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Peptide-based Targeting of Connexins and Pannexins for Therapeutic Purposes

Abstract

Introduction: Connexin and pannexin (hemi)channels play an important role in paracrine and autocrine signalling pathways. The opening of these cellular pores is linked to a wide range of diseases. Therefore, pharmacological closing of connexin and pannexin (hemi)channels seems a promising therapeutic strategy. However, available inhibitors of connexin and pannexin (hemi)channels cope with recurring problems concerning selectivity, specificity, stability and/or solubility.

Areas covered: A number of peptides that mimic specific regions in the native sequence of connexins and pannexins have the potential to overcome some of these hurdles. In this paper, an overview is provided on these peptide-based inhibitors of connexin and pannexin (hemi)channels for therapeutic purposes.

Expert opinion: Peptide mimetics can become valuable tools in the treatment of connexin-related and pannexin-related diseases, provided that available peptides are optimised, and new peptide mimetics are designed based on knowledge of the mechanisms underlying the gating control of connexin and pannexin (hemi)channels.

Key words: connexins, (hemi)channel inhibition, pannexins, peptide mimetics.

1. Introduction

In human, and in vertebrates in general, intercellular communication is mediated by gap junctions, which facilitate transport of small molecules and ions, such as glutamate, adenosine triphosphate (ATP) and calcium, between the cytoplasm of opposing cells [1]. Gap junctions are formed by the docking of 2 connexin (Cx) hemichannels, each consisting of 6 transmembrane proteins of the Cx family (Figure 1) [2]. Over the years, it has become clear that Cx hemichannels are not merely building blocks of gap junctions but can also function as single membrane channels. Cx hemichannels enable a similar exchange of small molecules and ions as gap junctions, though between the cytosol of an individual cell and its extracellular environment (Figure 1) [3]. Today, 21 Cx family members have been identified in human, named according to their molecular weight. All Cx subtypes share a common topology consisting of 4 transmembrane domains, 2 extracellular loops, 1 cytoplasmic loop and a cytoplasmic *N*- and *C*-terminal tail (Figure 2), and undergo post-translational modifications such as phosphorylation, *S*-nitrosylation and ubiquitination [2], [4]. These post-translational modifications are key mechanisms in Cx hemichannel regulation. In this context, phosphorylation of the *C*-terminal tail by protein kinase A and C alters Cx hemichannel permeability [5], [6]. Undocked Cx hemichannels are, in contrast to gap junctions, generally closed. However, their activation can be triggered by pathological stimuli, such as oxidative and mechanical stress, a decrease in extracellular calcium concentration or an elevation of intracellular calcium concentration [7], [8].

In 2000, a new protein family with a similar topological structure as Cx was identified in vertebrates, called pannexin (Panx) proteins (Figure 3). The Panx family comprises of 3 subtypes, namely Panx1, Panx2 and Panx3, named according to the timeline of their discovery. Like Cxs, Panx proteins also oligomerise into multimeric channels (Figure 1) [9]. However, extensive glycosylation at the second extracellular loop prevents the formation of gap junctions

[10]. Hence, they are called Panx channels, and not Panx hemichannels. Post-translational modifications such as *N*-glycosylation, *S*-nitrosylation and phosphorylation regulate Panx trafficking and opening [4]. Panx channels open under both physiological and pathophysiological conditions [11], [12]. In physiological conditions, Panx-mediated release of ATP and potassium contributes to normal homeostatic cell function. In certain pathological pathways, interactions between Panx channels and purinergic receptors can lead to high levels of extracellular ATP and potassium, and an influx of calcium resulting in inflammasome activation [12], [13].

Both Cx and Panx (hemi)channels contribute to paracrine and autocrine signalling pathways during inflammation and cell death through the release of ATP and other signalling molecules [14]–[19]. These channel types are therefore considered emerging targets in the treatment of various diseases (Table 1) [20]–[22]. Several chemical-based, RNA-based as well as antibody-based blockers are at hand. However, most of these compounds show non-specific and/or non-selective characteristics by inhibiting multiple Cx species or Cx hemichannels, gap junctions, Panx channels and/or other targets at once, which in some cases can lead to increased cell death [23], [24]. A group of peptide-based inhibitors was proven to be an exception, as a number of peptide mimetics showed specific and selective channel inhibition [25]. These peptides mimic channel-specific regions of the native protein sequence and can thereby potentially alter Cx or Panx (hemi)channel properties. Cx43 and Panx1 have been the main focus of peptide mimicry due to their high abundance and expression in a wide range of human tissues [26], [27]. In this paper, an overview is provided on peptide mimetics targeting Cx and Panx (hemi)channels and their potential use in the treatment of a Cx-related and Panx-related diseases, with particular attention being paid to Cx43 and Panx1.

2. Connexin peptide mimetics

2.1. Peptides mimicking sequences of the extracellular loops

The extracellular loop of Cx hemichannels appeared to be the most favourable target for the design of more selective inhibitors due to their accessibility in contrast to their full channel counterparts. Nevertheless, peptides containing the conserved motives QPG and SHVR of the first extracellular loop and the SRPTEK motif of the second extracellular loop still interfered with the formation of gap junctions [28]. This led to the development of currently known peptide mimetics ⁴³Gap26, ^{37,40}Gap26, ³²Gap27, ⁴⁰Gap27, ⁴³Gap27 and ⁴³Peptide5 [28]. Of note, the superscript in the nomenclature of these peptide analogues refers to the Cx subtype they are targeting.

The conserved SHVR motif of the first extracellular loop is incorporated in the sequence of Gap26 peptide mimetics. The 2 slightly different sequences are both categorised under the Gap26 code, one targeting Cx37 and Cx40, and the other targeting only Cx43 (Table 2 and Figure 2) [29], [30]. Cells treated with either of these Gap26 peptides showed Cx hemichannel inhibition within minutes. However, upon longer exposure times, decreased gap junction activity was equally observed [28], [31]. This effect may occur due to the high turn-over rate of Cx proteins, through which peptides can bind to the extracellular loops of a new Cx hemichannel before assembling into gap junctions [29]. Gap26 has been suggested to inhibit Cx hemichannels by shifting the voltage dependent opening to higher voltages, yet solid substantiating data are lacking [31].

There are 3 Gap27 peptides, each targeting different Cx types, namely Cx32, Cx40 and Cx43 [28], [30], [32]. These peptides mimic the conserved SRPTEK motif of the second extracellular loop, but have the same time-dependent effect on gap junction activity as Gap26 (Table 2 and

Figure 2) [31]. $^{43}\text{Gap27}$ and $^{40}\text{Gap27}$ were shown to decrease osteoclastic activity and angiogenesis in mouse retina, respectively [31], [33].

Like Gap27, Peptide5 contains the SRPTEK motif. However, the mimicked sequence of Peptide5 is shifted in the direction of the *N*-terminal tail in comparison to that of Gap27 (Table 2 and Figure 2) [28]. Peptide5 inhibits Cx43 hemichannels at a concentration of 5-10 μM , yet incubation at higher concentration (100 μM or higher) also leads to inhibition of gap junctions [34]. *In vivo* tests in mice have shown that Peptide5 reduces tissue damage after spinal cord injury and attenuates the permeability of vessels after retinal ischemia/reperfusion [35]. The exact mechanism of Cx43 hemichannel inhibition by Peptide5 remains unravelled, but the peptide is currently being tested in preclinical trials as PeptagonTM (OcuNexus Therapeutics Inc.) for use in the treatment of diabetic retinopathy [35].

2.2. Peptides mimicking sequences of intracellular regions

The interaction between the cytoplasmic loop and *C*-terminal tail mediates the gating mechanism of Cx hemichannels and gap junctions. Gap junctions are in an open state when there is no interaction between the *C*-terminal tail and cytoplasmic loop, while such interaction is critical for Cx hemichannel opening [36]. Experiments in HeLa cells transfected with Cx43 showed that Cx hemichannels, which lack their *C*-terminal tails, can be reopened when exposed to a peptide named CT10 peptide, also known as Cx43CT (Table 2 and Figure 2). CT10 reproduces the last 10 amino acids of the *C*-terminal tail of Cx43. Inhibition of Cx43-mediated ATP release by a peptide mimetic, called TAT-L2, pinpointed its mimicked L2 region (amino acid 119 to 144) as an essential sequence of the cytoplasmic loop in the interaction with the *C*-terminal tail (Table 2 and Figure 2). Moreover, amino acids H126 and I130 were proven to be essential for the binding of the L2 region to the *C*-terminal tail, as peptides mutated at these amino acid positions lack the inhibitory capacity of TAT-L2 [36]. This interaction is of utmost importance for the regulation of Cx43 hemichannel opening, but an additional trigger is

required, such as mechanical stress, decrease of extracellular calcium concentration or moderate elevations in intracellular calcium concentrations [7], [8], [37]. To date, 2 peptides mimicking the L2 region are available, namely ⁴³Gap19 and ³²Gap24 (Table 2 and Figure 2).

⁴³Gap19 inhibits Cx43 hemichannel currents by binding to the C-terminal tail, thereby preventing the cytoplasmic loop/C-terminal tail interaction, although not to the full extent. Nonetheless, ⁴³Gap19 has the advantage of being a selective inhibitor, as it does not affect gap junction or Panx1 channel activity [38], [39]. *In vitro* and *in vivo* tests showed that ⁴³Gap19 is capable of inhibiting Cx43 hemichannels in acute and chronic liver disease [39]–[41]. It also protects against myocardial ischemia/reperfusion injury [42].

³²Gap24 is a peptide that mimics a 13 amino acid long stretch of the L2 region of Cx32 (Table 2 and Figure 2) [8]. *In vitro* studies showed that Cx32 hemichannel-mediated ATP release is inhibited by ³²Gap24 at concentrations of 17 μ M without affecting gap junctions [8]. However, ³²Gap24 does inhibit Panx1 channels at higher concentrations [43]. *In vivo* administration of ³²Gap24 to mice resulted in alleviation of non-alcoholic steatohepatitis, liver fibrosis and acetaminophen-induced liver injury [39]–[41]. Its mode-of-action is still unknown but might involve a mechanism similar to that of ⁴³Gap19.

Peptides targeting intracellular regions of Cxs need to access the intracellular environment. Cell-penetrating peptides (CPP), such as the TAT-peptide, an oligoarginine tag and Xentry peptide, have been anchored to Cx-derived peptide sequences in order to enhance the uptake into the cell *via* endocytosis [44], [45]. ⁴³Gap19 can enter the cell on its own due to the KKFK cell-translocation motif of the L2 region. Nonetheless, comparison of the IC₅₀ (half maximal inhibitory concentration) of ⁴³Gap19 itself (47 μ M) and TAT-⁴³Gap19 (7 μ M) for the inhibition of ATP release in glioma cells showed that the entry of ⁴³Gap19 into the cell, and its effect accordingly, might be improved by linking to a TAT-tag. These results emphasise the importance of CPPs in the design of peptide mimetics targeting intracellular domains [42].

Importantly, the CPP itself can have effects on the target as suggested for the TAT-tag [46]. *In vivo* tests showed increased toxicity of TAT-Gap19 when administrated in higher concentrations [46].

The length of the C-terminal tail differs strongly among the different Cx subtypes. In this context, Cx26 has a C-terminal tail merely consisting of 10 amino acids, while Cx62 has a C-terminal tail of more than 250 amino acids [47], [48]. Mimicry of the C-terminal region can therefore result in more specific peptides. However, other proteins, such as tubulin, zonula-occludens 1 (ZO-1) or β -Catenin, are known to interact with the C-terminal tail of Cx43. The interference of the peptide mimetics with the interaction between the C-terminal tail and the other proteins might consequently alter other cellular pathways [49].

All 5 available peptides mimicking the C-terminal tail are derived from Cx43. CT10 and CT9 mimic the last 10 or 9 amino acids of the C-terminal tail, respectively, while the Src homology 3 binding domain (SH3) of Cx43 is reproduced by a peptide named Δ SH3 (Table 2 and Figure 2) [36], [50]. CT10, CT9 as well as Δ SH3 promote a “ready-to-open” conformational state of Cx hemichannels and are thus not suitable as therapeutics. Nevertheless, they are interesting tools to investigate the function of Cx hemichannels and gap junctions [36], [50].

The juxtamembrane 2 (JM2) peptide, which mimics a sequence close to the fourth transmembrane domain, inhibits trafficking of Cx43 to the cell surface and hence reduces Cx hemichannel-mediated transport (Table 2 and Figure 2) [51]. However, a decrease in Cx hemichannel abundance at the cell surface also affects gap junction formation and might therefore lower cell viability [24], [51].

α CT1 mimics the last 9 amino acids of Cx43 and is linked to an antennapedia sequence that facilitates cellular internalisation of the peptide mimetic (Table 2 and Figure 2). The interaction between Cx43 and the PDZ-domain of ZO-1, a region that is suggested to be involved in the

regulation of Cx trafficking and gap junction assembly, is disrupted by α CT1 [52], [53]. This interference leads to increased gap junction plaque formation and decreased Cx hemichannel activity. α CT1 is currently in clinical trials as Granexin™ (FirstString Research Inc.) for the treatment of diabetic foot ulcer closure, since the peptide mimetic was reported to accelerate wound healing, while reducing inflammation and scarring [54].

3. Pannexin peptide mimetics

3.1. Peptides mimicking sequences of the extracellular loops

Panx-related research mainly focuses on Panx1. In 2006, a series of peptides, containing 8 to 21 consecutive amino acids of the native Panx1 sequence, were tested *in vitro*. Through measurements of ATP-evoked dye uptake and current measurements, ¹⁰Panx1 was identified as a potent Panx1 inhibitor (Table 3 and Figure 3) [13]. Since then, the 10 amino acid long stretch of the first extracellular loop has been used to prove that inhibition of Panx1 channels prevents inflammation-induced neuron cell death in the enteric nervous system, hereby identifying Panx1 as a potential new target for inflammatory bowel disease treatments [55]. Results of animal studies also confirmed the significance of Panx1 inhibitors, such as ¹⁰Panx1, in the treatment of drug-induced liver toxicity [56].

Another set of 5 peptides, namely PanxE1a, PanxE1b, PanxE1c, PanxE2a and PanxE2b (Table 3 and Figure 3), mimicking sequences of the 2 extracellular loops of Panx1, was synthesised and screened *in vitro*. In spite of the differences in sequence (a longer sequence that is shifted towards the *N*-terminal end), PanxE1b inhibited Panx1 channel currents to the same extent as ¹⁰Panx1. The efficiency of the scrambled versions of ¹⁰Panx1 and PanxE1b was tested against that of the native sequences. The observed decrease in Panx1 channel inhibition of the scrambled version in comparison to the native sequence suggests a sequence specific inhibition, which substantiates the value of peptide mimetics of the native sequence. Regardless of this

sequence-specific inhibition, both ¹⁰Panx1 and PanxE1b inhibit Cx46 hemichannels as well [43].

Targeting the 2 extracellular loops is the most straightforward approach for the design of Panx1 inhibitory peptide mimetics. Over the years, research has proven the involvement of several amino acids of the extracellular loops in the activation and inhibition mechanisms of Panx1 channels. Peptide mimetics can also reach these target sequences more easily due their extracellular localisation [57]–[61]. Apart from post-translational modification sites, such as the glycosylation site at residue N254, the extracellular loops also contain interesting target sites for peptide mimetics [10]. An example is the binding site of extracellular ATP, which is known to block Panx1 channels at high concentrations [58].

3.2. Peptides mimicking sequences of the intracellular regions

Although mimicry of the extracellular loops seems promising, efforts have also been made to design peptides based on the intracellular regions of Panx1. To identify the essential amino acid motifs in α 1 adrenoreceptor (α 1DAR)-mediated activation of Panx1 channels, 2 novel peptides were synthesised, called IL1 and IL2 (Table 3 and Figure 3). These peptides mimic sequences of the intracellular loop of mouse Panx1, which are to a great extent conserved in human. Only IL2 significantly decreased phenylephrine-induced contractile responses and inhibited ATP release in murine pressurised thoracodorsal arteries. Thereafter, clusters of 3 to 4 consecutive amino acids of the IL2 sequence were substituted by alanines. This so-called “Ala-scan” was used to determine which amino acids are important for activation and thus of relevance for inhibition. Only the cells co-transfected with α 1DAR and a Panx1 mutated at the YLK motif showed no phenylephrine stimulation of Panx1 channel currents, identifying this 3 amino acid long stretch as a possible target for inhibition of α 1DAR-mediated activation of Panx1 channels [62].

A TAT-like sequence was anchored onto the sequences of both IL1 and IL2 to facilitate entry into the cell. In order to exclude the tag's influence on the channel inhibition, the sequence on its own was tested and showed no significant effect on ATP release and other phenylephrine-induced responses. There was also no significant effect observed for the scrambled version of IL2, which confirms sequence-specific inhibition, as was seen for ¹⁰Panx1 and PanxE1b [43], [62]. In comparison with ¹⁰Panx1, the intracellular loop-derived peptide was less effective in reducing the phenylephrine-induced atrial constriction. Nonetheless, these data suggest that inhibitors, such as IL2 or other Panx1 peptide mimetics targeting the intracellular YLK sequence, should be considered as potential therapeutics for blood pressure disorders [62].

The C-terminal tail contains multiple interesting target sequences, such as an auto-inhibitory region near the caspase cleavage site [63]. The discovery that the cleavage of the C-terminus by caspases is sufficient to activate Panx1 channels gave rise to the hypothesis of a ball-and-chain mechanism, in which the C-terminal tail functions as a Panx1 channel blocker by interacting with the pore. The removal of a group of 12 specific residues immediately downstream of the cleavage site appeared to be critical for the activation by caspase 3. Hence, the question arose whether this sequence on its own could block Panx1 channels. First, a peptide mimicking only the auto-inhibitory region was tested using whole-cell recordings of Panx1 channel currents, but no inhibitory effect was detected (Table 3). Subsequently, 2 larger Panx1-derived constructs were synthesised. One mimicked the complete C-terminal tail (hPanx1(Ct)) and was linked to an enhanced green fluorescent protein to ensure entry into the cell (Table 3 and Figure 3). The other was a FLAG-tagged construct of the C-terminal tail up to amino acid 391 (hPanx1(Ct) Δ 391) (Table 3 and Figure 3). Inhibition of Panx1 currents by both constructs indicates that there are important activation regions located more upstream in the sequence. Additional tests, using the purified C-terminal region in a cell-free system, substantiated channel blocking by the intracellular C-terminal tail. Although amino acid

stretches of more than 50 residues are typically not categorised as peptides, these results still highlight the potential of developing C-terminal-derived peptides for the treatment of diseases in which Panx1-mediated signalling is implicated, such as cancer and auto-immune disorders [63].

Another interesting target of the Panx1 C-terminal tail is the Src Family Kinase (SFK) consensus-like sequence containing a putative phosphorylation site at residue Y308. As phosphorylation is one of the mechanisms of Panx1 activation and SFK activity increases in hippocampal neurons during ischemia, it is likely that anoxia-induced Panx1 channel opening in neurons is regulated by this family of kinases. Panx₃₀₅₋₃₁₈ was synthesised and anchored to a TAT-tag in order to test if peptides containing the putative phosphorylation site could prevent anoxia-induced Panx1 channel opening (Table 3 and Figure 3). Bath application of TAT-Panx₃₀₅₋₃₁₈ showed decreased anoxic depolarisation of pyramidal neurons, thereby confirming the hypothesis. To exclude effects on the entire brain slice and to ascertain specificity of the phosphorylation site in single neurons, the peptide was also tested in whole-cell patch-clamp recordings. Measurements in these hippocampal neurons showed extensive blocking of the anoxic depolarisation currents. Inclusion of the TAT-tag itself in the patch pipettes in turn excluded interference of the sequence on the reported inhibition by TAT-Panx₃₀₅₋₃₁₈. Inhibition of Panx1 channels through targeting of the phosphorylation site was put forward as a potential new treatment of pathological neuronal depolarisation. Peptides, such as the interfering peptide TAT-Panx₃₀₅₋₃₁₈, could therefore be promising new tools in the prevention of cell death and ischemic core expansions after a stroke. [64].

4. Conclusion and Expert opinion

Cx and Panx (hemi)channels have a central role in the underlying mechanisms of various diseases associated with inflammation and cell death (Table 1). Many efforts have been made over the past 2 decades to identify potent inhibitors of these cellular pores, yet undesirable

inhibitor characteristics such as non-selective and/or non-specific inhibition often impede therapeutic development [64]. Cx mimetic peptides Gap26 and Gap27 not only inhibit Cx hemichannels, but also inhibit gap junctions in a time-dependent way [28], [31]. Peptide5, although also reported to affect gap junction activity, has reached the preclinical stage for the treatment of diabetic retinopathy as Peptagon™ (OcuNexus Therapeutics Inc.) [34]. As this peptide only inhibits gap junctions at higher concentrations, intravitreal injection was selected as the route of administration to have better control over the final concentration of the peptide in the target tissue. Despite its non-selective properties, Peptide5 still qualifies as a potential therapeutic in the treatment of Cx hemichannel-related disease [35].

Nevertheless, peptide mimetics of the intracellular regions seem more promising for several reasons. The amino acid sequences of the cytoplasmic loop and the C-terminal tail are not as conserved between the different Cx family members compared to the amino acid sequences of the extracellular loops. These regions differ considerably between the different Cx subtypes and are therefore potential targets in the design of more Cx-specific peptide mimetics [47], [48]. Furthermore, specific intramolecular interactions between the cytoplasmic loop and the C-terminal tail have been reported to control opening of Cx hemichannels, while the opposite holds true for gap junctions [36]. Targeting the interaction regions might therefore provide a potential solution for the selectivity problems of currently available inhibitors [36]. ³²Gap24 and ⁴³Gap19 have been reported to inhibit Cx hemichannels in several cell types without affecting gap junctions by interacting with the last 10 amino acids of the C-terminal tail. Nonetheless, ⁴³Gap19 is not able to completely inhibit Cx43 hemichannels, which can be possibly linked to the involvement of the SH3 binding domain that binds to the cytoplasmic loop [50]. This highlights the complexity of the cytoplasmic loop/C-terminal tail gating mechanism and its inhibition. Nevertheless, mimicking the C-terminal tail has proven to be promising in the case of the α CT1 peptide, which is currently being tested in clinical trials under

the name of Granexin™ (FirstString Research Inc.) for the treatment of diabetic foot ulcers [54]. A disadvantage of mimicry of the C-terminal tail lies with its interaction with several Cx-binding proteins [49]. Interference of Cx-based peptides with these interactions and their associated pathways must be excessively assessed to avoid possible side and/or adverse effects. The optimisation of Cx peptide mimetics of the intracellular regions also deserves further scrutiny. Selecting suitable CPPs that facilitate entry into the cell is an important aspect in this respect, as it can potentially boost the effects of peptides due to an increased accessibility of target sites [42], [44]. However, a possible effect of the CPP itself at the cellular level should always be taken into account during the selection process, since increased toxicity of compounds have been reported when linked to this kind of tags [46]. To avoid using a CPP, it might be feasible to design peptide mimetics that can enter the cell through open Cx hemichannels. This mechanism of internalisation was suggested for ³²Gap24, as it enters the cell without a cell-translocation motif in its sequence or CPP [8].

With Cx mimetic peptides already in clinical trials, it is clear that research on Panx channel inhibitors still has a long way to go. Peptides that mimic intracellular and extracellular Panx sequences have been reported to inhibit Panx1 channels, but specificity problems persist. New insights into the gating mechanisms of Panx1 channels enables a more rational design of peptide mimetics in the future by targeting amino acids or motifs essential for the channel opening and/or closing. For the extracellular loops, great promise lies in targeting the amino acids that are part of the extracellular binding site of ATP [58]. Part of this area was already covered by peptides such as ¹⁰Panx1 and PanxEb1. At the time of their introduction, this knowledge was lacking, but now can be used to optimise ¹⁰Panx1 to create a more specific inhibitor by shifting or expanding the sequence. Another potential approach can rely on the design of peptide mimetics that are able to interact with possible allosteric binding sites within the extracellular loops and/or transmembrane regions of Panx1, including the binding site of extracellular ATP

[65]. These Panx1 peptide mimetics could decrease Panx1 channel activity by allosteric modulation.

In summary, Cx and Panx peptide mimetics have the potential to overcome some of the hurdles other Cx and Panx (hemi)channel inhibitors are facing, provided that available peptides are optimised and new peptide mimetics are designed based on knowledge of the mechanisms underlying the gating control of Cx and Panx (hemi)channels. At present, most of these mechanisms are still unclear. The pharmacological characterisation of peptide mimetics is also crucial for further optimisation, yet experiments determining the pharmacological properties of these compounds are scarce. This equally applies to the crystal structures of the different Cx and Panx (hemi)channels. The crystal structure of Cx26 was published more than a decade ago, yet still is the only one in its kind thus far [66]. Recently, the cryo-EM structure of Panx1 was characterised [67], [68]. The structure of Cx26 shows that the *N*-terminal tails of the Cx proteins form the pore funnel of the resulting channel. Therefore, no peptide mimetics have been developed to mimic this intracellular region [66]. The *N*-terminal tail of Panx1, on the other hand, is of significant importance for its gating mechanism, but until today this area remains unexplored in the field of peptide mimicry [69]. Cx and Panx research mainly focused on Cx32, Cx43 and Panx1. Nevertheless, Panx3 has been identified as a possible target for the treatment of osteoarthritis, hence peptide-based inhibitors mimicking Panx3 could represent promising therapeutics (Table 1) [70]. The same might apply for Cx37 and Cx26 peptide mimetics, which represent potential drugs for the treatment of atherosclerosis, and skin disease and deafness, respectively (Table 1) [21], [71]. It can be anticipated that further exploration of these areas will open great perspectives for large patient populations worldwide in the years to come.

Highlights box: Priorities to be set regarding future development of peptide-based inhibitors of Cx and Panx (hemi)channels.

- Optimisation of existing peptides to improve stability and increase potency and selectivity
- Incorporation of amino acids and/or motifs important in gating mechanisms of Cxs and Panxs into the sequence of new peptide mimetics to obtain a more rational design approach
- Elucidation of gating mechanisms
- Pharmacological characterisation of peptide mimetics
- Determination of crystal and/or Cryo-EM structures

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Conflict of interest

The authors declare that the research was conducted in the absence of any commercial or financial relationship that could be construed as a potential conflict of interest.

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Table 1: Diseases linked to the opening of Cx and Panx (hemi)channels

Disease	Cx/Panx	Reference
Alzheimer's disease	Cx43, Panx1	[72]
Demyelination	Panx1	[73]
Epilepsy	Cx36, Panx1	[74], [75]
Encephalomyelitis	Panx1	[76]
Glioma	Panx1, Panx2	[77], [78]
Ischemia/stroke	Panx1, Panx2, Cx43	[21], [79]
Migraine	Panx1	[80]
Overactive bladder	Panx1	[81]
Glaucoma	Panx1	[82]
Crohn's disease/colitis	Panx1	[55]
Atherosclerosis	Cx37, Panx1	[21]
Cardiomyopathy	Cx43	[83]
Hypertension	Panx1	[21]
Myocardial ischemia/reperfusion	Cx43	[21]
Inflammation	Cx32, Cx43	[42], [84]
Microbial infection	Cx43, Panx1	[85], [86]
HIV/AIDS	Cx43, Panx1	[87], [88]
Multiple sclerosis	Cx43	[89]
Acute liver failure	Cx32, C43, Panx1	[39], [56]
Liver fibrosis and cirrhosis	Cx43	[40]
Non-alcoholic steatohepatitis	Cx32, Cx43, Panx1	[41], [90], [91]
Diabetes	Cx43, Panx1	[72]
Osteoarthritis	Panx3	[70]
Melanoma	Panx1	[92]
Non-syndromic deafness	Cx26	[71]
Syndromic deafness associated with skin disorders	Cx26	[71]

Cx, connexin; Panx, pannexin

Table 2: Cx peptide mimetics

Peptide	Target sequence	Cx	Target	Inhibits	Cell type	Reference
^{37,40} Gap26	VCYDQAFPISHIR	Cx37 Cx40	EL1	HC/GJ	Rat hepatocytes, HAEC	[30], [93]
⁴³ Gap26	VCYDKSFPISHVR	Cx43	EL1	HC/GJ	EVC304 human epithelial bladder cancer cells, chick corneal epithelial cells, chick neural retina cells, COS- 1, chick myocytes, HAEC	[28], [29], [94], [95]
³² Gap27	SRPTEKTVFT	Cx32	EL2	HC/GJ	Chick myocytes, xenopus oocytes	[28], [32]
⁴⁰ Gap27	SRPTEKNVFIV	Cx40	EL2	HC/GJ	HAEC, human endothelial cells	[33], [93]
⁴³ Gap27	SRPTEKTIFII	Cx43	EL2	HC/GJ	Rat osteoclasts, mice dendritic cells, A7r5 rat aortic smooth muscle cells, ECV304 human epithelial bladder cancer cells	[8], [96]– [98]
⁴³ Peptide5	VDCFLSRPTEKT	Cx43	EL2	HC/GJ	Rat neural cells, rat astrocytes, chick myocytes	[28], [34], [99]
⁴³ L2	DGANVDMHLKQIEIK KFKYGIEEHGK	Cx43	CL	HC	BCEC	[36]
⁴³ Gap19	KQIEIKKFK	Cx43	CL	HC	Rat C6 cells, pig cardiomyocytes, mouse hepatocytes	[39]–[42]
³² Gap24	GHGDPLHLEEVKC	Cx32	CL	HC	ECV304 human epithelial bladder cancer cells, rat hepatocytes, Xenopus oocytes	[8], [39], [41], [43]
⁴³ CT10 (Cx43CT)	SRPRPDDLEI	Cx43	CT	GJ	Rat C6 cells	[42]
⁴³ CT9	RPRPDDLEI	Cx43	CT	GJ	Rat smooth muscle cells, BCEC, HeLa cells	[50], [99]
⁴³ ΔSH3	SSPTAPLSPMSPPG	Cx43	CT	GJ	BCEC, HeLa cells	[50]
⁴³ JM2	VFFKGVKDRVKGRSD	Cx43	CT	HC/GJ	HeLa cells	[51]
⁴³ αCT1	RQPKOWFPNRRKPWK KRPRPDDLEI	Cx43	CT	HC	Rat cardiomyocytes, HeLa cells	[53], [54]

Cx, Connexin; HC, hemichannel; GJ, gap junction; EL, extracellular loop; CL, cytoplasmic loop; CT, C-terminal tail; BCEC, bovine corneal endothelial cells; HAEC, human aortic endothelial cells; COS-1, CV-1 origin carrying SV40; HeLa, Henrietta Lacks

Table 3: *Panx1* peptide mimetics

Peptide	Target sequence	Target	Inhibits Panx1 channels	Cell type	Reference
¹⁰ Panx1	WRQAAFVDSY	EL1	Yes	HEK293 cells, rat CA1 pyramidal neurons, xenopus oocytes, mice smooth muscle cells	[13], [43], [62], [64], [92], [100]
Panx1-1	GTQISCFSPS	EL1	No	HEK293 cells	[100]
Panx1-2	CFSPSSFWRQAA	EL1	No	HEK293 cells	[100]
Panx1-3	QKNSLQSESGNLP	EL1	No	HEK293 cells	[100]
Panx1-4	YCWAAVQQKNSLQSESGNLP	EL1	No	HEK293 cells	[100]
Panx1-5	LRNDSTVDPDQFQ	EL2	No	HEK293 cells	[100]
¹⁴ Panx1	SGILRNDSTVDPDQF	EL2	No	HEK293 cells	[13], [100]
PanxE1a	AQEISIGTQIS	EL1	No	Xenopus oocytes	[43]
PanxE1b	SSFSWRQAAFVDS	EL1	Yes	Xenopus oocytes	[43]
PanxE1c	SESGNLPLWLHK	EL1	No	Xenopus oocytes	[43]
PanxE2a	SSLSDEFVCSIKS	EL2	No	Xenopus oocytes	[43]
PanxE2b	KSGILRNDSTVDPDQ	EL2	No	Xenopus oocytes	[43]
IL1	VGQSLWEISE	CL	No	Mice smooth muscle cells	[62]
IL2	KYPIVEQYLK	CL	Yes	HEK293 cells/ mice smooth muscle cells	[62]
Panx1 auto-inhibitory region	GKTPMSAEMREE	CT	No	HEK293 cells	[63]
hPanx1(Ct)	F299-C426	CT	Yes	HEK293 cells	[63]
hPanx1(Ct) Δ391	F299-E391	CT	Yes	HEK293 cells	[63]
Panx₃₀₅₋₃₁₈	LKVYEILPTFDVLH	CT	Yes	Rat CA1 pyramidal neurons	[64]

Panx, pannexin; EL, extracellular loop; IL, intracellular loop; Ct, C-terminal tail; CL; cytoplasmic loop, HEK, human embryonic kidney; CA1, cornu ammonis1

Figure 1: Conformation of Cx hemichannels, gap junctions and Panx channels: Gap junctions are formed by the assembly of 2 Cx hemichannels, which in turn consist of 6 Cx proteins. Like Cxs, Panxs also oligomerise into multimeric structures. Both Cx and Panx(hemi)channels function as single membrane channels that facilitate transport between the intracellular and extracellular environment, while gap junctions connect the cytoplasm of opposing cells.

Figure 2: Cx topology and mimetic peptides: Cxs consist of 4 transmembrane domains, 2 extracellular loops, 1 cytoplasmic loop and a cytosolic N- and C-terminal tail. The first extracellular loops of Cx37, Cx40 as well Cx43 are mimicked by peptides under the Gap26 code. Gap27 and Peptide5, on the other hand, mimic regions of the second extracellular loop. Gap27 targets Cx32, Cx40 and Cx43, while Peptide5 is used for Cx43 inhibition. JM2, ΔSH3, CT9, CT10, αCT mimic the C-terminal tail of Cx43 and Gap24 reproduces a sequence of the cytoplasmic loop of Cx32. Both L2 and Gap19 also mimic the cytoplasmic loop but of Cx43.

Figure 3: Panx topology and mimetic peptides of Panx1: Panxs consist of 4 transmembrane domains, 2 extracellular loops, 1 cytoplasmic loop and a cytosolic N- and C-terminal tail. Peptide mimetics ¹⁰Panx1 and PanxE1b reproduce sequences of the first extracellular loop of Panx1. There is only 1 peptide that mimics Panx1's cytoplasmic loop, namely IL2 and Panx₃₀₅₋₃₁₈, hPanx(Ct) as well as hPanx1(Ct)Δ391 mimic sequences of its C-terminal tail.