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## Gap junction gene and protein families: Connexins, innexins, and pannexins

**Eric C. Beyer\*** and **Viviana M. Berthoud**

Department of Pediatrics, University of Chicago, Chicago, IL 60637, United States

### Abstract

Gap junction channels facilitate the intercellular exchange of ions and small molecules. While this process is critical to all multicellular organisms, the proteins that form gap junction channels are not conserved. Vertebrate gap junctions are formed by connexins, while invertebrate gap junctions are formed by innexins. Interestingly, vertebrates and lower chordates contain innexin homologs, the pannexins, which also form channels, but rarely (if ever) make intercellular channels. While the connexin and the innexin/pannexin polypeptides do not share significant sequence similarity, all three of these protein families share a similar membrane topology and some similarities in quaternary structure. This article is part of a Special Issue entitled: Gap Junction Proteins edited by Jean Claude Herve.

### Keywords

Connixin; Innixin; Pannixin

### 1. Introduction

Intercellular communication through gap junction channels is critical for coordinating the functions of cells in the tissues of all multicellular organisms by allowing direct exchange of ions and small molecules (including second messengers like  $\text{Ca}^{2+}$ ,  $\text{IP}_3$  and cyclic nucleotides and oligonucleotides). Gap junction mediated coupling allows groups of cells to respond to a ligand synchronously, even when only a few cells express the ligand receptor. During development, gap junctions form communication compartments in which coupled cells differentiate together, while those that are not coupled acquire a different fate.

### 2. Connexins

In vertebrates, gap junctions are formed by members of a family of proteins that are called connexins (Cx). Twenty connexins are expressed in humans and in mice (Table 1). The corresponding genes are identified with a symbol starting with “*GJ*” (for gap junction), while the most commonly used protein nomenclature employs an abbreviation beginning

\*Corresponding author at: University of Chicago, 900 E. 57th St. KCBD 5152, Chicago, IL 60637, United States.  
ecbeyer@uchicago.edu (E.C. Beyer).

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with “Cx” (for connexin) followed by a number corresponding to the molecular mass of the predicted polypeptide in kilodaltons [10]. The connexins form a closely related family exhibiting extensive amino acid identity and similarity within their transmembrane and extracellular domains. The similarities in their extracellular loops can be described by two connexin signatures (PS00407 and PS00408, <http://prosite.expasy.org/PDOC00341>). Differences and similarities in the connexin sequences have been used to define connexin subfamilies [7,30], and sequence comparisons between different species have been used to identify orthologs [18]. Currently, five connexin subfamilies are recognized ( $\alpha$ ,  $\beta$ ,  $\gamma$ ,  $\delta$ , and  $\epsilon$  or *GJA*, *GJB*, *GJC*, *GJD*, and *GJE*) (Table 1).

A wide range of genetic diseases have been mapped to mutations of the connexin encoding genes (including deafness, neuropathies, cataracts, skeletal abnormalities, and skin diseases) (reviewed in [9,31,37,38,46,48,53,55]). Connexins have sometimes been identified by abbreviations corresponding to these diseases, such as ODDD (oculodentodigital dysplasia), CMTX (X-linked Charcot-Marie-Tooth disease), and Erythrokeratoderma variabilis (EKV). Many of these abbreviations are included as synonyms in Table 1.

The ability of connexins to form intercellular channels is well documented in many different tissues and expression systems. Connexins can also form plasma membrane channels in unapposed cells [36]; these connexin “hemi-channels” have been implicated in a variety of physiological and pathological processes (reviewed in [47]).

### 3. Innexins

Cell-to-cell junctions and the process of direct intercellular communication are present even in some of the most primitive multicellular organisms [22,23,25,26]. Indeed, some of the first demonstrations of direct intercellular communication came from studies in invertebrates [22]. Although they perform similar functions to their vertebrate counterparts, invertebrate gap junctions are encoded by members of a very different gene family, the innexins (reviewed in [5,42]). The innexins do not exhibit significant sequence similarity to the connexins.

The innexins have been most extensively studied in model organisms like the fruit fly (*Drosophila melanogaster*), the nematode (*Caenorhabditis elegans*), and the medicinal leech (*Hirudo verbana*). Their members are listed in Tables 2–4. Unlike most of the connexin genes (which usually contain the full coding sequence in a single exon), several innexin genes contain the coding region in more than one exon. The number of introns can vary among members of the family (e.g., innexin genes from *Hirudo verbana* [28] and *Drosophila melanogaster* [51]). The presence of multiple introns within the DNA encoding the coding region allows the generation of different protein products through alternative RNA splicing (e.g., the *Drosophila shak-B* locus [17]). Interestingly, the *Drosophila melanogaster inx2* gene locus localizes in opposite orientation in the longest intron of the *inx7* gene; this structural organization has been proposed to serve for reciprocal control of gene expression of these innexins [16].

Like the connexins, the innexins are expressed with overlapping patterns allowing the formation of heteromeric hemichannels and heterotypic gap junction channels. Their wide expression in many different tissues reflects their involvement in many different cellular processes. Studies of innexins in invertebrates have particularly emphasized the importance of innexins in the nervous system. Many different innexins are expressed in the nervous system of invertebrates (at least 15 in the leech [28] and 8 in the octopus [2]). Mutations of some invertebrate innexins cause characteristic behavioral changes like *shaking* mutants in *Drosophila melanogaster* and *uncoordinated* mutants in *Caenorhabditis elegans* (reviewed in [42]). Innexins are differentially expressed during development [20]. The spatial and temporal expression differences may establish communication compartments that contribute to developmental patterning [45,54].

#### 4. Pannexins

Surprisingly, genes and expressed transcripts with substantial sequence similarity to the invertebrate innexins have also been identified in vertebrates [35]. These genes and proteins are called pannexins [35]. Three different pannexins are expressed in human and mouse tissues (Table 5). For human PANX2, two mRNA variants have been reported that encode proteins with different C-terminal amino acids (loci, NM\_001160300.1 and NM\_052839.3).

Like the connexins, the pannexins form oligomeric polypeptide assemblies and traffic to the plasma membrane, where they can form channels that connect the cytoplasm to the extracellular space [13]. Although PANX1 can form functional gap junction channels when expressed in *Xenopus* oocytes [13], pannexins do not form intercellular channels in transfected mammalian cells [50].

Unlike the connexins, pannexins undergo glycosylation within their extracellular regions. This modification may be important for the targeting of pannexins to the plasma membrane [11,39]. Pannexin glycosylation may effectively impede cell-to-cell channel formation and regulate pannexin intermixing [40]. Some innexins may also be glycosylated; for example, two yellow fever mosquito (*Aedes aegypti*) innexins (AeInx3 and AeInx7) contain predicted N-glycosylation sites, and immunoblots of AeInx3 show multiple immunoreactive bands. This similarity to the pannexins suggests that some innexins might have other functional roles besides intercellular communication [15].

Pannexins have been implicated in several pathologies including cardiovascular diseases, inflammation, cancer and neuropathies [6,41,57]. Due to their wide expression in many tissues and organs, deleterious pannexin gene mutations might be expected. The only human gene mutation reported to date encodes a non-functional PANX1 variant that does not inhibit the function of wild type PANX1; it was found in a patient (homozygous for this allele) with disorders in several organs [49]. Investigations of pannexin-null mice have also implicated pannexins in contributing to protection from ischemic stroke injury [4,21], modulation of neuronal excitability and learning [43,44], bone development [27], narcotic withdrawal [14], and sleep-wake cycle regulation and behavior [29].

## 5. Shared features of connexins, innexins, and pannexins

Despite their lack of amino acid sequence similarities, the connexins and the innexins/pannexins share structural and functional commonalities. All of these genes encode polytopic membrane proteins that have similar topologies within the membrane (Fig. 1). They each contain four transmembrane domains with their N- and C-termini on the cytoplasmic side of the membrane, leading to the formation of two extracellular loops and one intracellular loop. The connexin topologies were originally predicted from hydropathy plots of the cloned sequences and supported by mapping of regions using site-directed antibodies [24,56]. Determination of the crystal structures of some connexins and innexins supported the topological models [32,33,34,52]. Studies confirm that connexins, pannexins and innexins form channels with similar quaternary structures [3,12,19,32,33,52]. However, while connexin hemi-gap junction channels contain 6 subunits regardless of the connexin isoform, innexin hemi-gap junction channels and pannexin channels can have 6 or 8 subunits depending on the isoform (e.g. *C. elegans* inx-6 forms octamers, rat Panx1 forms hexamers and rat Panx2 most likely forms octamers) [3,33,34].

The connexins, innexins and pannexins all contain cysteines in their extracellular loops, but they differ in the numbers of cysteines in each loop: connexins contain three, whereas innexins and pannexins contain two. The connexins, innexins and pannexins contain an invariant proline residue in the second transmembrane domain. This proline forms part of a motif (PXXXW) that is conserved between vertebrate pannexins and most innexins. The connexins, innexins, and pannexins are all multi-member families; within the families, sequence differences between members confer unique channel and regulatory properties.

Both connexins and pannexins participate in several processes including propagation of calcium waves, inflammation, memory consolidation and neurodegeneration. Knowledge of the sequences and structures of the connexins, pannexins, and innexins is facilitating elucidation of their individual, shared, and complementary roles in physiology and pathophysiology.

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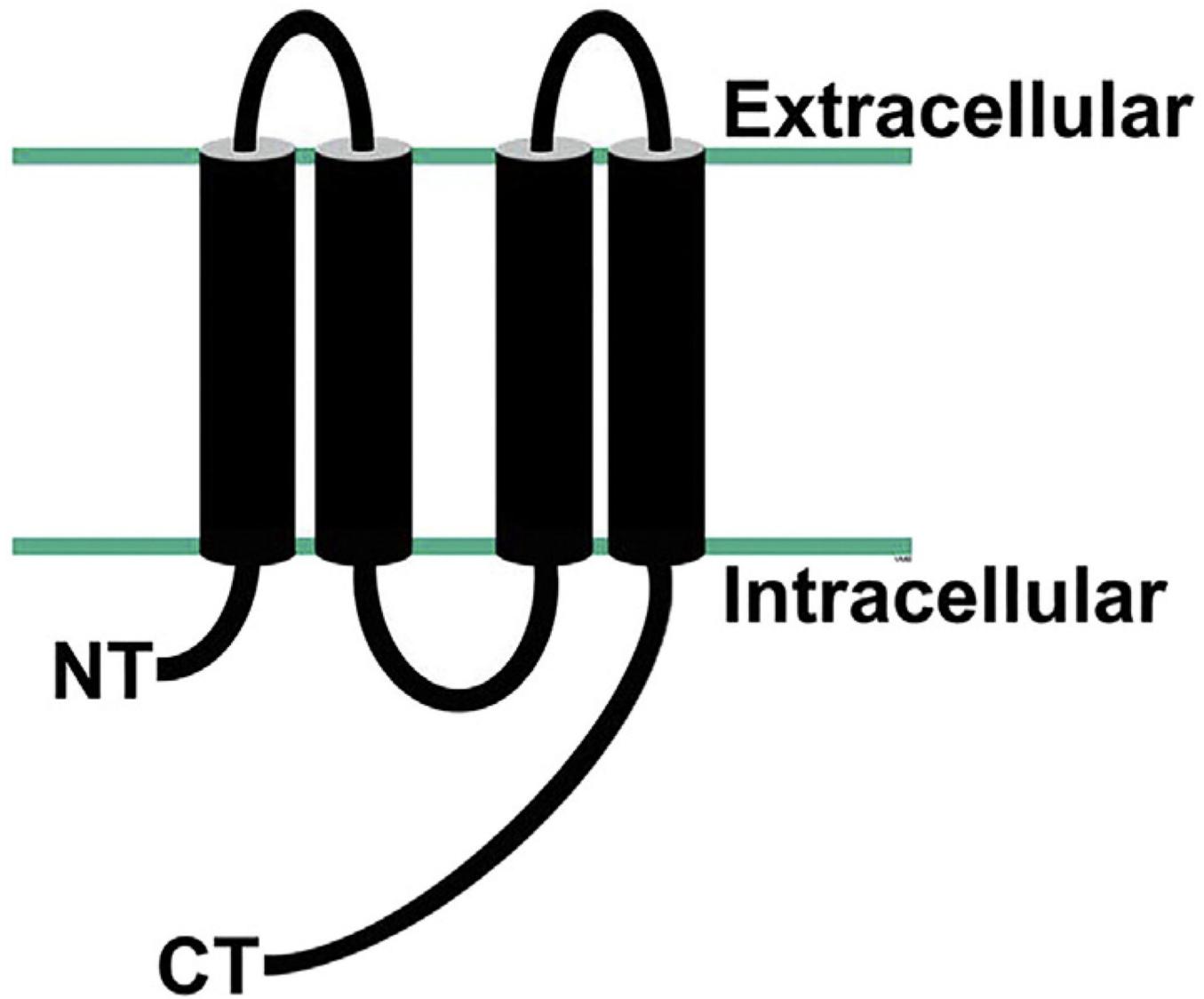
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**Fig. 1.**

Membrane topology of a connexin/innexin/pannexin. Transmembrane domains are depicted as cylinders that span the plasma membrane (boundaries indicated by teal lines). NT, N-terminus; CT, C-terminus.

**Table 1**

The connexin protein and gene families in humans and mice.

Human			Mouse	
Gene symbol	Protein name	Synonyms	Gene symbol	Protein name
<i>GJB1</i>	CX32	CMTX1, CMTX	<i>Gjb1</i>	Cx32
<i>GJB2</i>	CX26	DFNB1, DFNA3, NSRD1	<i>Gjb2</i>	Cx26
<i>GJB3</i>	CX31	DFNA2, EKV	<i>Gjb3</i>	Cx31
<i>GJB4</i>	CX30.3		<i>Gjb4</i>	Cx30.3
<i>GJB5</i>	CX31.1		<i>Gjb5</i>	Cx31.1
<i>GJB6</i>	CX30	DFNA3, ED2, EDH, HED	<i>Gjb6</i>	Cx30
<i>GJB7</i>	CX25		–	–
<i>GJA1</i>	CX43	ODDD, ODOD, SDTY3	<i>Gja1</i>	Cx43
<i>GJA3</i>	CX46	CZP3	<i>Gja3</i>	Cx46
<i>GJA4</i>	CX37		<i>Gja4</i>	Cx37
<i>GJA5</i>	CX40		<i>Gja5</i>	Cx40
–	–		<i>Gja6</i>	Cx33
<i>GJA8</i>	CX50	CAE1, CZP1, CAE	<i>Gja8</i>	Cx50
<i>GJA9</i>	CX59		–	–
<i>GJA10</i>	CX62		<i>Gja10</i>	Cx57
<i>GJC1</i>	CX45		<i>Gjc1</i>	Cx45
<i>GJC2</i>	CX47	SPG44	<i>Gjc2</i>	Cx47
<i>GJC3</i>	CX30.2/31.3		<i>Gjc3</i>	Cx29
<i>GJD2</i>	CX36		<i>Gjd2</i>	Cx36
<i>GJD3</i>	CX31.9		<i>Gjd3</i>	Cx30.2
<i>GJD4</i>	CX40.1		<i>Gjd4</i>	Cx39
			<i>Gje1</i>	Cx23

Modified from Beyer and Berthoud [8] and from <http://www.genenames.org/genefamilies/GJ>. Cx has been generally used as an abbreviation for Connexin. Many of the synonyms refer to genetic diseases or syndromes linked to mutations of the connexins.

**Table 2**

*Drosophila melanogaster* innexins.

Gene symbol	Gene name	Synonyms
<i>inx2</i>	Innixin 2	kropf, prp33, l(1)G0043, l(1)G0035, l(1)G0118
<i>inx3</i>	Innixin 3	<i>Dm-Inx3</i> , inx-3
<i>inx5</i>	Innixin 5	
<i>inx6</i>	Innixin 6	prp6
<i>inx7</i>	Innixin 7	prp7
<i>ogre</i>	Optic ganglion reduced	l(1)ogre, inx1
<i>shakB</i>	<i>Shaking B</i>	Pas, shak-B, R-9-29, shB, R9-29, <i>inx8</i>
<i>zpg</i>	Zero population growth	<i>inx4</i>

Modified from <http://flybase.org/reports/FBgg0000112.html> and based on Abascal and Zardoya [1]. These proteins are also identified as Passover protein homologs ([http://www.membranetransport.org/other\\_family.php?ffID=Innixin&oOID=dme11](http://www.membranetransport.org/other_family.php?ffID=Innixin&oOID=dme11)).

**Table 3***Caenorhabditis elegans* innexins.

Locus	Sequence	Synonyms
<i>inx-1</i>	C16E9.4	CELE_C16E9.4, <i>opu-1</i> , pcr55
<i>inx-2</i>	F08G12.10	CELE_F08G12.10, XL914, <i>opu-2</i>
<i>inx-3</i>	F22F4.2	<i>opu-3</i> , CELE_F22F4.2
<i>inx-5</i>	R09F10.4	CELE_R09F10.4, <i>opu-5</i>
<i>inx-6</i>	C36H8.2	CELE_C36H8.2, <i>opu-6</i>
<i>inx-7</i>	K02B2.4	CELE_K02B2.4, <i>opu-7</i>
<i>inx-8</i>	ZK792.2	<i>opu-8</i> , CELE_ZK792.2
<i>inx-9</i>	ZK792.3	<i>opu-9</i> , CELE_ZK792.3
<i>inx-10</i>	T18H9.5	<i>opu-10</i> , CELE_T18H9.5
<i>inx-11</i>	W04D2.3	CELE_W04D2.3, <i>opu-11</i>
<i>inx-12</i>	ZK770.3	<i>opu-12</i> , <i>let-368</i> , CELE_ZK770.3
<i>inx-13</i>	Y8G1A.2	CELE_Y8G1A.2, <i>let-585</i> , <i>opu-13</i>
<i>inx-14</i>	F07A5.1	CELE_F07A5.1, <i>opu-14</i>
<i>inx-15</i>	R12E2.9	<i>opu-15</i> , CELE_R12E2.9
<i>inx-16</i>	R12E2.5	CELE_R12E2.5, <i>opu-16</i>
<i>inx-17</i>	R12E2.4	<i>opu-17</i> , CELE_R12E2.4, 1E733
<i>inx-18</i>	C18H7.2	<i>opu-18</i> , CELE_C18H7.2
<i>inx-19</i>	T16H5.1	<i>nsy-5</i> , CELE_T16H5.1, <i>opu-19</i>
<i>inx-20</i>	T23H4.1	CELE_T23H4.1, <i>opu-20</i>
<i>inx-21</i>	Y47G6A.1	CELE_Y47G6A.1, <i>opu-21</i>
<i>inx-22</i>	Y47G6A.2	CELE_Y47G6A.2
<i>unc-9</i>	R12H7.1	CELE_R12H7.1
<i>unc-7</i>	R07D5.1	<i>unc-124</i> , <i>unc-12</i> , CELE_R07D5.1
<i>eat-5</i>	F13G3.8	CELE_F13G3.8
<i>che-7</i>	F26D11.10	<i>inx-4</i> , CELE_F26D11.10

Modified from [http://www.wormbase.org/resources/gene\\_class/inx#01-10](http://www.wormbase.org/resources/gene_class/inx#01-10), [http://www.wormbase.org/species/c\\_elegans/gene/WBGene00006749#0-9g-3](http://www.wormbase.org/species/c_elegans/gene/WBGene00006749#0-9g-3), [http://www.wormbase.org/species/c\\_elegans/gene/WBGene00006747#0-9g-3](http://www.wormbase.org/species/c_elegans/gene/WBGene00006747#0-9g-3), [http://www.wormbase.org/species/c\\_elegans/gene/WBGene00001136#0-9g-3](http://www.wormbase.org/species/c_elegans/gene/WBGene00001136#0-9g-3), and [http://www.wormbase.org/species/c\\_elegans/gene/WBGene00000488#0-9g-3](http://www.wormbase.org/species/c_elegans/gene/WBGene00000488#0-9g-3).

**Table 4**

*Hirudo verbana* innexins.

Symbol	Name
<i>inx1</i>	Innexin 1
<i>inx2</i>	Innexin 2
<i>inx3</i>	Innexin 3
<i>inx4</i>	Innexin 4
<i>inx5</i>	Innexin 5
<i>inx6</i>	Innexin 6
<i>inx7</i>	Innexin 7
<i>inx8</i>	Innexin 8
<i>inx9A</i>	Innexin 9A
<i>inx9B</i>	Innexin 9B
<i>inx10</i>	Innexin 10
<i>inx11A</i>	Innexin 11A
<i>inx11B</i>	Innexin 11B
<i>inx12</i>	Innexin 12
<i>inx13</i>	Innexin 13
<i>inx14</i>	Innexin 14
<i>inx15</i>	Innexin 15
<i>inx16</i>	Innexin 16
<i>inx17</i>	Innexin 17
<i>inx18</i>	Innexin 18
<i>inx19</i>	Innexin 19

Based on Kandarian et al. [28].

**Table 5**

Pannexins.

Symbol	Name	Synonyms
PANX1	Pannexin 1	MRS1, UNQ2529, PX1
PANX2	Pannexin 2	hPANX2, PX2
PANX3	Pannexin 3	Px3

Modified from <http://www.genenames.org/cgi-bin/genefamilies/set/228> and <http://www.genenames.org/genefamilies/PANX>