior ventral fragment that contains the liver rudiment, the ventral walls of midgut and postanal gut, and ventral mesoderm and epidermis (Nieuwkoop and Faber, 1975). Although the significance of this distribution is not known, it is possible that the gene product plays some role in morphogenesis of the respiratory, alimentary, and urogenital tract organs where it is later stably expressed. A better understanding of the embryonic distribution of the putative gap junction mRNA will require analysis by in situ hybridization.
junctional coupling (Michalke and Loewenstein, 1971; Epstein and Gilula, 1977).

Comparison of diverse gap junction proteins also shows a similar pattern of structural divergence. A region between the second and third putative transmembrane domains (around residues 100–140 in Xenopus) is highly variable in primary sequence. This domain also differs in its length between the major liver gap junction protein and that predicted for the heart gap junction in mammals (Beyer et al., 1987). The combined proteolytic and immunochemical studies of Zimmer et al. (1987) indicate that this part of the molecule is exposed on the cytoplasmic surface of the junctional membrane. The carboxy-terminal sequences (after residue 220) are highly divergent, although careful alignment reveals partial identity between the frog protein and the mammalian liver molecule. This variable region is also thought to reside on the cytoplasmic surface of the native gap junction (Zimmer et al., 1987).

Phosphorylation of gap junction proteins has been proposed to be an important modulator of junction number and conductance (Johnson et al., 1986; Saez et al., 1986). Thus, it may be significant that despite extreme sequence divergence in cytoplasmic domains, a consensus protein kinase A modification site (Krebs and Beavo, 1979) between positions 220 and 240 exists in both the human liver and frog embryonic junction proteins (at residue 227 in Xenopus). In contrast, the two consensus tyrosine phosphorylation sites (Patience et al., 1987) in the cytoplasmic domains, a consensus protein kinase A modification site (at amino acid 171 of the frog protein) lies in one of the putative extracellular regions. The functional significance of these primary sequence features remains to be determined.

The availability of the coding sequences for embryonic gap junction proteins will greatly facilitate detailed study of the regulation of junctional conductance and its role in development. Specific antibody probes are being developed to determine the number and distribution of different gap junction proteins in the embryo. A combination of in vitro mutagenesis and in vivo expression studies are now possible to locate the structural determinants of junctional assembly and conductance. Genomic sequences encoding diverse embryonic gap junction proteins have been cloned (Kumar, N. M., and N. B. Gilula, unpublished data) and the genetic regulatory determinants of junction biosynthesis are being identified. These approaches will form a basis for understanding the complex physiological control of cell–cell interactions during embryogenesis.

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Gimlich et al. Xenopus Embryonic Gap Junctions