Conus Venom Peptide Pharmacology

Richard J. Lewis, Sébastien Dutertre, Irina Vetter, and MacDonald J. Christie

Institute for Molecular Bioscience, the University of Queensland in St. Lucia, Brisbane, Queensland, Australia (R.J.L., S.D., I.V.); and Discipline of Pharmacology, the University of Sydney, Sydney, New South Wales, Australia (M.J.C.)

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Address correspondence to: Richard J. Lewis, Institute for Molecular Bioscience, the University of Queensland, Q4072, Australia. E-mail: r.lewis@imb.uq.edu.au

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Abstract—Conopeptides are a diverse group of recently evolved venom peptides used for prey capture and/or defense. Each species of cone snails produces in excess of 1000 conopeptides, with those pharmacologically characterized (~0.1%) targeting a diverse range of membrane proteins typically with high potency and specificity. The majority of conopeptides inhibit voltage- or ligand-gated ion channels, providing valuable research tools for the dissection of the role played by specific ion channels in excitable cells. It is noteworthy that many of these targets are found to be expressed in pain pathways, with several conopeptides having entered the clinic as potential treatments for pain [e.g., pyroglutamate1-MrIA (Xen2174)] and one now marketed for intrathecal treatment of severe pain [ziconotide (Prialt)]. This review discusses the diversity, pharmacology, structure-activity relationships, and therapeutic potential of cone snail venom peptide families acting at voltage-gated ion channels (α-, μ-, δ-, γ-, and ε-conotoxins), ligand-gated ion channels (α-conotoxins, σ-conotoxin, ikot-ikot, and canan-tokins), G-protein-coupled receptors (ρ-conopeptides, conopressins, and contulakins), and neurotransmitter transporters (γ-conopeptides), with expanded discussion on the clinical potential of sodium and calcium channel inhibitors and α-conotoxins. Expanding the discovery of new bioactives using proteomic/transcriptomic approaches combined with high-throughput platforms and better defining conopeptide structure-activity relationships using relevant membrane protein crystal structures are expected to grow the already significant impact conopeptides have had as both research probes and leads to new therapies.

I. Introduction

The interrogation of chemical diversity with therapeutically relevant screens remains the dominant discovery engine for the pharmaceutical industry. Although most success with this approach has been achieved by exploring natural product extracts composed mostly of smaller organic molecules, there is a growing realization that peptides are an underused source of leads for new therapeutics. This realization is now gaining momentum following the disappointments of combinatorial chemistry, increasing failure rates of small molecules in clinical development, and the limitations of small-molecule–based approaches for many druggable targets. Sources of peptides include plant cyclotides (Henriques and Craik, 2010), phage display libraries (Pande et al., 2010), and venom peptides (Lewis and Garcia, 2003). Among these sources, venom peptides provide arguably the largest source of chemical diversity, being driven by evolutionary pressure for improved prey capture and/or defense. This diversity has arisen multiple times in nature as diverse as sea anemones, jellyfish, centipedes, spiders, scorpions, cone snails, cephalopods, echinoderms, snakes, lizards, fish, platypus and arguably even fleas, mosquitoes, kissing bugs, leeches, ticks, and vampire bats (Fry et al., 2009). Ensuring their successful implementation, venom peptides have coevolved with sophisticated and specialized envenomation machinery comprising fangs, barbs, modified teeth, harpoons, nematocysts, spines, or sprays. Not surprisingly, given that most venoms are delivered intravenously, there are multiple examples of convergent evolution of a relatively small number of structural scaffolds that possess the requisite stability to remain intact, both within the venom and in plasma after envenomation. These “privileged” structural frameworks have provided the scaffolds for an explosion in sequence diversity that explains much of the chemical diversity found in present-day venoms.

Among the venomous species, cone snails within the family Conidae are unique for their ability to use a diverse array of small disulfide-bridged peptides (conopeptides or conotoxins) for prey capture (Fig. 1). Conopeptides have evolved across all phylogenetic clades and feeding strategies of cone snails from at least 16 genetically distinct superfamilies, many of which are subject to extensive post-translational modifications (Table 1). This highly evolved hunting strategy, developed in parallel with the deployment of a hollow, barbed harpoon, allows normally herbivorous molluscs to prey on animals as diverse as worms (vermivorous species), fish (piscivorous species), and other molluscs (molluscivorous species). Successful implementation of this strategy has allowed this single genus of widely distributed marine molluscs to evolve into more than 500 Conus species. Cone snails hunt prey mostly at night and once prey is located by smell they skillfully inject small quantities of venom (up to ~50 μl) to paralyze prey within seconds using a rich cocktail of conopeptides that are cleaved from propeptides by specialized venom endoproteases (Milne et al., 2003). Their small molecular size (typ-
ically <5 kDa), relative ease of synthesis, structural stability and target specificity make them ideal pharmacological probes (Adams et al., 1999). This broadly evolved bioactivity provides a unique source of new research tools and potential therapeutic agents, with \( \omega - \text{MVIIA} \) [ziconotide (Prialt; Azur Pharma Inc., Philadelphia, PA)] already approved for clinical use in the treatment of severe pain (Miljanich, 2001).

Somewhat surprisingly, many of these classes of conotoxins act on pain targets, allowing the specific dissection of key ion channels and receptors underlying pain and providing new ligands with potential as pain therapeutics (Fig. 2). Each species of cone snail produces in excess of 1000 conopeptides, with an estimated 5\% overlap in conopeptides found between species (Davis et al., 2009) (see Fig. 1). At the moment, only ~0.1\% of conopeptides have been characterized pharmacologically, yet many have already been identified with clinical potential, as highlighted in Table 2. The use of advanced transcriptomic/proteomic approaches combined with high throughput and multiplexed high content screens is expected to accelerate ligand and target discovery. One caveat is that many conotoxins will preferentially target prey species over related mammalian targets and are likely to be missed in screens relevant to human diseases. This review expands and updates the last comprehensive review of Conus spp. venoms in 2004 (Terlau and Olivera, 2004). Here we discuss the diversity, pharmacology, structure-activity relationships, and therapeutic potential of cone snail venom peptide families acting at voltage-gated ion channels (\( \omega - \), \( \mu - \), \( \mu O - \), \( \delta - \), \( \nu - \) and

![Fig. 1. The cone snail, venom apparatus, and venoms. A, shell of C. textile, a typical tented molluscivorous cone snail. B, dissected venom apparatus from C. textile, showing the long and convoluted venom duct, radular sac, proboscis, and salivary glands. C, high-performance liquid chromatography/mass spectrometry separation of venom peptides from the milked venom of C. textile. D, matching liquid chromatography/mass spectrometry of the venom duct from the same C. textile.](image-url)
\(\alpha\)-conotoxins), ligand-gated ion channels (\(\alpha\)-conotoxins, \(\sigma\)-conotoxin, ikot ikot, and conantokins), GPCRs\(^1\) (\(\rho\)-conopeptides, conopressins and contulakins), and neurotransmitter transporters (\(\chi\)-conopeptides), and we discuss the potential of sodium and calcium channel inhibitors and \(\alpha\)-conotoxins to modulate pain pathways.

### Table 1

Superfamilies of conopeptides, occurrence in different Conus spp. clades and prey targets, and post-translational modifications (PTMs)

<table>
<thead>
<tr>
<th>Superfamily</th>
<th>Cysteine Framework</th>
<th>Family</th>
<th>Species</th>
<th>Clades</th>
<th>Diet</th>
<th>PTMs</th>
</tr>
</thead>
<tbody>
<tr>
<td>A</td>
<td>I, II, IV, XIV</td>
<td>(\alpha, \kappa, \rho)</td>
<td>43</td>
<td>E, I, II, III, V, VI, VII, X, XII, XIV, XV, XVII</td>
<td>V, M, P</td>
<td>O, (\gamma), G, Z, Ys</td>
</tr>
<tr>
<td>B</td>
<td>XX</td>
<td>(\alpha)</td>
<td>6</td>
<td>XII</td>
<td>V</td>
<td>O, (\gamma)</td>
</tr>
<tr>
<td>C</td>
<td>VI/VII, XI</td>
<td>(\kappa)</td>
<td>11</td>
<td>E, I, V, X, XIV, XVII</td>
<td>V, M, P</td>
<td>O, BrW, (\gamma), D</td>
</tr>
<tr>
<td>D</td>
<td>XI, XII</td>
<td>(\kappa)</td>
<td>17</td>
<td>I, V, VI, X, XII, XIII, XVII</td>
<td>V, M, P</td>
<td>O, (\gamma)</td>
</tr>
<tr>
<td>E</td>
<td>VI/VII, VI</td>
<td>(\kappa)</td>
<td>3</td>
<td>XIV</td>
<td>V</td>
<td></td>
</tr>
<tr>
<td>F</td>
<td>XIV</td>
<td>(\kappa)</td>
<td>2</td>
<td>IX</td>
<td>V</td>
<td>*</td>
</tr>
<tr>
<td>G</td>
<td>XIV</td>
<td>(\kappa)</td>
<td>2</td>
<td>E</td>
<td>V, P</td>
<td></td>
</tr>
<tr>
<td>H</td>
<td>III, IV, VI/VII, IX, XVI</td>
<td>(\alpha, \kappa, \mu)</td>
<td>28</td>
<td>E, I, II, III, IV, V, VI, VII, X, XII, XIV, XV, XVI, XVII</td>
<td>V, M, P</td>
<td>O, (\gamma), D</td>
</tr>
<tr>
<td>I</td>
<td>VI/VII, XII</td>
<td>(\delta, \gamma, \kappa, \mu, \omega)</td>
<td>53</td>
<td>E, I, II, III, V, VI, VII, IX, X, XI, XII, XIII, XIV, XV, XVI, XVII</td>
<td>V, M, P</td>
<td>O, BrW, (\gamma)</td>
</tr>
<tr>
<td>J</td>
<td>VI/VII, XV</td>
<td>(\delta)</td>
<td>15</td>
<td>I, V, VI, VII, X, XII, XIII, XIV, XVI</td>
<td>V, M, P</td>
<td>O, BrW, (\gamma)</td>
</tr>
<tr>
<td>K</td>
<td>VI/VII</td>
<td>(\gamma)</td>
<td>6</td>
<td>V, VII, XIV, XVI</td>
<td>V, M, P</td>
<td></td>
</tr>
<tr>
<td>L</td>
<td>IX</td>
<td>(\gamma)</td>
<td>6</td>
<td>V, X, XVII</td>
<td>V, M</td>
<td>*</td>
</tr>
<tr>
<td>M</td>
<td>VIII</td>
<td>(\alpha, \sigma)</td>
<td>6</td>
<td>I, II, V, XIV</td>
<td>V, M, P</td>
<td>O, BrW, (\gamma)</td>
</tr>
<tr>
<td>N</td>
<td>I, V, X, XVI</td>
<td>(\alpha, \sigma, \mu)</td>
<td>24</td>
<td>E, II, III, V, VI, VII, X, XII, XIII, XIV, XVI, XV, XVII</td>
<td>V, M, P</td>
<td>O, BrW, (\gamma, G, Z)</td>
</tr>
<tr>
<td>O</td>
<td>XV</td>
<td>(\alpha)</td>
<td>2</td>
<td>XII</td>
<td>V</td>
<td>*</td>
</tr>
<tr>
<td>P</td>
<td>XVII</td>
<td>(\alpha)</td>
<td>1</td>
<td>XIV</td>
<td>V</td>
<td>O</td>
</tr>
</tbody>
</table>

E, early clade; P, fish; M, molluscs; V, worms; \(\gamma\), C-terminal amidation; O, hydroproline; BrW, bromotryptophane; D, \(\delta\)-amino acid; \(\gamma\), \(\gamma\)-carboxyglutamate; \(\gamma\)-Val, \(\gamma\)-hydroxyvaline; G, glycosylation; Z, pyroglutamate; Ys, sulfo-t-tyrosine.

\(\kappa\)-conotoxins

Fig. 2. Peripheral and spinal pain pathways amenable to conopeptide modulation. A number of selected targets on peripheral nociceptive terminals and afferent neurons as well as descending facilitatory and inhibitory pathways originating in the medulla are shown. Therapeutic targets with known conotoxin modulators are highlighted in blue, and those targeted by peptides derived from other species are highlighted in green. Targets with therapeutic potential but no known specific peptide modulators are shown in yellow, and targets that are modulated by venom peptides but in an undesirable manner (e.g., inhibition of K\(_{1.4}\) by \(\kappa\)-conotoxins and activation of TRPV1 by \(\kappa\)-theraphotoxin-Pc1a) are highlighted in orange. ASIC, acid-sensing ion channel; P2X2/3, purinocepor 2X2 and 2X3; TRP, transient receptor potential channel; \(\alpha\)2\(
\beta\)1, auxiliary Ca\(_{\text{v}}\) subunit; GlyR, glycine receptor.
II. \(\omega\)-Conotoxin Inhibitors of Voltage-Gated Calcium Channels

The Ca\(_v\) channels are assemblies of the various pore-forming \(\alpha\)-subunits associated with single transmembrane \(\alpha\)28-subunits and intracellular \(\beta\)-subunits (Catterall et al., 2005b, 2007) (Table 3). Calcium channel (Ca\(_v\)) inhibitors are used as antihypertensive, antiarrhythmic, and anti-convulsant agents and in chronic pain management, and other potential uses are in development (Triggle, 2007). The therapeutic potential of \(\omega\)-conotoxins is based on their ability to selectively inhibit mammalian Ca\(_v\) isoforms (Table 4) expressed in ascending pain pathways (especially Ca\(_v\)2.2, which underlies the N-type current present in sensory neurons) and to produce antinociception in animal models of pain. Our understanding of the pharmacology of \(\omega\)-conotoxins has arisen mostly from studies on GVIA, MVIIA, CVIF, and MVIIC. Although these peptides are considered to function as simple pore blockers, their pharmacology is reminiscent of \(\omega\)-conotoxins, because coexpression of the pore-forming \(\alpha\) subunit with auxiliary \(\beta\) or

<table>
<thead>
<tr>
<th>Class</th>
<th>Mode of Action</th>
<th>Name</th>
<th>Clinical Potential</th>
</tr>
</thead>
<tbody>
<tr>
<td>(\omega)</td>
<td>Ca,2.2 inhibitor</td>
<td>MVIIA</td>
<td>Pain (intrathecal; phase IV)</td>
</tr>
<tr>
<td>(\mu)</td>
<td>Na, inhibitor</td>
<td>SIIIA</td>
<td>Pain (intravenous)</td>
</tr>
<tr>
<td>(\mu)O</td>
<td>Na,1.8 inhibitor</td>
<td>MrVIB</td>
<td>Pain (intrathecal/intravenous)</td>
</tr>
<tr>
<td>(\delta)</td>
<td>Na, enhancer</td>
<td>EVIA</td>
<td>?</td>
</tr>
<tr>
<td>(\kappa)</td>
<td>K, inhibitor</td>
<td>PVIIA</td>
<td>Cardiac reperfusion (intrathecal; phase II)</td>
</tr>
<tr>
<td>(\chi)</td>
<td>NET inhibitor</td>
<td>Xen2174</td>
<td>Pain (intrathecal; phase IV)</td>
</tr>
<tr>
<td>(\alpha)</td>
<td>nACHr inhibitor</td>
<td>Vcl11</td>
<td>Pain (intravenous)</td>
</tr>
<tr>
<td>(\sigma)</td>
<td>5HT, receptor</td>
<td>GVIIIA</td>
<td>Pain (intravenous)</td>
</tr>
<tr>
<td>(\rho)</td>
<td>(\alpha)-Adrenoceptor inhibitor</td>
<td>TIA</td>
<td>Cardiovascular/BPH</td>
</tr>
<tr>
<td>Conantok</td>
<td>NMDA-R antagonist</td>
<td>Con-G</td>
<td>Pain/epilepsy (intrathecal)</td>
</tr>
<tr>
<td>Conopressin</td>
<td>Vasopressin-R agonist</td>
<td>Cono-G</td>
<td>Cardiovascular/mood</td>
</tr>
<tr>
<td>Contulakin</td>
<td>Neurotensin-R agonist</td>
<td>Cont-G</td>
<td>Pain (intrathecal)</td>
</tr>
</tbody>
</table>

\(\omega\)-conotoxins, because coexpression of the pore-forming \(\alpha\) subunit with auxiliary \(\beta\) or

### Table 3

<table>
<thead>
<tr>
<th>Ca(_v), Isoform</th>
<th>Distribution</th>
<th>Selective Toxin Inhibitors</th>
<th>Effects/Side Effects of Inhibition</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Ca,1.1–1.4 (L-type)</td>
<td>Skeletal muscle (1.1), (T-tubules), Cardiac muscle (1.2–1.3), smooth muscle (1.2), CNS (1.1–1.3), DRG (1.2–1.4), retina (1.4)</td>
<td>None known (dihydropyridines)</td>
<td>Widespread effects on cardiovascular system, 1.2 implicated in neuropathic pain in spinal cord.</td>
<td>Kim et al., 2001; Catterall et al., 2005b, 2007; Fossat et al., 2010</td>
</tr>
<tr>
<td>Ca,2.1 (P/Q type)</td>
<td>Brain, spinal cord, sympathetic neurons, DRG, endocrine cells, contribution to presynaptic neurotransmitter release at CNS, PNS, and neuromuscular junction.</td>
<td>(-)Conotoxins MVIC \sim MVID &gt; CVIB &gt; CVIC &gt; MVIA &gt; GVIA &gt; CVID</td>
<td>Mutations in several neurological disorders, blockers produce partial inhibition of synaptic transmission. Peripheral side effects expected from autonomic and neuromuscular block.</td>
<td>Bourinet et al., 1999; Nudler et al., 2003; Catterall et al., 2005b, 2007 (For selectivity see Table 4)</td>
</tr>
<tr>
<td>Ca,2.2 (CACHIA)</td>
<td>Brain, spinal cord, sympathetic neurons, DRG, contribution to presynaptic neurotransmitter release in CNS and PNS.</td>
<td>(-)Conotoxins CVIE = CVID &gt; GVIA &gt; CVIA &gt; MVIA &gt; CVID &gt; CVIC</td>
<td>Blockers produce inhibition of synaptic transmission throughout the nervous system.</td>
<td>Catterall et al., 2005b, 2007 (For selectivity see Table 4)</td>
</tr>
<tr>
<td>Ca,2.3 (CACHIA)</td>
<td>Brain, spinal cord, sympathetic neurons, DRG, minor role in presynaptic neurotransmitter release in CNS and PNS, synaptic plasticity.</td>
<td>No conotoxins</td>
<td>Spiders: SNX-482</td>
<td>Blocks modulate synaptic plasticity at plasticity in some brain synapses.</td>
</tr>
<tr>
<td>Ca,3.1 (CACHIA)</td>
<td>Brain neurons localized to soma and dendrites. High expression in cerebellum and thalamus.</td>
<td>No conotoxins</td>
<td>(pimoizide, mibebradil, TTA-P2)</td>
<td>Small-molecule modulators may be useful for some CNS neurological disorders.</td>
</tr>
<tr>
<td>Ca,3.2 (CACHIAF)</td>
<td>CNS, DRG neurons: localized to soma and dendrites. Modulates action potential firing. Also heart, liver, kidney, lung, skeletal muscle, pancreas.</td>
<td>No conotoxins</td>
<td>Scorpion: kurtxin (pimoizide, mibebradil, Z123212 * TTA-P2)</td>
<td>Pain modulation. Relaxation of coronary arteries, potential side effects from actions in other tissues.</td>
</tr>
<tr>
<td>Ca,3.3 (CACHIA)</td>
<td>CNS neurons: localized to soma and dendrites. Modulates action potential firing.</td>
<td>No conotoxins</td>
<td>(pimoizide, TTA-P2, mibebradil very weak)</td>
<td>Presumably many side effects.</td>
</tr>
</tbody>
</table>

\*Clinical development suspended.
TABLE 4

ω-Conotoxins targeting Ca, calcium channels (loop formula C6C5–9CC2–4C3–6C)

Residues identified as being significant for affinity are underlined.

<table>
<thead>
<tr>
<th>Species</th>
<th>Name</th>
<th>Diet</th>
<th>Sequence Disulfide Bonded (1–4/2–5/3–6)</th>
<th>Cα Selectivity</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. consors</td>
<td>GVIIA</td>
<td>P</td>
<td>--GKGQGKQTLRMYD--CC--HOSCSSSGGRG*</td>
<td>2.2 &gt; 2.1</td>
<td>Favreau et al., 2001</td>
</tr>
<tr>
<td>C. catus</td>
<td>CVIA</td>
<td>P</td>
<td>--SNSGASRHTSYD--CC--TSQRS--GRC*</td>
<td>2.2 &gt; 2.2</td>
<td>Lewis et al., 2000</td>
</tr>
<tr>
<td></td>
<td>CVID</td>
<td>P</td>
<td>--CNGKSKSLKMRYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.2</td>
<td>Lewis et al., 2000</td>
</tr>
<tr>
<td></td>
<td>CVIC</td>
<td>P</td>
<td>--CNGKSKSLKMRYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.2</td>
<td>Lewis et al., 2000</td>
</tr>
<tr>
<td></td>
<td>CVIE-2</td>
<td>P</td>
<td>--CNGKSKSLKMRYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.2</td>
<td>Berecki et al., 2010</td>
</tr>
<tr>
<td></td>
<td>GVIVF</td>
<td>P</td>
<td>--CGGTGKSKSRIYNN--CC--BSCNTRYC*</td>
<td>2.2 &gt; 2.1</td>
<td>Lee et al., 2010</td>
</tr>
<tr>
<td></td>
<td>GVIA</td>
<td>P</td>
<td>--GSOSSSCSOTSYN--CC--BSCNTRYC*</td>
<td>2.2 &gt; 2.1</td>
<td>Olivera et al., 1984</td>
</tr>
<tr>
<td>C. magus</td>
<td>MVIIA</td>
<td>P</td>
<td>--GKGKSGRLMYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Olivera et al., 1985</td>
</tr>
<tr>
<td></td>
<td>MVIB</td>
<td>P</td>
<td>--GKGKSGRLMYD--CC--TGSSG2RGRC*</td>
<td>N.D.</td>
<td>Olivera et al., 1987</td>
</tr>
<tr>
<td></td>
<td>MVIIIC</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.1 &gt; 2.2</td>
<td>Hillyard et al., 1992</td>
</tr>
<tr>
<td></td>
<td>MVIID</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.1 &gt; 2.2</td>
<td>Nielseni et al., 1999a</td>
</tr>
<tr>
<td></td>
<td>GVIA</td>
<td>P</td>
<td>--GKGKASCGRLMYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Olivera et al., 1987</td>
</tr>
<tr>
<td></td>
<td>GVIIA</td>
<td>P</td>
<td>--GKGKASCGRLMYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Kim et al., 1995</td>
</tr>
<tr>
<td></td>
<td>GVIIIB</td>
<td>P</td>
<td>--GKGKASCGRLMYD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Nielsen et al., 1999</td>
</tr>
<tr>
<td></td>
<td>GVIIIC</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.1 &gt; 2.2</td>
<td>Haack et al., 1993</td>
</tr>
<tr>
<td></td>
<td>GVIIID</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.1 &gt; 2.2</td>
<td>Monje et al., 1993</td>
</tr>
<tr>
<td>C. pennaceus</td>
<td>PnVIA</td>
<td>M</td>
<td>--CLOEVDYFCGIFPANNLCL--CC--SGNCEPVV--CCTPQ</td>
<td>Molluscan N-type</td>
<td>Kits et al., 1996</td>
</tr>
<tr>
<td></td>
<td>PnVIB</td>
<td>M</td>
<td>--DDECFPPNGFPGHTFP--CC--SGNCFPFA--CA</td>
<td>Molluscan N-type</td>
<td>Kits et al., 1996</td>
</tr>
<tr>
<td>C. pulicarius</td>
<td>PsIA</td>
<td>V</td>
<td>--RCRFPQYQYQYPVRKWSNC--SGLA11--CVS</td>
<td>N.D.</td>
<td>Zhao and Huang, 2000</td>
</tr>
<tr>
<td></td>
<td>PsIIA</td>
<td>V</td>
<td>--TCNPQCTCFLHRH--CC--SLYCHKTHCA</td>
<td>N.D.</td>
<td>Zhao and Huang, 2000</td>
</tr>
<tr>
<td>C. radiatus</td>
<td>RVIA</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.2</td>
<td>Abbott and Litzinger, 1994</td>
</tr>
<tr>
<td>C. striatus</td>
<td>SO3</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>Naα ~ Kα ~ 2.2 &gt; 2.1 &gt; 2.3</td>
<td>Li et al., 1999; Li et al., 2003b; Wen et al., 2005</td>
</tr>
<tr>
<td></td>
<td>SO4</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>SO5</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>SVIA</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Ramilo et al., 1992</td>
</tr>
<tr>
<td></td>
<td>SVIB</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.2</td>
<td>Woppmann et al., 1994; Nadasdi et al., 1995</td>
</tr>
<tr>
<td>C. tulipa</td>
<td>TVIA</td>
<td>P</td>
<td>--GKGKAPCRGTYMD--CC--TGSSG2RGRC*</td>
<td>2.2 &gt; 2.1</td>
<td>Chung et al., 1995; Wang et al., 1998</td>
</tr>
<tr>
<td>C. textile</td>
<td>TxO1</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO2</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO3</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO4</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO5</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO6</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO7</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
<tr>
<td></td>
<td>TxO8</td>
<td>M</td>
<td>--LGAGEVCDCIDFPF--CC--GVCILLF--CA</td>
<td>N.D.</td>
<td>Lu et al., 1999</td>
</tr>
</tbody>
</table>

P, fish; M, molluscs; V, worms; *, C-terminal amidation; N.D., not determined.

α2δ subunits can significantly alter their channel affinity (Lewis et al., 2000; Mould et al., 2004; Motin et al., 2007). Such differences may have particular relevance in disease states such as pain, where α2δ subunits, particularly α2δ1, are up-regulated (see section II.C). ω-Conotoxins remain the only class of conotoxins with FDA approval to date, the registration of MVIIA (ziconotide) for the treatment of intractable pain having been approved in 2004. Unfortunately, dose-limiting neurological side effects have limited the clinical applications for ω-conotoxins.

A. Subtype Selectivity

ω-Conotoxins with defined activity at mammalian Caα isoforms have so far been isolated only from piscivorous cone snails, where they are likely to have evolved as part of the motor cabal (Olivera et al., 1985). Based on the behav-
ioral phenotype elicited after intracerebral injection in mice they were termed “shaker” peptides. It is now appreciated that \(\omega\)-H9275-conotoxins represent some of the most selective known inhibitors for the neuronal Cav isoforms 2.2 and 2.1. Specifically, \(\omega\)-H9275-conotoxins CVID, CVIE, CVIF, GVIA, and MVIIA are particularly selective for Cav2.2, whereas MVIIC and MVIID show a preference for Cav2.1 underlining P/Q-type calcium currents (Monje et al., 1993; Woppmann et al., 1994; Nadasdi et al., 1995; Nielsen et al., 1996; Flinn et al., 1999; Lewis et al., 2000; Berecki et al., 2010). The binding site of \(\omega\)-H9275-conotoxins to the Cav subtypes has been mapped primarily to the external vestibule of the channel in the domain III S5–S6 region (Ellinor et al., 1994), consistent with preliminary results obtained from docking of \(\omega\)-MVIIA to a homology model of \(\omega\)-Cav2.2 (Fig. 3A) built from the recently reported crystal structure of a bacterial sodium channel (Payandeh et al., 2011). Residues immediately outside this region seem to also contribute to Cav2.2 inhibition by GVIA, most notably Gly1326, which contributes to the reversibility of \(\omega\)-conotoxin block (Feng et al., 2001). Intracellular domains (Kaneko et al., 2002; McDonough et al., 2002) are also reported to modulate binding kinetics and \(\omega\)-conotoxin affinity for Cav2.2 and, in addition, the presence of subunits seems to not only modify Ca, gating characteristics and kinetics but also the interaction of \(\omega\)-conotoxins with the channel.

The high-affinity block of Cav2.2 by CVID was found to be reversible in heterologous systems expressing only the pore-forming \(\alpha\)-subunit, but irreversible in DRG neurons, an effect that is mimicked in expression systems where the \(\alpha\)-subunit is coexpressed with auxiliary \(\beta3\) and \(\alpha2\delta1\) subunits (Lewis et al., 2000; Mould et al., 2004; Motin et al., 2007). Likewise, inhibition of Cav2.2 by CVIE and CVIF was found to be virtually irreversible in the presence of \(\beta3\) subunits but reversible in systems coexpressing the \(\beta2\) subunit (Berecki et al., 2010). Intriguingly, these effects parallel modification of channel characteristics by auxiliary subunits, suggesting that altered block characteristics of \(\omega\)-conotoxins in the presence of auxiliary subunits reflect altered channel kinetics. In addition to altered binding kinetics, many \(\omega\)-conotoxins also have lower affinity for Cav2.2 in the presence of auxiliary subunits, especially \(\alpha2\delta1\) (Lewis et al., 2000; Berecki et al., 2010). However, the precise mechanisms contributing to these intriguing characteristics of \(\omega\)-conotoxins, as well as the effect of these pharmacological differences on the therapeutic potential of these peptides, remain to be elucidated.

Although the vast majority of \(\omega\)-conotoxins isolated to date are selective, to varying degrees, for mammalian...
Cav2.1 and Cav2.2, only TxVII, isolated from the molluscivorous Conus textile, blocks molluscan dihydropyridine-sensitive channels, which are homologous to mammalian L-type voltage-gated calcium channels (Fainzilber et al., 1996). However, this \( \omega \)-conotoxin seems to display phyllic selectivity, as TxVII was found to be inactive at rat L-type channels expressed in PC12 cells (Fainzilber et al., 1996; Sasaki et al., 1999). Likewise, PnVIA and PnVIB were isolated from the molluscivorous Conus pennaceus, but in contrast to TxVII, they inhibit the molluscan dihydropyridine-insensitive high-voltage activated Ca\(^{2+} \) current (Kits et al., 1996). Not surprisingly, the sequences of these related peptides are distinct from conotoxins from piscivorous cone snails targeting mammalian channels. Indeed, molluscan channels are usually insensitive to GVIA, suggesting distinct phylum-selective pharmacologies resulting from these divergent sequences. Accordingly, \( \omega \)-conotoxins from molluscivorous cone snails seem to represent a distinct subclass of \( \omega \)-conotoxins with specificity for molluscan calcium channels.

Other structurally diverse \( \omega \)-conotoxins include PuIA and PuIIA from the worm-hunting Conus pulicarius, as well as several peptides identified from the molluscivorous C. textile and piscivorous Conus striatus. The precise pharmacological target and subtype selectivity of these conotoxins remains to be determined; however, their homology to the functionally promiscuous SO3, which also inhibits sodium and potassium channels in hippocampal neurons (Li et al., 2003b; Wen et al., 2005), suggests that their pharmacological classification as \( \omega \)-conotoxins may be premature.

B. Structure-Activity Relationships

The pharmacological activity of \( \omega \)-conotoxins has been attributed primarily to Tyr13 and Lys2, both of which are highly conserved in \( \omega \)-conotoxins derived from piscivorous cone snails (Table 4) and are proposed to form a two-point pharmacophore (Sato et al., 1993; Kim et al., 1994; Lew et al., 1997; Flinn et al., 1999) (Fig. 4). The hydroxyl group of Tyr13 in particular seems critical for high-affinity binding of \( \omega \)-conotoxins to Ca\(_{2.2} \), although the aromatic moiety also seems to contribute to binding (Kim et al., 1994; Flinn et al., 1999). The positive charge of the second most important residue, Lys2, which is conserved in all \( \omega \)-conotoxins except MVIIID and TVIA, also contributes significantly to activity (Sato et al., 1993; Lew et al., 1997; Flinn et al., 1999). Detailed structure-activity relationship studies in GVIA showed that the precise location of this positive charge is less important, both lengthening and shortening of the side chain being tolerated. However, bulkier substitutions in this position greatly reduced activity (Flinn et al., 1999).

In addition, several other residues in loop 2 and 4 also contribute to varying degrees to \( \omega \)-conotoxin affinity and selectivity (Gandía et al., 1997; Lew et al., 1997; Nielsen et al., 1999a). Loop 4 residues with a significant effect on \( \omega \)-conotoxin affinity include Arg21 in MVIIA and Arg17, Tyr22, and Lys24 in GVIA, whereas the residue at position 10 in loop 2 seems to play a key role in determining subtype selectivity (Nielsen et al., 1999a). Biotinylation of Lys10 in the P/Q-selective MVIID significantly decreased binding affinity (Haack et al., 1993), and the importance of this residue for Ca\(_{\alpha} \) subtype selectivity was also confirmed by several independent studies (Nadasdi et al., 1995; Nielsen et al., 1996). The residue at position 10 is consistently a lysine in \( \omega \)-conotoxins with high affinity for Ca\(_{2.1} \), but often an arginine or hydroxyproline in Ca\(_{2.2} \)-selective peptides (Nadasdi et al., 1995; Nielsen et al., 1996). However, it remains to be determined if the subtype selectivity of Ca\(_{2.1} \)-selective MVIIIC and MVIID are significantly altered by a K10R swap. It is noteworthy that an arginine in position 10 was reported to reduce recovery from Ca\(_{2.2} \) block for both MVIIA and CVID, suggesting that the effect of this residue on subtype selectivity could be due to altered recovery characteristics (Mould et al., 2004).

Although the pharmacophore of \( \omega \)-conotoxins responsible for affinity and subtype selectivity at Ca\(_{\alpha} \)s is becoming...
increasingly clear, residues responsible for any splice variant selectivity of \( \omega \)-conotoxins have not been determined to date. Nonetheless, our understanding of these structure-activity relationships are being applied to the design of small molecule, orally active \( \omega \)-conotoxin peptidomimetics with the hope of engineering novel analgesic molecules based on the unique pharmacological properties of \( \omega \)-conotoxins (Schroeder et al., 2004; Andersson et al., 2009).

C. Calcium Channel Inhibition by Conotoxins in Pain Management

There is strong evidence that Ca\(_{\text{a},2.2}\) channels on nociceptive primary afferent nerves are an target for pain management. Some of the most effective nonopioid analgesics for chronic pain management, gabapentin and pregabalin, interact with Ca\(_{\text{a}}\) channel \( \alpha_2\delta \) subunits, which is thought to disrupt trafficking of Ca\(_{\text{a},2.2}\) channels (Bauer et al., 2010). Indeed, in the spinal cord, opioids act predominantly on Ca\(_{\text{a},2.2}\) channels via \( \mu \)-opioid receptors expressed on nociceptive primary afferent nerve terminals to produce presynaptic inhibition and analgesia (Heinke et al., 2011). Many \( \omega \)-conotoxins exhibit high potency and selectivity for different subtypes of voltage-gated calcium channels (Oli vera et al., 1994). The development of the N-type (Ca\(_{\text{a},2.2}\)) antagonist, \( \omega \)-conotoxin MVIIA (SNX-111; ziconotide), as an intrathecal analog to manage to moderate severe chronic pain, provided the first validation of the use of \( \omega \)-conotoxins and established Ca\(_{\text{a},2.2}\) as new target for pain therapeutics (Lewis and Garcia, 2003; Winquist et al., 2005). Although ziconotide is potent and does not induce addiction or tolerance as opioids do (Malmberg and Yaksh, 1995; Bowersox et al., 1996), its use is limited because of the need for intrathecal administration combined with significant dose-limiting neurological side effects (Penn and Paice, 2000). This side-effect profile likely arises, at least in part, from the spread of peptide from the intrathecal space to higher (supraspinal) brain centers including cerebellum and the dependence of a significant component of synaptic neurotransmission on Ca\(_{\text{a},2.2}\) at many CNS synapses, including inhibitory spinal synapses (Penn and Paice, 2000; Schmidtko et al., 2010). However, as discussed below, other properties of \( \omega \)-conotoxins could additionally contribute to their side-effect profile and therapeutic index. The distribution of Ca\(_{\text{a}}\) channel types (Catterall et al., 2005b, 2007), potential actions of inhibitors, as well as selective conotoxins and other inhibitors are summarized in Table 3. The role of Ca\(_{\text{a},1}\) to 3 and Ca\(_{\text{a},2}\delta\) in pain pathways and their potential for selective targeting by conotoxins is outlined below.

The Ca\(_{\text{a},1}\) channel \( \alpha \)-subunits encode L-type channels but evidence for their involvement in pain states is still very limited (Yaksh, 2006). L-type calcium channel subtypes are expressed in sensory neurons and dorsal horn of the spinal cord, where they could potentially modulate the development of neuropathic pain (Kim et al., 2001). Intrathecal L-type channel antagonists have mixed effects in pain models (see Yaksh, 2006), possibly because nonselective Ca\(_{\text{a},1}\) inhibitors have little effect on afferent substance P release (Takasusuki and Yaksh, 2011) or the role of Ca\(_{\text{a},1}\) changes in different models of pain. More recently, antisense knockdown and microRNA regulation of the Ca\(_{\text{a},1.2}\) in spinal cord has been shown to reverse the development of mechanical signs of neuropathic pain, hyperexcitability of deep dorsal horn neurons, phosphorylation of cAMP response element-binding protein, and induction of cyclooxygenase-2 mRNA in the spinal cord (Fossat et al., 2010), consistent with Ca\(_{\text{a},1.2}\) expression predominantly in neuronal somata and dendrites and its role in gene regulation and plasticity (Murakami et al., 2004; Zhang et al., 2006a). These findings suggest that specific peptide inhibitors of Ca\(_{\text{a},1.2}\) may be useful for management and perhaps reversal of central adaptations responsible for maintenance of neuropathic pain when applied directly to the dorsal spinal cord.

Ca\(_{\text{a},2.1}\) encodes the \( \alpha \)-subunit of high-voltage activated P/Q-type calcium channels, with alternative splicing generating the P and Q phenotypic variants (Bourinet et al., 1999). Together with Ca\(_{\text{a},2.2}\) and Ca\(_{\text{a},2.3}\), P/Q-type channels contribute to the calcium influx, triggering synaptic neurotransmission at many synapses including nociceptive synapses (Heinke et al., 2004; Rycroft et al., 2007) and thus may be considered as a target for potential pain therapeutics (e.g., Vanegas and Schaible, 2000; Yaksh, 2006). However, P/Q channels are more densely expressed in non-nociceptive than in nociceptive sensory neurons and are the major Ca\(_{\text{a}}\) channels mediating synaptic neurotransmission at neuromuscular synapses (Uchitel et al., 1992; Westenbroek et al., 1998; Nudler et al., 2003). P/Q channel inhibitors would therefore be expected to produce neuromuscular and non-nociceptive sensory side effects after systemic or intrathecal administration. This might suggest a greater role in sensory modalities other than nociception. Indeed, intrathecal administration of the highly selective Ca\(_{\text{a},2.1}\) inhibitor, agatoxin IVA, in a variety of pain models has produced mixed results (Malmberg and Yaksh, 1994; Vanegas and Schaible, 2000; Yaksh, 2006).

The most promising calcium channel regulating pain pathways is arguably Ca\(_{\text{a},2.2}\), which encodes the \( \alpha \)-subunit of high voltage activated N-type calcium channels. Ca\(_{\text{a},2.2}\) inhibitors have been developed as pain therapeutics, because Ca\(_{\text{a},2.2}\) is the predominant channel supporting nociceptive primary afferent neurotransmission in the dorsal horn of the spinal cord (Fig. 2). Although Ca\(_{\text{a},2.2}\) is sometimes considered the only calcium channel mediating synaptic transmission at nociceptive synapses, other Ca\(_{\text{a}}\) channels, including P/Q-type, R-type, and to a small extent L-type, contribute ~50% of neurotransmitter release at nociceptive synapses (Heinke et al., 2004; Rycroft et al., 2007). Among a diverse group of \( \omega \)-conotoxins, MVIIA was established to be highly efficacious after intrathecal administration in a range of animal pain models (Malmberg and Yaksh, 1994; Scott et al., 2002; Yaksh, 2006), although severe behavioral side effects of apparent neurological origin were observed within the effective dose-range for pain...
relief (Smith et al., 2002). In humans, optimal use of ziconotide (MVIIA) requires slow and careful titration of dose and rate of intrathecal infusion. The adverse effects of ziconotide on the central nervous system include dizziness, nystagmus, confusion, abnormal gait, somnolence, speech difficulties, amnnesia, and abnormal thought processes (Penn and Paice, 2000; Schmidtke et al., 2010). Small-molecule Ca_{2.2} inhibitors may suffer from similar side-effect issues in addition to the peripheral side effects observed after intravenous administration of ziconotide. These include orthostatic hypotension, dizziness, sinus bradycardia, rhinitis, and nausea (McGuire et al., 1997). Preclinical testing of other \( \omega \)-conotoxins suggest improvements are possible. For example, CVID (AM336, CNSB004, lecnotocon) has potency to inhibit Ca\(_{2.2}\) channels and relieve neuropathic pain signs in animal models comparable to that of MVIIA but has been reported to exhibit a better (approximately 5-fold) therapeutic index for analgesia versus side effects (Scott et al., 2002; Smith et al., 2002). Some of the potential reasons for improved therapeutic index and potential applications of novel \( \omega \)-conotoxins are explored below.

Although CVID has similar potency at Ca\(_{2.2}\) as MVIIA, it is approximately 100-fold more selective for N-type than P/Q type channels (Lewis et al., 2000). This has been suggested as a reason for its improved side effect profile both in the CNS and periphery (Smith et al., 2002; Kolosov et al., 2010). However, MVIIA is already nearly 10,000-fold selective for N-type versus P/Q-type channels based on radioligand-binding studies using rat brain membrane (Lewis et al., 2000), so this might not be the explanation for better selectivity of CVID versus MVIIA and GVIA. Further systematic investigation of the relationship between N and P/Q selectivity and therapeutic index will be required to determine whether this is important.

The target residence time of a drug can strongly influence its therapeutic index (Copeland et al., 2006). The rate of reversal of inhibition of Ca\(_{2.2}\) by \( \omega \)-conotoxins certainly influences the extent to which side effects can be managed clinically (Penn and Paice, 2000). Many \( \omega \)-conotoxins, including MVIIA and GVIA, seem to bind nearly irreversibly to the N-type channel. However, reversibility can be induced by hyperpolarizations to potentials more negative than the minimum of the steady-state inactivation curve; i.e., \( \omega \)-conotoxins bind with higher affinity to the inactivated state of the N-channel than the resting state (Stocker et al., 1997). Such voltage-dependent recovery from block varies for different \( \omega \)-conotoxins and is strongly influenced for some by the \( \alpha_{2\delta} \)- and \( \beta \)-subunits, in particular \( \alpha_{2\delta} \), \( \beta_2 \), and \( \beta_3 \), coexpressed with the \( \alpha \)-subunit (Mould et al., 2004; Berecki et al., 2010). Reversibility of GVIA and MVIIA is only weakly influenced by \( \alpha_{2\delta} \)- and \( \beta_2 \)- or \( \beta_3 \)-subunit coexpression, and both appear to have a narrower therapeutic index than for CVID, which is strongly influenced by the presence of these subunits (Mould et al., 2004; Berecki et al., 2010). Two more recently identified \( \omega \)-conotoxins from Conus catus, CVIF and CVID, show greater voltage-dependent reversal in the presence of \( \alpha_{2\delta} \)- and \( \beta \)-subunits than CVID (Berecki et al., 2010). The implications of this property for modulation of primary afferent nociceptive neurotransmission will remain uncertain until the therapeutic indices of these novel \( \omega \)-conotoxins are determined. The importance of this property in nerve terminals is also uncertain because Ca\(_{2.2}\) channels in some nerve terminals seem to be resistant to voltage-dependent inactivation (Chan et al., 2007). Nonetheless, it is of interest that GVIA and MVIIA apparently irreversibly inhibit primary afferent synaptic neurotransmission, whereas CVID is partly reversible. CVIE and CVIF are fully reversible after removal of the peptides but show similar efficacy to CVID in pain models (Motin et al., 2007; Berecki et al., 2010). If the therapeutic indices for CVIE and CVIF were significantly better than for both CVID and MVIIA, it would suggest that reversibility of block is an important factor in therapeutic index. A novel \( \omega \)-conotoxin, FVIA from Conus fulmen, may be useful because it is fully reversible within the normal steady-state inactivation range of Ca\(_{2.2}\) (\(-80 \text{ mV}\)). However, its voltage- and \( \alpha_{2\delta} \)-\( \beta \)-subunit dependence and therapeutic index have not been determined (Lee et al., 2010).

Ca\(_{2.2}\) \( \alpha_{2\delta} \)-subunits also strongly influence the potency of some \( \omega \)-conotoxins but not others, independently of \( \beta \)-subunit coexpression (Mould et al., 2004; Motin et al., 2007; Motin and Adams, 2008; Berecki et al., 2010). The potency (with coexpression of \( \beta \)-subunits) of MVIIA, CVID, CVIF, and MVIIA are reduced approximately 100-fold by coexpression of \( \alpha_{2\delta} \)-subunits in oocytes, whereas the potency of CVIE is only reduced approximately 10-fold (Mould et al., 2004; Berecki et al., 2010). This may be important because \( \alpha_{2\delta} \)-subunit expression is profoundly up-regulated in the central terminals of primary afferent nerves in neuropathic pain (Bauer et al., 2010) so that the potency of some \( \omega \)-conotoxins in pain states might be strongly modulated. Consistent with such an effect, CVID and MVIIA at maximal effect doses are less effective at nociceptive primary afferent synapses in a rat inflammatory pain model (Rycroft et al., 2007). Other conotoxins and neuropathic models remain to be examined at this level.

The highly specific binding of \( \omega \)-conotoxins to Ca\(_{2.2}\) suggests that specific interaction with splice variants may be possible. The Ca\(_{2.2}\) gene contains several alternative 3-subunit coexpression, and both appear to have a narrower therapeutic index than for CVID, which is strongly influenced by the presence of these subunits (Mould et al., 2004; Berecki et al., 2010). Two more recently identified \( \omega \)-conotoxins from Conus catus, CVIF and
codes a distinct pair of 32 amino acid sequences in the intracellular, C-terminal region of the channel, the prospects for developing selective \(\omega\)-conotoxins for these isoforms may be limited given these peptides bind extracellularly (see Fig. 3A). The function and tissue distribution of other splice variants have been less extensively studied. A long C-terminal splice variant of Cav2.2 has been identified in presynaptic membranes (Gardezi et al., 2010) and other variants lacking a synaptic protein interaction site within the intracellular SII-SIII linker domain are presumably not targeted to synaptic nerve terminals (Kaneko et al., 2002). It is noteworthy that the \(\Delta 1\) variant (SII-SIII domain truncation) was less sensitive to inhibition by both MVIIA and GVIA (Kaneko et al., 2002), suggesting that it may be possible to selectively target \(\omega\)-conotoxins to Cav2.2 splice variants, even when sequence variations are within intracellular domains.

The efficacy of \(\omega\)-conotoxins in pain management is generally considered to be due exclusively to inhibition of N-type channels at primary afferent synapses in the dorsal horn of the spinal cord. Until recently, the possibility that pain relief could be achieved with systemic administration was not considered because MVIIA produces serious systemic cardiovascular and other side effects mediated by the peripheral nervous system (McGuire et al., 1997). However, in conscious rabbits and isolated, sympathetically innervated tissues, CVID was much less potent than MVIIA at producing sympathetic and cardiovascular effects (Wright et al., 2000), suggesting it may be safer after systemic administration. Indeed, intravenous CVID has recently been shown to produce modest antihyperalgesia in pain models at doses producing no cardiovascular effects (Kolosov et al., 2010) and synergizes strongly with other analgesics, including morphine (Kolosov et al., 2010; Kolosov et al., 2011). The reasons for the greater therapeutic index of systemic CVID are not known. It could be due to greater N- versus P/Q-channel selectivity (but see selectivity section above) or to influences of auxiliary subunits expressed selectively in sympathetic neurons (Kolosov et al., 2010). Using GVIA and CVID to probe N-channels, different contributions of N-channels to vasoconstrictor versus vasodilator neurons have been noted (Jobling et al., 2004; Morris et al., 2004) but sensitivities to conotoxins differentially influenced by auxiliary subunit expression, such as CVD, CVIE, and CVIF, have not been examined. Resolution of differential effects in relevant sympathetic nerve terminal preparations may produce a more rational approach to the development of safe, systemically active \(\omega\)-conotoxin pain therapeutics.

In contrast to Ca\(_{2.2}\), Ca\(_{2.3}\) has not been extensively explored in pain models and no highly selective \(\omega\)-conotoxins targeting this channel are known. R-type channels do contribute to nociceptive primary afferent synaptic transmission (Heinke et al., 2004; Rycroft et al., 2007), and the selective Ca\(_{2.3}\) inhibitor SNX-482 from the tarantula, Hysterocrates gigas, has been shown to be antinociceptive after intrathecal administration (Murakami et al., 2004) and to inhibit nociceptive neural responses in the spinal cord dorsal horn in vivo in a neuropathic pain model (Matthews et al., 2007).

Conotoxins acting at other calcium channel types, notably Ca\(_{3.3}\) subtypes, could also be developed as pain therapeutics (Yakh, 2006; Triggle, 2007; Zamponi et al., 2009). Ca\(_{3.3}\) \(\alpha\)-subunits encode the family of low-voltage-activated calcium channel currents that modulate action potential burst firing in CNS neurons and contribute to Ca\(_{2+}\) mediated plasticity. Ca\(_{3.2}\) is the predominant type expressed in nociceptive and mechanosensitive sensory neurons (see Todorovic and Jevtovic-Todorovic, 2011). In neuropathic pain models, T-type channel current density is up-regulated, and this contributes to sensory neuron hyperexcitability (Jagodic et al., 2007, 2008). T-type channels are also expressed by neurons in the dorsal horn of the spinal cord (see Todorovic and Jevtovic-Todorovic, 2011) and have been shown to be crucial for induction of plasticity at nociceptive primary afferent synapses that could contribute to persistent pain (Ikeda et al., 2003, 2006). Consistent with this role, knockdown of Ca\(_{3.2}\) in sensory neurons reduced signs of thermal and mechanical pain in neuropathic pain models (Bourinet et al., 2005; Messinger et al., 2009). Nonselective, small-molecule T-type channel inhibitors also reduce neuropathic pain signs in animal models, and antisense knockdown experiments in sensory neurons have confirmed that this effect is mediated by Ca\(_{3.2}\) (Dogrul et al., 2003; Choi et al., 2007; Choe et al., 2011). Thus, evidence implicating Ca\(_{3.2}\) in sensory neuron hyperexcitability in neuropathic pain suggests that peripherally administered conotoxins selectively targeting Ca\(_{3.2}\), if they can be identified, may be useful therapeutics.

### II. Conotoxins Interacting with Voltage-Gated Sodium Channels

To date, four classes of conotoxins targeting Na\(_n\) channels (\(\mu\), \(\muO\), \(\delta\), and \(\iota\) conotoxins) have been isolated from cone snail venom (Cruz et al., 1985; Painzilber et al., 1994b; McIntosh et al., 1995; Fiedler et al., 2008). Although these venom peptides exhibit activity at the same pharmacological targets, they are structurally distinct and vary in their mechanism of action, with two families producing inhibition (\(\mu\)- and \(\muO\)-conotoxins) and two families activation (\(\delta\)- or \(\iota\)-conotoxins) of Na\(_n\) channels (Table 5). The \(\mu\)-conotoxins elicit Na\(_n\) inhibition through direct pore block overlapping with tetrodotoxin at site 1, consistent with preliminary docking of A15-TIIIA to a homology model of Na\(_{1.4}\) built from the crystal structure of a bacterial sodium channel (Fig. 3B). In contrast, \(\muO\)-conotoxins seem to interfere with the voltage sensors in domain II of Na\(_n\) to restrict channel opening, \(\delta\)-conotoxins cause a delay in Na\(_n^+\) inactivation by binding to site 6 resulting in action potential prolongation and persistent neuronal firing, whereas the \(\iota\)-conotoxins enhance channel opening by shifting the voltage dependence of Na\(_n^+\) activation to more hyperpolar-
### Table 5

**μ- and μO-Conotoxins inhibiting Na$_{1.1,x}$ sodium channels (μ-conotoxin loop formula CC1–8CC3–4C2–5C)**

Cysteines are boldered and aligned separately for μ- and μO-conotoxins, with residues affecting sodium channel affinity underlined.

<table>
<thead>
<tr>
<th>Species</th>
<th>Name</th>
<th>Diet</th>
<th>Sequence (Disulfide Bonded 1-4/2-5/3-6)</th>
<th>Na$_{1.1,x}$ Selectivity</th>
<th>Reference</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>μ-Conotoxins</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. bulittus</em></td>
<td>BuIII A</td>
<td>P</td>
<td>VTRDRC-K---GKRCGFW-CRDHSRC-c*</td>
<td>2 &gt; 4 &gt; 1 &gt; 3 &gt; 6 &gt; 5 &gt; 7 &gt; 8</td>
<td>Holford et al., 2009; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>BuIII B</td>
<td>P</td>
<td>VGERCCKN---GKRCGFW-CRDHSRC-c*</td>
<td>4 &gt; 2 &gt; 3 &gt; 1 &gt; 6 &gt; 5 &gt; 7 &gt; 8</td>
<td>Holford et al., 2009; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>BuIII C</td>
<td>P</td>
<td>IVDRCCKNKGKRGFW-CRDHSRC-c*</td>
<td>4 &gt; ?</td>
<td>Holford et al., 2009</td>
</tr>
<tr>
<td><em>C. catus</em></td>
<td>CII A</td>
<td>P</td>
<td>--GRCCGPN---GCSRSWCREDHAS-c*</td>
<td>Amphibian skeletal/</td>
<td>Zhang et al., 2006b</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>cardiac, TTX-R</td>
<td></td>
</tr>
<tr>
<td></td>
<td>C. consors</td>
<td>CIII A</td>
<td>--GRCCDVPA----CSGRGRCDHADQ-c*</td>
<td>2 &gt; 4 &gt; 6 &gt; 5 &gt; 3 &gt; 1 &gt; 7 &gt; 8</td>
<td>Zhang et al., 2006b; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>C. geographus</td>
<td>GIIB</td>
<td>P --RDCCTOORK---CRDROCK-OGDC-CA*</td>
<td>(&lt; 25%)</td>
<td>Cruz et al., 1985; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>GII B</td>
<td>P</td>
<td>--RDCCTOORK---CRDROCK-OMKDC-CA*</td>
<td>4 &gt; 2 &gt; 3 &gt; 5 &gt; 7 &gt; 8 &gt; ?</td>
<td>Cruz et al., 1985; Zhang et al., 2007</td>
</tr>
<tr>
<td></td>
<td>GIIIC</td>
<td>P</td>
<td>--RDCCTOORK---CRDROCK-OLRDC-CA*</td>
<td>4 &gt; 2 &gt; N.D.</td>
<td>Bulaj et al., 2005; Zhang et al., 2007; Wilson et al., 2011a</td>
</tr>
<tr>
<td><em>C. kinoshitai</em></td>
<td>KIII A</td>
<td>P</td>
<td>---CC-------CSDKRCHDHSRC-c*</td>
<td>2 &gt; 4 &gt; 6 &gt; 1 &gt; 7 &gt; 3 &gt; 5 &gt; 8</td>
<td></td>
</tr>
<tr>
<td><em>C. magus</em></td>
<td>MII A</td>
<td>P</td>
<td>--ZGCNVPMK---CSGRGCRDHADQ-c*</td>
<td>4 &gt; 2 &gt; 3 &gt; 6 &gt; 1 &gt; 5 &gt; 7 &gt; 8</td>
<td>Zhang et al., 2006b; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>MII B</td>
<td>P</td>
<td>--ZGCNVPMK---CSGRGCRDHADQ-c*</td>
<td>4 &gt; 6 &gt; 1 &gt; 2 &gt; 3 &gt; 5 &gt; 7 &gt; 8</td>
<td>Shon et al., 1998a; Wilson et al., 2011a</td>
</tr>
<tr>
<td><em>C. purpurascens</em></td>
<td>PHIA</td>
<td>P</td>
<td>--ZLCCGFKS---CRDROCK-OGHC-c*</td>
<td>4 &gt; 6 &gt; 1 &gt; 2 &gt; 3 &gt; 5 &gt; 7 &gt; 8</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. pennaceus</em></td>
<td>PhIVA</td>
<td>M</td>
<td>----cckygt---c-llge-sp-ccc</td>
<td>Molluscan</td>
<td>Fainzilber et al., 1995b</td>
</tr>
<tr>
<td></td>
<td>PhIVB</td>
<td>M</td>
<td>----cckygt---c-wlge-sp-ccc</td>
<td>Molluscan</td>
<td>Fainzilber et al., 1995b</td>
</tr>
<tr>
<td><em>C. striatus</em></td>
<td>SIIIA</td>
<td>P</td>
<td>--ZNCNGG---CSKWRCHDHSRC-c*</td>
<td>2 &gt; 4 &gt; 6 &gt; 1 &gt; 3 &gt; 7 &gt; 5 &gt; 8</td>
<td>Bulaj et al., 2005; Yao et al., 2008; Leipoldt et al., 2011; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>SIIIB</td>
<td>P</td>
<td>--ZNCNGG---CSKWRCHDHSRC-c*</td>
<td>4 &gt; 2 &gt; ?</td>
<td>Schroeder et al., 2008</td>
</tr>
<tr>
<td><em>C. stercusmuscarum</em></td>
<td>SmIIIA</td>
<td>P</td>
<td>--ZRCNGRRG---CSGRGCRDHAS-cc</td>
<td>4 &gt; 2 &gt; 1 &gt; 3 &gt; 6 &gt; 5 &gt; 7 &gt; 8</td>
<td>West et al., 2002; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>SxIII A</td>
<td>P</td>
<td>--RCCGKGGS---CSGRARCHK-LKCC-c*</td>
<td>4 &gt; 1 &gt; 6 &gt; 2 &gt; 3 &gt; 5 &gt; 7 &gt; 8</td>
<td>Walewska et al., 2008; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>SxIII B</td>
<td>P</td>
<td>--RCCGKGGS---CSGRARCHK-LKCC-c*</td>
<td>N.D.</td>
<td>Walewska et al., 2008</td>
</tr>
<tr>
<td><em>C. tulipa</em></td>
<td>TIIB A</td>
<td>P</td>
<td>--RGCCGKGGS---CSGRARCHK-OGCC-c*</td>
<td>2 &gt; 4 &gt; 1 &gt; 3 &gt; 6 &gt; 5 &gt; 7 &gt; 8</td>
<td>Lewis et al., 2007; Wilson et al., 2011a</td>
</tr>
<tr>
<td></td>
<td>TIIB B</td>
<td>P</td>
<td>--RGCCGKGGS---CSGRARCHK-OGCC-c*</td>
<td>4 &gt; 2 &gt; ?</td>
<td></td>
</tr>
<tr>
<td><strong>μO-Conotoxins</strong></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>C. litteratus</em></td>
<td>LtVIA</td>
<td>V</td>
<td>GECGNWNYCTHSICCSGCGECSLRSYCDI</td>
<td>N.D.</td>
<td>Pi et al., 2007</td>
</tr>
<tr>
<td></td>
<td>LtVd</td>
<td>V</td>
<td>--DC------CPAKLKCNCP</td>
<td>TTX-S &gt; TTX-R</td>
<td>Liu et al., 2007a</td>
</tr>
<tr>
<td></td>
<td>LAVIC</td>
<td>V</td>
<td>WPCMVAFSFGSLVECGCSSP--CFLNRCY</td>
<td>N.D.</td>
<td>Wang et al., 2008</td>
</tr>
<tr>
<td><em>C. marmoreus</em></td>
<td>MrVIA</td>
<td>M</td>
<td>--AGBRDMYETVPTITPCGRLCCPGFPVCV</td>
<td>8 &gt; 7 &gt; 4 &gt; 2 &gt; TTX-S</td>
<td>Fainzilber et al., 1995c; McIntosh et al., 1995; Safo et al., 2000; Daly et al., 2004; Zorn et al., 2006</td>
</tr>
<tr>
<td></td>
<td>MrVIB</td>
<td>M</td>
<td>--CSHKWEYCVPTILGFYVCSPGLRCSPFPCV</td>
<td>8 &gt; 4 &gt; 2 &gt; 3 &gt; 5 &gt; 7 &gt; 9</td>
<td>Fainzilber et al., 1995b; Fainzilber et al., 1995c; McIntosh et al., 1995; Eckberg et al., 2006; Zorn et al., 2006</td>
</tr>
<tr>
<td><em>C. geographus</em></td>
<td>Conotoxin-GS</td>
<td>P</td>
<td>--ACGSRGSRCCQCCMMGLRGCGRNPQKCIAGHCDV</td>
<td>4 &gt; 2 &gt; N.D.</td>
<td>Yanagawa et al., 1988; Hill et al., 1997</td>
</tr>
</tbody>
</table>

P, fish; M, molluscs; V, worms; *, C-terminal amidation; N.D., not determined; TTX-S TTX-sensitive; TTX-R, TTX-resistant.
izated potentials. It is noteworthy that conotoxins provide some of the most subtype-selective Na\textsubscript{v} modulators, especially for Na\textsubscript{v}1.4, Na\textsubscript{v}1.2, and more recently Na\textsubscript{v}1.8 and have proven to be invaluable tools to dissect the physiological roles and pharmacologies of Na\textsubscript{v}1.1 to Na\textsubscript{v}1.9. The potential of Na\textsubscript{v}-targeting conotoxins as drug leads is only now beginning to be explored.

A. \textit{\textmu}-Conotoxin Inhibitors of Voltage-Gated Sodium Channels

Of the conotoxins targeting Na\textsubscript{v}, the \textit{\textmu}-conotoxins are the most numerous and best characterized, with 20 different \textit{\textmu}-conotoxins described to date. \textit{\textmu}-Conotoxins belong to the M superfamily of conopeptides and comprise 16 to 26 residues including 3 conserved disulfide bonds that stabilize their three-dimensional structure (see Table 5, Fig. 5). The \textit{\textmu}-conotoxins are generally characterized by an overall net positive charge, which contributes to their ability to bind through electrostatic interactions to the outer vestibule of Na\textsubscript{v} to inhibit ionic conductance (Hui et al., 2002; Hui et al., 2003; Li et al., 2003a).

\textit{\textmu}-Conotoxins are the only venom peptides that bind to site 1 on Na\textsubscript{v}, a site originally defined by the guanidinium pore blockers tetrodotoxin (TTX) and saxitoxin (see Fozzard and Lipkind, 2010). Although TTX (and saxitoxin) only distinguishes between TTX-sensitive (Na\textsubscript{v}1.1, -1.2, -1.3, -1.4, -1.6, and -1.7) and TTX-resistant (Na\textsubscript{v}1.5, -1.8, and -1.9) isoforms, \textit{\textmu}-conotoxins display further subtype selectivity among mammalian TTX-sensitive Na\textsubscript{v} subtypes (see Table 5). This difference in pharmacology arises because the binding sites of TTX and \textit{\textmu}-conotoxins only partially overlap and involve multiple Na\textsubscript{v} residues in the case of the larger \textit{\textmu}-conotoxins (Sato et al., 1991; Dudley et al., 1995; Li et al., 1997), whereas TTX binding is crucially defined by relatively few residues deep in the pore of the Na\textsubscript{v} (see Fozzard and Lipkind, 2010). Not surprisingly, \textit{\textmu}-conotoxin binding to Na\textsubscript{v} involves multiple interacting peptide side chains (see below). This larger surface area of interaction at the entrance to the channel opens up prospects to engineer further Na\textsubscript{v} subtype selectivity, which has been considered challenging to date because of the overall high homology between Na\textsubscript{v} subtypes in the pore region.

The first \textit{\textmu}-conotoxins discovered were GIIIA to GIIIC, which selectively target the skeletal muscle subtype Na\textsubscript{v}1.4 (Cruz et al., 1985). In recent years, the Na\textsubscript{v} subtype selectivity of \textit{\textmu}-conotoxins has been studied with renewed interest; many have now shown subtype selectivity for neuronal subtypes, including PIIIA, KIIIA, MIIIA, CIIIA, CnIIIA, CnIIIB, SIIIA, SmIIIA, and TIIIA. To date, no \textit{\textmu}-conotoxins have been identified with affinity for the TTX-resistant mammalian subtypes Na\textsubscript{v}1.5, -1.9, and -1.8 (Lewis et al., 2007; Schroeder et al., 2008; Leipold et al., 2011; Wilson et al., 2011a) despite a number showing activity at amphibian TTX-resistant isoforms (Zhang et al., 2006b) (see Table 5). The least susceptible isoforms include Na\textsubscript{v}1.3, -1.7, and -1.5, and no \textit{\textmu}-conotoxins have yet been found to block recombinantly expressed Na\textsubscript{v}1.8 (Lewis et al., 2007; Schroeder et al., 2008; Leipold et al., 2011; Wilson et al., 2011a). Instead, the \textit{\textmu}-conotoxins seem to either target the mammalian skeletal muscle isoform Na\textsubscript{v}1.4 and/or the mammalian brain isoform Na\textsubscript{v}1.2 with highest affinity. However, the modest variations in potency at the other neuronal Na\textsubscript{v} subtypes (Table 5) may allow the development of analogs that target therapeutically relevant Na\textsubscript{v}s.

Coexpression of the pore-forming \(\alpha\) subunits with relevant \(\beta\) subunits does not seem to affect \textit{\textmu}-conotoxin selectivity or affinity, at least in the case of KIIIA (Wilson et al., 2011a), although comprehensive studies using other \textit{\textmu}-conotoxins are lacking. It is noteworthy that for many \textit{\textmu}-conotoxins, Na\textsubscript{v} subtype selectivity seems to critically depend on dissociation rate constants. For example, the high affinity of KIIIA for Na\textsubscript{v}1.2 relates to its extremely slow dissociation constant, resulting in essentially irreversible high-affinity block of Na\textsubscript{v}1.2 but lower affinity reversible block of other TTX-sensitive channels (McArthur et al., 2011).
The pharmacophore of the μ-conotoxins GIIXIA, PIIXIA, and TIIXIA with five residues in loop 1 has been mapped to a critical Arg13 or Arg14 in similar positions on a turn in loop 2 (Chahine et al., 1995; Shon et al., 1998a; Lewis et al., 2007). In contrast, the pharmacophore of μ-conotoxins with one to three residues in loop 1 has been mapped to an α-helical motif formed by loops 2 and 3, with the equivalent loop 2 arginine playing only a minor role in affinity (Zhang et al., 2007; Schroeder et al., 2008). Reflecting the more extended surface of interaction with Na⁺ for these small μ-conotoxins, several residues have been found to contribute critically to Na⁺ affinity and/or selectivity of μ-conotoxins, opening up perhaps the best opportunities for the development of subtype specific inhibitors. Lys7 in KIIIA and the equivalent Lys11 in SIIIA contribute mostly to the direct binding of this residue in the pore of Navs (McArthur et al., 2011; Van Der Haegen et al., 2011); substitutions also affected the extent of Na⁺ inhibition by KIIIA, the decrease in efficacy correlating with the residue size (Zhang et al., 2010). The corresponding Arg14 in PIIXIA and TIIXIA also significantly decreased Na⁺ affinity, again most prominently at Na⁺,1.4 (Shon et al., 1998a; Lewis et al., 2007; Schroeder et al., 2008), consistent with direct binding of this residue in the pore of Na⁺,s (McArthur et al., 2011). Not surprisingly, substitution of the analogous residue in GIIXIA (Arg13) produced a striking loss of activity at Na⁺,1.4 in this peptide (Sato et al., 1991; Becker et al., 1992), with interaction with Glu758 in domain II and Glu403 in domain I identified in Na⁺,1.4 (Chang et al., 1998).

Another residue with important implications for Na⁺ affinity and selectivity is Trp8 in KIIIA and the equivalent Trp12 in SIIIA (Lewis et al., 2007; Schroeder et al., 2008; McArthur et al., 2011; Van Der Haegen et al., 2011); substitution of this residue in KIIIA and SIIIA decreases affinity and favors Na⁺,1.2 selectivity over Na⁺,1.4. In contrast, the unusual negative charge (Glu15) in loop 2 of TIIXIA seems to introduce an unfavorable interaction or clash, with [E15A]TIIXIA having enhanced affinity, especially for Na⁺,1.2, where it is the most potent μ-conotoxin inhibitor of neuronal Na⁺,s identified to date (Lewis et al., 2007). The smaller μ-conotoxins KIIIA (SIIIA) are also affected by alanine substitutions at Arg10 (Arg14) and Asp11 (Asp15), which favor Na⁺,1.2 selectivity over Na⁺,1.4 (Zhang et al., 2007; Schroeder et al., 2008). It is noteworthy that the sequence of SIIIA and SIIIB differ only in residues at this position (Arg14 and Asp15 for SIIIA, and Lys14 and Gly15 for SIIIB); accordingly, the major difference between these toxins is the preferential inhibition of Na⁺,1.2 over Na⁺,1.4 by SIIIA and the reversed selectivity for SIIIB (Schroeder et al., 2008).

Several μ-conotoxin analogs have been identified that have striking effects on subtype selectivity beyond Na⁺,1.2/1.4. Most notably, KIIIA[R14A] has been found to preferentially inhibit Na⁺,1.7 over Na⁺,1.2 and Na⁺,1.4, albeit with decreased affinity overall (McArthur et al., 2011). Nonetheless, this finding indicates that it is possible to engineer smaller μ-conotoxins with tailored subtype selectivity, especially as our understanding of the precise structural requirements for Na⁺ subtype binding are improved after the report of the first voltage-gated sodium channel structure (see Fig. 3B).

B. μ-O-Conotoxin Inhibitors of Voltage-Gated Sodium Channels

The μ-O-conotoxins belong to the O superfamily of conopeptides and possess an ICK motif with appropriate disulfide bond connectivity (Table 5). Despite the relatively few peptides identified in this class, μ-O-conotoxins MrVIA and MrVIB have received considerable attention, because their analgesic effects in animal models of pain were ascribed to their relative selectivity for Na⁺,1.8 over other TTX-sensitive Na⁺ subtypes expressed in DRG neurons (Daly et al., 2004; Bulaj et al., 2006; Ekberg et al., 2006). Significant differences in their affinity at native Na⁺,1.8 expressed in DRG neurons and heterologously expressed Na⁺,1.8 have been reported. These presumably arise because of the presence of auxiliary β subunits, particularly β2, which has recently been shown to significantly increase the rate of Na⁺,1.8 inhibition by MrVIB and to increase its potency accordingly (Wilson et al., 2011b). It is noteworthy that μ-O-conotoxins can also differentiate between the TTX-resistant subtypes Na⁺,1.8 and -1.9, because the persistent Na⁺,1.9 current in DRG neurons was unaffected by MrVIB (Ekberg et al., 2006). Although MrVIA and MrVIB have been found to affect molluscan Ca⁺, (Fainzilber et al., 1995c), this mechanism does not seem to contribute to the analgesic effect, because mammalian Ca⁺, in DRG neurons were unaffected (Daly et al., 2004).

The μ-O-conotoxin binding site remains to be fully defined but seems to overlap at least partially with site 6, in that MrVIA was able to displace δ-conotoxin TxVIA binding (Ekberg et al., 2006). In addition, selectivity of MrVIA at Na⁺,1.4 over Na⁺,1.2 has been attributed to the SS2 loop of domain III (Zorn et al., 2006). It is noteworthy that this site is also involved in β scorpion toxin binding to site 4 (Leipold et al., 2006), and both Na⁺,1.4 and Na⁺,1.8 share a homologous residue in this domain that is distinct from the other Na⁺ subtypes and may contribute to the relative selectivity of MrVIA and MrVIB (Ekberg et al., 2006). Accordingly, functional overlap with the β scorpion toxin Ts1 was recently described, suggesting μO conotoxins interact with the voltage sensor of Na⁺,s (Leipold et al., 2007). Indeed, voltage-dependent relief of Na⁺,1.4 inhibition by MrVIB was attributed to the voltage sensor of domain II (Leipold et al., 2007), another site shared with β scorpion toxins. Similar effects were also reported for Na⁺,1.8, where the Kₐff of MrVIB was also accelerated by strong depolarizations (Wilson et al., 2011b). However, compared with Na⁺,1.4, the Kₐff of MrVIB at Na⁺,1.8 was significantly slower and required repeated depolarizations to relieve block (Wilson et al., 2011b).

In contrast to the μ-conotoxins, relatively little is known about the structure-activity relationships of μO-conotoxins, in part because only MrVIA and MrVIB, which differ
by only three residues (Ser3/Arg3; Leu14/Ile14; Val17/Ile17), have been available for pharmacological evaluation, and their effects remain to be evaluated across all Na\textsubscript{v} subtypes in parallel. In addition, difficulties synthesizing, correctly folding, and purifying hydrophobic \(\mu\)O-conotoxins have thwarted attempts to identify their pharmacophore through alanine-scanning approaches. However, recent improvements in oxidative folding of synthetic MrVIB through regioselective synthesis using selenocysteines may provide an accelerated avenue for the generation of \(\mu\)O-conotoxin analogs, allowing residues contributing to their affinity and subtype selectivity to be identified (de Araujo et al., 2011).

C. Other Conotoxin Inhibitors of Voltage-Gated Sodium Channels

Conotoxin GS was identified as an O-superfamily conotoxin; however, in contrast to MrVIA and MrVIB, conotoxin GS seems to share a binding site with TTX and GIIIA, suggesting that this conotoxin is distinct both in structure and mode of action (Yanagawa et al., 1988; Hill et al., 1997). In addition, two novel O-superfamily conotoxins, LtVIC and LtVIIA, were identified from Conus litteratus using a DNA-sequencing approach (Pi et al., 2007; Wang et al., 2008). Both recombinant peptides inhibited sodium currents in DRG neurons in a manner similar to that of MrVIA and MrVIB, suggesting that they are novel \(\mu\)O-conotoxins, but their subtype selectivity and structure-activity relationships remain to be investigated. Even more unusual is the \(\mu\)T-conotoxin, LtVD, which is reported to inhibit TTX-sensitive Na\textsubscript{v}, and is thus classified as the first \(\mu\)-conotoxin from the large class of small T-superfamily conopeptides (Liu et al., 2007a).

D. \(\delta\)-Conotoxin Activators of Voltage-Gated Sodium Channels

The \(\delta\)-conotoxins, ICK peptides structurally related to the \(\mu\)O- and \(\omega\)-conotoxins, exhibit functional similarities to the site 3 \(\alpha\)-scorpion toxins; they inhibit fast Na\textsubscript{v} inactivation and shift the voltage-dependence of activation to more negative potentials, resulting in a prolongation of action potentials and persistent neuronal firing (Leipold et al., 2005). Structural analysis has shown that several hydrophobic residues conserved across the \(\delta\)-conotoxins are present on the external surface of the peptides (Shon et al., 1994), where they could potentially interact with hydrophobic residues in the S3/S4 linker of domain IV, which form part of the \(\delta\)-conotoxin binding pocket, site 6 (Leipold et al., 2005).

Little is known about Na\textsubscript{v} subtype selectivity of the \(\delta\)-conotoxins. \(\delta\)-Conotoxins isolated from molluscivorous cone snails, with the exception of Am2766 (Sudarsal et al., 2003; Sarma et al., 2005), target only molluscan Na\textsubscript{v}, and are inactive at mammalian targets, whereas \(\delta\)-conotoxins from piscivorous cone snails seem to also inhibit inactivation of mammalian Na\textsubscript{v}. Intriguingly, although \(\delta\)-conotoxins from molluscivorous cone snails, such as TxVIA and GmVIA, showed no activity at mammalian Na\textsubscript{v}, they still bind to mammalian tissues, suggesting that subtle differences in the \(\delta\)-conotoxin binding site lead to profound effects on activity (Fainzilber et al., 1995a; Hasson et al., 1995; Shichor et al., 1996). A number of \(\delta\)-conotoxins with activity at mammalian Na\textsubscript{v,2} and Na\textsubscript{v,4} have been described previously (Bulaj et al., 2001; Sudarsal et al., 2003; Leipold et al., 2005; Sarma et al., 2005), although detailed selectivity studies have not been conducted for the majority of these peptides. A recent report that EVIA displayed selectivity for neuronal subtypes Na\textsubscript{v,1.2}, 1.3 and 1.6 over muscle and cardiac subtypes Na\textsubscript{v,1.4} and Na\textsubscript{v,1.5} promises that subtype selectivity may be found for other \(\delta\)-conotoxins (Barbier et al., 2004).

Reminiscent of the \(\mu\)O-conotoxins, difficulties relating to the synthesis and purification of the hydrophobic \(\delta\)-conotoxins and their analogs again results in low yields of correctly folded peptide that have limited progress on both Na\textsubscript{v} subtype-selectivity and structure-activity relationships. High sequence homology between \(\delta\)-conotoxins from piscivorous cone snails has been noted, particularly in the central hydrophobic region of these peptides (Bulaj et al., 2001). It is noteworthy that the PVIA[9F]A and PVIA[12A] analogs lost activity at mammalian Na\textsubscript{v}, consistent with the hypothesis that these hydrophobic residues interact with hydrophobic residues that form part of site 6, whereas analogs of the adjacent residues T8A and K13A retained activity (Bulaj et al., 2001). However, the substantial reduction in affinity upon replacing Ile12 with an alanine is surprising if only hydrophobic interactions are involved, suggesting the possibility that this change may have in fact altered the structure of PVIA. It remains to be determined to what degree, if any, these residues affect Na\textsubscript{v} subtype selectivity, or whether these findings apply to \(\delta\)-conotoxins from molluscivorous cone snails that have divergent sequences.

E. \(\iota\)-Conotoxin Activators of Voltage-Gated Sodium Channels

Two \(\iota\)-conotoxins have recently been identified as Na\textsubscript{v} activators with a mechanism of action distinct from that of the \(\delta\)-conotoxins. \(\iota\)-RXIA is a large, 46-residue peptide from the I superfamily that forms an ICK motif, whereas LtIIIA is a small, 17-residue peptide belonging to the M superfamily of conotoxins (Jimenez et al., 2003; Buzcek et al., 2007; Wang et al., 2009). Despite these sequence and structural differences, both \(\iota\)-conotoxins activate Na\textsubscript{v} without significantly affecting inactivation, in contrast to the \(\delta\)-conotoxins. Specifically, LtIIIA enhanced the amplitude of TTX-sensitive whole-cell Na\textsuperscript{+} currents in DRG without any apparent effects on inactivation (Wang et al., 2009), whereas RXIA shifted the voltage dependence of activation of Na\textsubscript{v,1.6} and Na\textsubscript{v,1.2} to more hyperpolarized potentials without affecting inactivation (Fiedler et al., 2008). It is noteworthy that the post-translationally modified Phe44 (\(\iota\)-Phe) was important for activity particularly at Na\textsubscript{v,1.2}, suggesting participation of the disordered C-terminal tail.
in binding to a yet to be defined Na\textsubscript{v} site (Fiedler et al., 2008). RXIA was also active at Na\textsubscript{v,1.7} but did not affect other Na\textsubscript{v} subtypes (Fiedler et al., 2008), suggesting that detailed structure-activity relationship and subtype selectivity studies of the 17 \( \tau \)-conotoxins identified in Conus radiatus (Jimenez et al., 2003) might shed further light on the mode of action of this potentially interesting family of excitatory conopeptides.

F. Sodium Channel Inhibition in Pain Management

Sodium channel (Na\textsubscript{v}) inhibitors are used as local anesthetics, analgesics, antiarrhythmics, and anticonvulsants. They are most widely used for regional anesthesia and analgesia, as well as systemically for chronic pain management. Until very recently, the utility of small-molecule Na\textsubscript{v} subtypes (Fiedler et al., 2008), suggesting that with highly selective expression in different tissues has provided a strong impetus to identify subtype selective Na\textsubscript{v} antagonists for pain management. The selectivity of conotoxins for different channel types may provide novel drugs for clinical use in regional anesthesia and for systemic or intrathecal administration in chronic pain states. The potential restriction of peptide distribution to systemic tissue compartments rather than central nervous or local application in restricted tissue compartments could provide advantages for these selective peptide Na\textsubscript{v} antagonists. Among the conotoxin classes,

<table>
<thead>
<tr>
<th>Isoform</th>
<th>Distribution</th>
<th>Potential Effects/Side Effects</th>
<th>Selective Toxin Inhibitors</th>
<th>References</th>
</tr>
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<tbody>
<tr>
<td>Na\textsubscript{v,1.1} (SCN1A)</td>
<td>Located primarily in neuronal soma. Found widely in CNS and peripheral neurons (including DRG) cardiac myocytes (T-tubules) (cortex, hippocampus, cerebellum), PNS, DRG, motor neurons.</td>
<td>Widespread effects on the nervous and cardiovascular systems.</td>
<td>No selective conotoxins</td>
<td>Catterall et al., 2005a; Catterall, 2010</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.2} (SCN2A)</td>
<td>Located primarily in axons, node of Ranvier. Found in CNS low expression in adult DRG.</td>
<td>Widespread effects on the nervous and cardiovascular systems.</td>
<td>( \mu )-Conotoxins</td>
<td>Catterall et al., 2005a; Catterall, 2010; Wilson et al., 2011a</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.3} (SCN3A)</td>
<td>Widely distributed in embryonic nervous system but declines postnatally; adult rat CNS, particularly dorsal spinal cord; also upregulated after injury; adult human CNS.</td>
<td>Limited evidence for analgesia. If restricted to periphery, side effects should be minimal; intrathecal CNS side effects possible.</td>
<td>No selective conotoxins</td>
<td>Felts et al., 1997; Hains et al., 2003; Catterall et al., 2005a; Catterall, 2010</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.4} (SCN4A)</td>
<td>Skeletal muscle</td>
<td>Muscle dysfunction</td>
<td>( \mu )-Conotoxins</td>
<td>Catterall et al., 2005a; Schroeder et al., 2008; Catterall, 2010; Wilson et al., 2011a</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.5} (SCN5A)</td>
<td>Cardiac muscle, embryonic DRG</td>
<td>Cardiac side effects</td>
<td>No selective conotoxins</td>
<td>Catterall et al., 2005a; Catterall, 2010</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.6} (SCN8A)</td>
<td>Highly localized in nodes of Ranvier in CNS and PNS, including DRG.</td>
<td>Widespread effects on the nervous and cardiovascular systems.</td>
<td>No selective conotoxins</td>
<td>Catterall et al., 2005a; Catterall, 2010</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.7} (SCN9A)</td>
<td>High expression in small sensory (DRG) neurons and autonomic neurons, also Schwann cells, CD1 + dendritic cells, and some endocrine cells (adrenal medulla).</td>
<td>Analgesic effects. Possible autonomic side effects but autonomic function seems normal with loss-of-function mutations; olfactory side effects.</td>
<td>No selective conotoxins (ProTx-II, huwentoxin-IV)</td>
<td>Catterall et al., 2005a; Cummins and Rush, 2007; Schmalhofer et al., 2008; Xiao et al., 2008a; Xiao et al., 2008b</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.8} (SCN10A)</td>
<td>Small- to medium-sized (presumably nociceptive) DRG neurons, also found in retina and cardiac myocytes.</td>
<td>Analgesic effects. Visual and cardiac side-effects likely from distributional and human mutation studies.</td>
<td>MrVIA, MrVIB</td>
<td>Ekberg et al., 2006; Cummins and Rush, 2007; O’Brien et al., 2008; Chambers et al., 2010</td>
</tr>
<tr>
<td>Na\textsubscript{v,1.9} (SCN11A)</td>
<td>Small-diameter, mostly unmyelinated DRG neurons, also found in retina.</td>
<td>Potential analgesic effects. Potential visual effects.</td>
<td>None known</td>
<td>Catterall et al., 2005a; Cummins and Rush, 2007; O’Brien et al., 2008</td>
</tr>
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PNS, peripheral nervous system.
some $\mu$- and $\mu$O-conotoxins show promise as selective Na$_v$ subtype inhibitors. A large number of $\mu$-conotoxins display considerable channel type selectivity. Most of those isolated inhibit Na$_v$1.2 and Na$_v$1.4 most potently (Schroeder et al., 2008; Wilson et al., 2011a). Although some $\mu$-conotoxins (e.g., KIIIA) have analgesic activity after systemic administration (Zhang et al., 2007), none to date have shown a clear Na$_v$ selectivity profile suitable for development as pain therapeutics. By contrast, several $\mu$O-conotoxins have shown a clear Na$_v$ selectivity profile suitable for development as pain therapeutics because of their established role in pain, selective expression in nociceptive neurons and nerve terminals, and/or their regulation in pain states (see reviews by Catterall et al., 2005a; Cummins and Rush, 2007; Dib-Hajj et al., 2009; England and de Groot, 2009; Catterall, 2010; Catterall et al., 2010). Other Na$_v$ types are also expressed in sensory neurons, including Na$_v$1.1, -1.6, and (at low levels) -1.5 (Catterall et al., 2005a; Catterall, 2010; Dib-Hajj et al., 2010), but inhibition studies with $\mu$-conotoxins have suggested that Na$_v$1.6 and Na$_v$1.7 are the major contributors to peripheral nerve action potentials (Wilson et al., 2011a). Widespread expression of these subtypes (except Na$_v$1.7, see below) in other excitable tissues is likely to preclude the application of inhibitors of these channels as pain therapeutics. The role of Na$_v$ subtypes in pain pathways and their potential for selective targeting by conotoxins is outlined below.

Of the potential Na$_v$ pain targets, Na$_v$1.7 is one of the most promising for pain management. Na$_v$1.7 is expressed almost exclusively in peripheral neurons (Catterall et al., 2005a) and selectively in nociceptive primary afferents (Raymond et al., 2004). Na$_v$1.7 gene deletion targeted to nociceptive sensory neurons (Na$_v$1.8 expressing) or knockdown reduces inflammatory pain and thermal hyperalgesia (Nassar et al., 2004) but not neuropathic pain (Nassar et al., 2005). The reason for this lack of effect in neuropathic pain is still unknown. Na$_v$1.7 expression is up-regulated in injured nerves and in sensory neuron cell bodies in inflammatory pain and may contribute to ectopic action potential discharge in painful neurones (Dib-Hajj et al., 2010). In humans, rare loss-of-function mutations of Na$_v$1.7 produce a complete absence of pain sensation (Cox et al., 2006; Goldberg et al., 2007) and, conversely, gain-of-function mutations are associated with painful neuropathies (Fertleman et al., 2006; Han et al., 2006). Polymorphisms in Na$_v$1.7 in normal humans are also significantly correlated with pain sensitivity (Reimann et al., 2010). The mechanism responsible for the profound loss of function for Na$_v$1.7 mutations in human pain remain uncertain, but these channels are concentrated in nerve endings and amplify small depolarizations; they therefore have the potential to play a major role in coupling generator potentials in nociceptive afferent nerves with action potential generation (Cummins et al., 1998).

There are already several relatively selective small-molecule inhibitors of Na$_v$1.7 that have shown efficacy in acute, inflammatory, and neuropathic pain models (Williams et al., 2007; London et al., 2008; Bregman et al., 2011; Chowdhury et al., 2011). Although many conotoxins can also inhibit Na$_v$1.7 (see above), no highly selective antagonists have been identified to date, although analogs of the smaller $\mu$-conotoxins have potential (see above). At the moment, spider venoms are more promising sources of selective Na$_v$1.7 inhibitors. For example, ProTx-II from the tarantula *Thrixopelma pruriens* is a potent and selective inhibitor of Na$_v$1.7 (~100-fold over other types) but shows limited efficacy in inflammatory pain models after intravenous or intrathecal administration (Schmalhofer et al., 2008). This lack of activity in pain models might suggest that selective Na$_v$1.7 inhibitors are not as useful as previously thought, but the possibility that the peptide distributes poorly from the circulation to nociceptive nerve endings cannot be excluded. Huwentoxin-IV, from the tarantula *Ornithoctonus huwena*, is also modestly selective for Na$_v$1.7 (it also inhibits Na$_v$1.2 and Na$_v$1.3), but actions in animal pain models have not been reported in detail (Xiao et al., 2008a,b).

Na$_v$1.7 is also expressed in several other tissues. A major off-target location of Na$_v$1.7 expression are olfactory neurons (Ahn et al., 2011), and loss-of-function mutations can cause anosmia (Weiss et al., 2011). However, such side effects may not be of major concern to persons suffering severe pain, but loss of smell would be expected to reduce quality of life during prolonged treatment. More recently Na$_v$1.7 expression in monocyte-derived dendritic cells has been shown to modify responses to cytokines (Kis-Toth et al., 2011), suggesting potential for immune modulation and potentially immunological side effects of Na$_v$1.7 inhibitors.

The TTX-resistant channel Na$_v$1.8 is also a promising target for pain management. It is expressed predominantly in small nociceptive primary afferent nerves (Catterall et al., 2005a; Cummins and Rush, 2007; Catterall, 2010; Dib-Hajj et al., 2010). Na$_v$1.8 contributes to the action potential and repetitive firing in small, nociceptive sensory neurons (Catterall et al., 2005a; Cummins and Rush, 2007; Catterall, 2010; Dib-Hajj et al., 2010). The activity of Na$_v$1.8 in sensory neurons is strongly enhanced by inflammatory mediators, both via up-regulation and/or modulation of channel kinetics by protein kinase A and C (see Dib-Hajj et al., 2010). Both protein and mRNA for Na$_v$1.8 are up-regulated locally in injured sciatic nerves in nerve injury models (Gold et al., 2003; Thakor et al., 2009). Na$_v$1.8 knockdown (Lai et al., 2002; Gold et al., 2003) and gene deletion (Akopian et al., 1999) studies have suggested an important role in neuropathic and inflammatory pain. Perhaps the most significant phenotype in Na$_v$1.8 knockout mice is a nearly complete loss of ectopic action potential activity in experimental neuromas (Roza et al., 2003). Together with the established redistribution of Na$_v$1.8 to sites of nerve injury and neuromas in animal models and
humans (e.g., Black et al., 2008), this finding may suggest a specific therapeutic use for Na\textsubscript{v}1.8 inhibitors in nerve injury-induced pain associated with neuromas.

\(\mu\text{O}-\text{conotoxins MrVIA and MrVIB inhibit Na}_{v}1.8\) in sensory neurons (Daly et al., 2004; Ekberg et al., 2006) and significantly reduce mechanical and thermal pain in both neuropathic and inflammatory pain models; selectivity over motor side effects is more than 30-fold greater than found for lidocaine (Ekberg et al., 2006). It is noteworthy that potentially more stable and easier to synthesize selencysteine analogs produced similar beneficial effects (de Araujo et al., 2011). These findings suggest that direct spinal administration of Na\textsubscript{v}1.8-selective conotoxins may have a place in pain management. MrVIB has also been shown to display local anesthetic actions after intraplantar administration (Bulaj et al., 2006). Although Na\textsubscript{v} inhibitors from other species have yet to show preferential Na\textsubscript{v}1.8 targeting, a chimeric scorpion toxin (drosotoxin) shows quite low potency but high selectivity for TTX-resistant (Na\textsubscript{v}1.8) versus TTX-sensitive Na\textsubscript{v}, currents in rat sensory neurons (Zhu et al., 2010). Consistent with results obtained using \(\mu\text{O}-\text{conotoxins, small-molecule antagonists preferentially targeting Na}_{v}1.8\) (Jarvis et al., 2007; Scanio et al., 2010) have since been reported to show efficacy in neuropathic pain models.

Although small-molecule and conotoxin inhibitors of Na\textsubscript{v}1.8 have produced efficacy in pain models, there are concerns about adverse side effects. For example, in addition to their selective expression in nociceptive sensory nerves, Na\textsubscript{v}1.8 and Na\textsubscript{v}1.9 is expressed in retina (O’Brien et al., 2008), where small-molecule antagonists could produce retinal side effects, although peptides are potentially excluded from this compartment. Of more concern is the recent finding that Na\textsubscript{v}1.8 is expressed in cardiac myocytes and that polymorphisms in the Na\textsubscript{v}1.8 gene influence QT interval, electrocardiogram conduction block, and ventricular fibrillation (Chambers et al., 2010), raising the potential for severe cardiac side effects from systemic use of Na\textsubscript{v}1.8 inhibitors that would complicate long-term use.

The tetrodotoxin-resistant channel, Na\textsubscript{v}1.9 is also a promising target for pain management but has been less thoroughly studied than Na\textsubscript{v}1.7 or Na\textsubscript{v}1.8, largely because attempts to express the channel in heterologous expression systems have been unsuccessful. It is expressed predominantly in small sensory neurons, particularly in a subclass of C-fiber nociceptors (Fang et al., 2006) and visceral sensory nerves (Rugiero et al., 2003). It has also been detected in retina (O’Brien et al., 2008). Na\textsubscript{v}1.9 produces a persistent sodium current that modulates resting membrane potential and amplifies small depolarizations, contributing to excitability of small nociceptive nerves. The activity of Na\textsubscript{v}1.9 is strongly enhanced by inflammatory mediators (e.g., Maingret et al., 2008; Ostman et al., 2008), although a number of Na\textsubscript{v}1.9 gene deletion studies have consistently found little or no effect on neuropathic pain, except for inhibition of cold allodynia (Leo et al., 2010). In contrast, thermal pain sensitivity is consistently blunted in inflammatory pain models in Na\textsubscript{v}1.9 knockout animals (Priest et al., 2005; Amaya et al., 2006). Na\textsubscript{v}1.9 inhibitors may therefore be useful for inflammatory and visceral pain. Because of the difficulties in heterologously expressing Na\textsubscript{v}1.9, no selective pharmacological tools, including conotoxins, have been identified to study its function in normal neurons and pain states. However, some spider and scorpion toxins including ProTxI and TsVII were recently found to interact with Na\textsubscript{v}1.9 endogenously expressed in DRG neurons in a nonselective manner (Bosmans et al., 2011).

Na\textsubscript{v}1.3 is also a potential target for pain therapeutics, although its role in the maintenance of pain remains controversial. It is highly expressed in embryonic DRG neurons but declines to very low levels in adult sensory neurons (Felts et al., 1997). Expression of Na\textsubscript{v}1.3 in sensory neurons is strongly up-regulated by nerve injury (Black et al., 1999; Lindia and Abbadie, 2003; Fukuoka et al., 2008) and is up-regulated in humans in painful neuromas (Black et al., 2008) and the spinal cord (Hains et al., 2003). Antisense knockdown of Na\textsubscript{v}1.3 in nerve-injured rats has been shown to attenuate signs of neuropathic pain (Hains et al., 2003), but in other studies, no effects of knockdown were found (Lindia et al., 2005). Moreover, both global and nociceptor-specific (Na\textsubscript{v}1.8 Cre mice) deletion of Na\textsubscript{v}1.3 in mice had no effect on neuropathic pain behavior or ectopic discharges from damaged nerves, suggesting Na\textsubscript{v}1.3 is neither necessary nor sufficient for development of nerve-injury related pain (Nassar et al., 2006). The latter findings have strongly questioned the importance of Na\textsubscript{v}1.3 in nerve injury-related pain and have reduced the impetus to develop Na\textsubscript{v}1.3 specific inhibitors. Although several \(\mu\text{O}-\text{conotoxins can inhibit Na}_{v}1.3, they all interact more potently with Na}_{v}1.2 or Na}_{v}1.4 (Wilson et al., 2011a), and more selective analogs are required before chemical dissection of the role of Na\textsubscript{v}1.3 in different pain states can be investigated.

In conclusion, the potential for identification and development of Na\textsubscript{v}1 subtype-selective conotoxins remains largely untapped. Conotoxins that selectively interact with Na\textsubscript{v}1.7, Na\textsubscript{v}1.9, and/or Na\textsubscript{v}1.3 need to identified; mixed block of these subtypes potentially produces greater efficacy than the selective block of a single subtype. It should also be noted that the potency of conotoxins may differ in injured versus uninjured neurons. As observed for \(\omega\)-conotoxins (see section II.C), interactions of \(\mu\text{O}-\text{conotoxins with Na}_{v}\) channel types are also influenced by auxiliary subunit expression. Na\textsubscript{v}1.8 molecules are up-regulated in sensory neurons in neuropathic pain models (Pertin et al., 2005) and interact with Na\textsubscript{v}s to increase the on-rate of MrVIB in heterologous systems (Wilson et al., 2011b), providing the \(\mu\text{O}-\text{conotoxins with a window of functional selectivity. It is noteworthy that Na}_{v}1.8 subunits are also up-regulated in pain states (Shah et al., 2000), and their expression levels influence gating of Na\textsubscript{v}1.3 (Cusdin et al., 2010) to potentially influence \(\mu\text{O}-\text{conotoxin pharmacology in a disease-dependent manner.}
III. \(\kappa\)-Conotoxins Interacting with Potassium Channels

Potassium channels comprise a vastly diverse family of ion channels, with a large number of genes encoding for the pore-forming \(\alpha\)-subunits, which are divided into channels with six, four, and two transmembrane domains. Accordingly, multiple families of \(\kappa\)-conotoxins targeting several different potassium channels have been isolated from cone snail venom (Table 7). Activity at potassium channels appears to constitute an important component of the “lightning-strike” cabal of piscivorous cone snails (Terlau et al., 1996); however, relatively little is known about subtype selectivity and structure-activity relationship of conotoxins targeting potassium channels, and potential therapeutic uses have not yet been determined.

A. \(\kappa\alpha\)-Conotoxins

The \(\kappa\alpha\)-conotoxins MIVA, SIVA, SIVB, SmIVA, SmIVB, PIVE, CcTx, and PIVF (Teichert et al., 2007a) are relatively short excitatory peptides that elicit potent effects after intramuscular injection in fish and direct exposure to amphibian neuromuscular preparations, but not in mammals. It remains unclear whether these observed differences are due to pharmacodynamic effects (such as restricted access to mammalian \(K_c\) channels expressed in juxtaparanodal regions of myelinated motor axons) or they reflect strong differences in subtype affinity (Teichert et al., 2007a). Although some of these peptides inhibit \(Shaker\) \(K_c\) channels, the precise target and structure activity relationship for many of the \(\kappa\alpha\)-conotoxins remains unclear.

B. \(\kappa\omega\)-Conotoxins

The \(\kappa\omega\)-conotoxin PVIIA has received particular attention because it was shown to exhibit cardioprotective properties in several animal models of ischemia-reperfusion injury (Lubbers et al., 2005). Arg2, Lys7, Phe9, and Phe23 were shown to contribute to voltage-dependent interactions with the \(Shaker\) potassium channel (Scanlon et al., 1997), which was identified as the molecular target of PVIIA and is highly homologous with mammalian \(K_c\) isoforms (Terlau et al., 1996; Shon et al., 1998b; Huang et al., 2005). These residues form part of a lysine-hydrophobic residue dyad, which is evolutionally conserved and contributes to activity at \(K_c\) channels in several other toxins, including charybdotoxin from scorpion and BgK from sea anemone (Savarin et al., 1998; García et al., 1999). Figure 6 shows a model of the interaction between PVIIA and the shaker potassium channel, revealing a likely model of interaction of the dyad comprising Lys7 and Phe9. It is surprising that the rat \(K_c\,1.1\) isofrom was resistant to...
PVIIA (Shon et al., 1998b), indicating that other presently unidentified mammalian \(K_v\) isoforms contribute to the cardioprotective effects of PVIIA.

C. \(\kappa M\)-Conotoxins

Like PVIIA, the \(\kappa M\)-conotoxin RIIIJ was found to exert cardioprotective effects, presumably due to the high affinity of this peptide for mammalian \(K_v1.2\) and \(K_v1.2\)-containing \(K_v1.1\), \(K_v1.5\), and \(K_v1.6\) heteromultimers (Chen et al., 2010). Lys9, in conjunction with other less clearly identified residues, contributes to the high affinity of RIIIJ for \(K_v1.2\). It is noteworthy that RIIIJ was less potent at \(K_v1.2/K_v1.7\)-heteromultimers than the related \(\kappa M\)-conotoxin RIIIK, demonstrating that different \(K_v\) channel heteromultimers are pharmacologically distinct. Several residues, including Leu1, Arg10, Lys18, and Arg19, were found to contribute critically to activity of RIIIK at the trout \(TSha1\) \(K^+\) channel, the \(K_v\) isoform most sensitive to block by RIIIK (Al-Sabi et al., 2004). It is surprising that these residues do not seem to form part of a functional dyad but interact with the channel by means of electrostatic interactions (Al-Sabi et al., 2004; Verdier et al., 2005). Based on docking interactions at the Shaker potassium channel, residues potentially involved in the pharmacophore are indicated in Fig. 6C.

D. \(\kappa J\)-Conotoxins

\(\kappa J\)-Conotoxin pl14a, a member of the J superfamily, is an unusual conotoxin in that it inhibits both \(K_v1.6\) and several isoforms of the nicotinic acetylcholine receptor (nAChR) (Imperial et al., 2006). Homology modeling suggests that this peptide possesses both the putative functional dyad, formed by residues Lys18 and Tyr19, and a ring of basic residues comprising Arg3, Arg5, Arg12, and Arg25, reminiscent of the pharmacophore found in the \(\kappa M\)-conotoxin RIIIK (Mondal et al., 2007). However, it remains to be determined whether these residues are involved in interactions with \(K_v\) channels as predicted. Based on docking
interactions at the Shaker potassium channel, residues potentially involved in the pharmacophore are indicated in Fig. 6B.

E. Kg(2)-Conotoxins

ViTx, sr11a, and BeTX belong to the Kg(2) class of conotoxins and constitute an interesting class of structurally related potassium channel modulators. ViTx inhibits K\textsubscript{r}1.1 and K\textsubscript{r}1.3 but not K\textsubscript{r}1.2 (Kauferstein et al., 2003), whereas the recently identified sr11a inhibits K\textsubscript{r}1.2 and K\textsubscript{r}1.6 but not K\textsubscript{r}1.3 (Aguilar et al., 2010). In contrast, BeTX displays an unusual potentiation of Ca\textsuperscript{2+} and voltage-dependent BK channel current by increasing the channel open probability (Fan et al., 2003). This effect was independent of channel inactivation and was readily reversible, suggesting an interaction with an extracellular binding site (Fan et al., 2003). The molecular basis of the unique subtype selectivity of the Kg(2) conotoxins remains unknown to date. The only lysine in ViTx occurs at the C terminus, suggesting that the conserved dyad motif is not involved and implicates alternate mechanisms of interaction with K\textsubscript{r} channels (Kauferstein et al., 2003). Likewise, sr11a seems to lack a functional dyad motif; however, homology modeling identified Arg17 and Arg29 as residues possibly involved in the biological activity of this novel peptide (Aguilar et al., 2010).

F. Contryphan-Vn

Contryphan-Vn was recently identified as a D-tryptophan-containing disulfide-constrained nonapeptide with activity at both voltage-gated and Ca\textsuperscript{2+}-dependent K\textsuperscript{+} channels, perhaps owing to the presence of a unique Lys-Trp dyad. However, the structural requirements for activity of Contryphan-Vn at these molecular targets, as well as its subtype-selectivity, remain to be determined (Massilia et al., 2003).

G. Conkunitzin-S1

The potassium channel-targeted toxin conkunitzin-S1 is a 60-amino acid peptide that, despite belonging to the Kunitz domain family of proteins, is stabilized by only two disulfide bonds (Bayrhuber et al., 2005). Conkunitzin-S1 was shown to inhibit the Shaker potassium channel by interacting with the ion channel pore through K427 (Bayrhuber et al., 2005).

IV. Conotoxins Interacting with Ligand-Gated Ion Channels

Cone snails have evolved multiple classes of conopeptides to target ligand-gated ion channels, including nAChR, 5-hydroxytryptamine\textsubscript{3} (5-HT\textsubscript{3}), and N-methyl-D-aspartate (NMDA) antagonists as well as \alpha-amino-3-hydroxy-5-methyl-4-isoxazole propionic acid (AMPA) enhancers. Of these, antagonists of nAChRs are the largest and most diverse and, along with the NMDA antagonists, show most potential as leads to new ligand-gated ion channel therapeutics (Table 8).

A. Conotoxin Inhibitors of Nicotinic Acetylcholine Receptors

All Conus spp. venoms investigated to date contain at least one conotoxin that inhibits the nAChR (McIntosh et al., 1999; Dutertre et al., 2007). Overall, seven different families of conotoxins are known to target the nAChR: \alpha-conotoxins, \alphaC-conotoxins, \alphaD-conotoxins, \psi-conotoxins, \alphaS-conotoxins, \alphaL-conotoxins, and \alpha\delta-conotoxins (Table 8). The \alpha-conotoxins are selective antagonists of the muscle-type (3/5) and neuronal-type (4/7, 4/4, and 4/3) nAChRs and arguably represent the largest group of characterized Conus spp. peptides (McIntosh et al., 1999) (Table 8). \alpha-Conotoxins selective for neuronal subtype of nAChR have significantly contributed to their characterization both in vivo and in vitro, and some of these peptides may have therapeutic potential (Livett et al., 2006). The pharmacophore of these \alpha-conotoxins has been thoroughly investigated and has been shown to be composed of a conserved hydrophobic patch in the first loop that determines binding and a more variable second loop that confers selectivity through pairwise interactions with different nAChR subunits (Dutertre et al., 2005).

One of the first structure-activity relationship studies on \alpha-conotoxin was carried out on the closely related PnIA and PnIB (Fainzilber et al., 1994a). The sequences differ by only two amino acids at position 10 and 11, yet PnIA is selective for \alpha3\beta2, whereas PnIB binds preferentially to \alpha7 nAChR. It was later determined that position 10 alone was responsible for the shift in nAChR selectivity (Hogg et al., 1999; Luo et al., 1999). In addition, sequential truncation of the second loop was shown to influence potency and ultimately significantly alter the structure of PnIA (Jin et al., 2008). On the receptor side, mutation of three residues on the \alpha3 nAChR subunit (Pro182, Ile188, and Gly198) affected the high affinity of PnIA (Everhart et al., 2003). These structure-activity relationship studies allowed the construction of a model of the interaction between PnIA and nAChR (Dutertre et al., 2004), which was consistent with the subsequent cocrystal structure of the acetylcholine binding protein (AChBP) and a variant of PnIA (Celie et al., 2005).

ImI is another \alpha-conotoxin for which structure-activity relationship studies have identified determinants that influence potency. Modification of Asp5, Pro6, Arg7, and Trp10 altered the potency of ImI at the \alpha7 nAChR (Quiram and Sine, 1998a, b). Later, thermodynamic mutant cycle analysis identified pairwise interactions between ImI and \alpha7 nAChR (Quiram et al., 1999). The results revealed a major interaction between Arg7 of ImI and Tyr195 in \alpha7, accompanied by smaller contributions between Asp5 of ImI and Trp149, Tyr151, and Gly153 of \alpha7, and between Trp10 of ImI and Thr77 and Asn111 of \alpha7. Again, most of these pairwise interactions were confirmed in the struc-
### TABLE 8

α-Conotoxins inhibiting nAChRs (loop formula COC3–4C3–7C, excluding 3 + disulfide bonded and framework XIV α-conotoxins)

Cysteines are bolded and aligned separately for the different α-conotoxin classes.

<table>
<thead>
<tr>
<th>Species</th>
<th>Diet</th>
<th>Name</th>
<th>Sequence (Disulfide Bonded 1–3/2–4)</th>
<th>nAChR select</th>
<th>References</th>
</tr>
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<tbody>
<tr>
<td>C. achatinus</td>
<td>P</td>
<td>α-Ac1.1a</td>
<td>-NGCXC-HPAC---HRHFC-C</td>
<td>Muscle nAChR</td>
<td>Liu et al., 2007b</td>
</tr>
<tr>
<td></td>
<td>P</td>
<td>α-Ac1.1b</td>
<td>-NGCXC-HPAC---HRHFC-C</td>
<td>Muscle nAChR</td>
<td>Liu et al., 2007b</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-AuA</td>
<td>-GGCXMHPACANNNQDyC</td>
<td>α3β2 &gt; α7</td>
<td>Loughnan et al., 2004</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-AuIB</td>
<td>-GGCXMHPACANNNQDyC</td>
<td>α3β2 &gt; α7</td>
<td>Loughnan et al., 2004</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-ArIA</td>
<td>IRRDCCCFPANKVNNPHVCRR</td>
<td>α7 ~ α3β2</td>
<td>Whiteaker et al., 2007</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-ArIB</td>
<td>-DDRCCCPANNNPHVCRR</td>
<td>α7 &gt; α3β2</td>
<td>Whiteaker et al., 2007</td>
</tr>
<tr>
<td>C. australis</td>
<td>M</td>
<td>α-AuA</td>
<td>-CSSYFPFCANTNSDyC</td>
<td>α3β4</td>
<td>Luo et al., 1998</td>
</tr>
<tr>
<td></td>
<td>M</td>
<td>α-AuIB</td>
<td>-CSSYFPFCANTNSDyC</td>
<td>α3β4 &gt; α7</td>
<td>Luo et al., 1998</td>
</tr>
<tr>
<td></td>
<td>M</td>
<td>α-AuIC</td>
<td>-CSSYFPFCANTNSDyC</td>
<td>α3β4</td>
<td>Luo et al., 1998</td>
</tr>
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<td>C. ballatus</td>
<td>P</td>
<td>α-BuA</td>
<td>---CSSTPFC---AVLYC-C</td>
<td>α6α3β2 &gt; α6α3β4 &gt; α3β2</td>
<td>Azam et al., 2005</td>
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<td>C. consors</td>
<td>P</td>
<td>α-CnIA</td>
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<td>Favreau et al., 1999</td>
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<td>C. ermineus</td>
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<td>α-EI</td>
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<td>Muscle nAChR (αδ &gt; αγ′)</td>
<td>Martinez et al., 1995</td>
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<td>M</td>
<td>α-Eπl</td>
<td>-CSSDPRCFMNNSNQPC-C</td>
<td>α7</td>
<td>Loughnan et al., 1988, 2003b</td>
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<td>P</td>
<td>α-GI</td>
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<td>Muscle nAChR</td>
<td>Gray et al., 1981</td>
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<td></td>
<td>P</td>
<td>α-GIA</td>
<td>---CC--N-PAC---GRHYS-C</td>
<td>Muscle nAChR</td>
<td>Gray et al., 1981</td>
</tr>
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<td></td>
<td>P</td>
<td>α-GIC</td>
<td>---CC--SHPACAGNHNHC-C</td>
<td>α3β2 &gt; α4β2</td>
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<td>M</td>
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<td>α-Iml</td>
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<td>McIntosh et al., 1994, 2004</td>
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<tr>
<td></td>
<td>V</td>
<td>α-IpI</td>
<td>---CSSDAR--RWR--C</td>
<td>α7, noncompetitive</td>
<td>Ellison et al., 2004</td>
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<td>C. leopoldi</td>
<td>V</td>
<td>α-Lp1</td>
<td>---CC--ARAACAGIQGEL-C</td>
<td>α3β2 &gt; α6β3β2</td>
<td>Peng et al., 2008</td>
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<td>C. litteratus</td>
<td>V</td>
<td>α-LtdA</td>
<td>---CC--ARAACAGHIEL-C</td>
<td>α3β2 &gt; α6β3β2</td>
<td>Luo et al., 2010</td>
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<td>C. magus</td>
<td>P</td>
<td>α-MI</td>
<td>---CGCXMHPAC---KGYSC-C</td>
<td>Muscle nAChR</td>
<td>McIntosh et al., 1982</td>
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<td>C. omnus</td>
<td>M</td>
<td>α-OmIA</td>
<td>---CC--SHPACAGNHNHC-C</td>
<td>α6α3β2β3 &gt; α3β2 &gt; α7</td>
<td>Cartier et al., 1996</td>
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<td>V</td>
<td>α-PeIA</td>
<td>IRRDCCCFPANKVNNPHVCRR</td>
<td>α6α10 &gt; α3β2 &gt; α3β4</td>
<td>McIntosh et al., 2005</td>
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<td>P</td>
<td>α-PIA</td>
<td>-RDDCCCPANTNSDyC-C</td>
<td>α6α3β2 &gt; α7</td>
<td>Dowell et al., 2003</td>
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<td>C. pennis etius</td>
<td>M</td>
<td>α-PnIA</td>
<td>---CSSLPACANNPDyC-C</td>
<td>α3β2 &gt; α7</td>
<td>Fainzilber et al., 1994a</td>
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<td>C. quercinus</td>
<td>V</td>
<td>α-Qc1.2</td>
<td>-CSSDPRCFMNNSNQPC-C</td>
<td>α3β2, α3β4</td>
<td>Peng et al., 2009</td>
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<tr>
<td>C. regius</td>
<td>V</td>
<td>α-Reg1β/C</td>
<td>---CC--SDOREKHC--C</td>
<td>N.D.</td>
<td>Franco et al., 2006</td>
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<td></td>
<td>V</td>
<td>α-Reg1δ</td>
<td>---CC--SDPDKEHC--C</td>
<td>N.D.</td>
<td>Franco et al., 2006</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-Reg1e</td>
<td>---CC--SDKRCYR--C</td>
<td>N.D.</td>
<td>Franco et al., 2006</td>
</tr>
<tr>
<td></td>
<td>V</td>
<td>α-Reg1f</td>
<td>---CC--SDKRCYR--C</td>
<td>N.D.</td>
<td>Franco et al., 2006</td>
</tr>
<tr>
<td>C. striatus</td>
<td>P</td>
<td>α-SI</td>
<td>---CC--N-PAC---GRKYS-C</td>
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<td>Zafaralla et al., 1988</td>
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<tr>
<td>C. spurius</td>
<td>V</td>
<td>α-SrA</td>
<td>---CC--HTPANCATT--C</td>
<td>Muscle nAChR</td>
<td>Myers et al., 1991</td>
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<td>C. tinarius</td>
<td>V</td>
<td>α-TIA</td>
<td>---CC--SHPACAGNHNHC-C</td>
<td>Muscleαγ2</td>
<td>López-Vera et al., 2007a</td>
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<td>C. textile</td>
<td>M</td>
<td>α-TxIA</td>
<td>---CSSRCPCTNNPDC-C</td>
<td>α3β2 &gt; α7</td>
<td>López-Vera et al., 2007</td>
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<tr>
<td>C. victoriae</td>
<td>M</td>
<td>α-VcIA</td>
<td>---CSSDPCKYNHDPEIC-C</td>
<td>Neuronal nAChR</td>
<td>Kauferstein et al., 2011</td>
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<td></td>
<td>M</td>
<td>α-VcII</td>
<td>---CSSDPCKYNHDPEIC-C</td>
<td>Neuronal nAChR</td>
<td>Dutterre et al., 2007</td>
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<tr>
<td>C. striatus</td>
<td>P</td>
<td>α-SI</td>
<td>---CC--SNAPAGNNYC--COTSGC</td>
<td>Muscle nAChR</td>
<td>Sandall et al., 2003</td>
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<tr>
<td>C. emineus</td>
<td>P</td>
<td>α-EIVIA</td>
<td>-CSSPYNACOCSCCOCSVROOYCROSGG-C</td>
<td>Muscle nAChR</td>
<td>Vincler et al., 2006</td>
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<tr>
<td></td>
<td>P</td>
<td>α-EIVB</td>
<td>-CSSPYNACOCSCCOCSVROOYCROSGG-C</td>
<td>Muscle nAChR</td>
<td>Vincler et al., 2006</td>
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<tr>
<td>C. obtusus</td>
<td>P</td>
<td>α-OIVIA</td>
<td>-CSSVONACICOSCCOCSVROOYCROSGG-C</td>
<td>Muscle nAChR</td>
<td>Jacobson et al., 1997</td>
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<td>C. pergrandinus</td>
<td>V</td>
<td>α-OFVIA</td>
<td>-CSSVONACICOSCCOCSVROOYCROSGG-C</td>
<td>Muscle nAChR</td>
<td>Jacobson et al., 1997</td>
</tr>
<tr>
<td>C. parvis</td>
<td>P</td>
<td>α-PFI</td>
<td>---CSSVONACICOSCCSRO--C</td>
<td>Fetal &gt; adult muscle nAChR</td>
<td>Teichert et al., 2005b</td>
</tr>
<tr>
<td>C. purpurascens</td>
<td>P</td>
<td>α-PFII</td>
<td>---CSSVONACICOSCCSRO--C</td>
<td>Fetal &gt; adult muscle nAChR</td>
<td>Teichert et al., 2006</td>
</tr>
<tr>
<td>C. littoralis</td>
<td>V</td>
<td>α-LlXIVA</td>
<td>---CC--PPKLEPS--CCNC--</td>
<td>Neuronal nAChR</td>
<td>Peng et al., 2006</td>
</tr>
<tr>
<td>C. planorbis</td>
<td>V</td>
<td>α-PXIVA</td>
<td>FPFRPPCNCZLARAGIHPYFCPCRIC-C</td>
<td>Muscle &gt; α3β2</td>
<td>Imperial et al., 2006</td>
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<tr>
<td>C. radiatus</td>
<td>P</td>
<td>α-RVIIIA</td>
<td>KCND6FDSKRGTGVCYCN-CYSCYCGCLNLHC</td>
<td>Muscle and neuronal nAChR</td>
<td>Teichert et al., 2005a</td>
</tr>
<tr>
<td>C. parvis</td>
<td>P</td>
<td>α-PFIIH</td>
<td>---CC--PPKLEPS--CCNC--</td>
<td>Neuronal nAChR</td>
<td>Lusiana et al., 2008</td>
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<td>C. caelatum</td>
<td>V</td>
<td>α-DVXXA</td>
<td>DDDQCCOCTYHGRGHCSCC-dimer</td>
<td>α7 &gt; α3β2</td>
<td>Loughnan et al., 2006</td>
</tr>
<tr>
<td>C. caelatum</td>
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<td>α7 &gt; α3β2</td>
<td>Loughnan et al., 2006</td>
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<td>V</td>
<td>α-DVXXCC</td>
<td>DLRCCTRANAPGSTQRNPCCLVRPMCGNCPFCPSAG</td>
<td>N.D.</td>
<td>Loughnan et al., 2006</td>
</tr>
</tbody>
</table>
ture of ImI bound to AChBP (Hansen et al., 2005; Ulens et al., 2006).

A third \(\alpha\)-conotoxin of particular interest is MI, which blocks \(\alpha3\beta2\)- and \(\alpha6\)-containing nAChRs (Cartier et al., 1996). A series of analogs were designed to selectively target the \(\alpha6\alpha3\beta2\beta3\) combination (McIntosh et al., 2004) and later used to determine the contribution of \(\alpha6\)-containing nAChR in dopamine release in the striatum and to reveal a down-regulation of this subtype upon long-term nicotine exposure (McCallum et al., 2005; Perry et al., 2007). Radiolabeled and fluoroescenently labeled MI/analogs have also been used to demonstrate down-regulation of these \(\alpha\)-conotoxin binding sites in nigrostriatal damaged animal models as well as in post mortem brain from humans with Parkinson’s disease (Quik et al., 2004). Residues involved in MI binding on the \(\alpha3\beta2\) nAChR have been identified, and these include Lys185 and Ile188 on \(\alpha3\), and Thr59, Val109, Phe117, and Leu119 on the \(\beta\) subunit, allowing a model of the interaction to be built (Harvey et al., 1997; Dutertre et al., 2005). More recently, ArlIB, which blocks both \(\alpha7\) and \(\alpha3\beta2\) nAChR, was compared with other \(\alpha\)-conotoxin sequences and rationally modified to increase \(\alpha 7\) nAChR selectivity (Whiteaker et al., 2007). This structure-function analysis yielded two analogs, V11L, V16A-ArlIB and V11L, V16D-ArlIB, which had low affinity for \(\alpha3\beta2\) but retained \(\alpha7\) nAChR activity as predicted, with an iodinated form developed as a pharmacological tool (Whiteaker et al., 2008).

GID is the only \(\alpha\)-conotoxin with relatively high affinity for the \(\alpha4\beta2\) nAChR subtype (Niec et al., 2003a). This \(\alpha\)-conotoxin is unusual in that it possesses an extended N terminus of four residues, as well as two post-translational modifications. A complete alanine scan of all noncysteine residues revealed that most analogs had at least a 10-fold reduced activity at the \(\alpha4\beta2\) subtype, implying a highly specific interaction (Millard et al., 2009). Docking of GID to \(\alpha4\beta2\) or its cocryrstallization with AChBP could reveal the specific interactions responsible for its \(\alpha4\beta2\) affinity and provide a rationale basis for the design of more selective analogs.

Newly discovered \(\alpha\)-conotoxins Vc1.1, RgIA, and PeIA target the \(\alpha9\alpha10\) nAChR subtype (McIntosh et al., 2005; Clark et al., 2006; Ellison et al., 2006), which may potentially be involved in immune responses and pain (Satkunanathan et al., 2005; McIntosh et al., 2009). Scanning mutagenesis of \(\alpha\)-conotoxin Vc1.1 revealed that Ser4 and Asn9 are important for \(\alpha9\alpha10\) nAChR potency (Halai et al., 2009), whereas for RgIA, Asp5, Pro6, and Arg7 were shown to be critical for both \(\alpha9\alpha10\) and \(\alpha7\) nAChR blockade (Ellison et al., 2008). It is noteworthy that these \(\alpha9\alpha10\)-selective \(\alpha\)-conotoxins are analgesic in different animal models of chronic pain, but there is an uncertainty about the true molecular target responsible for this effect. Indeed, whereas \(\alpha9\alpha10\) nAChR-selective small molecules were recently shown to also provide pain relief, N-type calcium channel inactivation through a novel interaction with GABA\(_B\) receptor has also been proposed (Callaghan and Adams, 2010; Zheng et al., 2011).

The determination of several X-ray crystal structures of AChBP/\(\alpha\)-conotoxin complexes significantly advanced our understanding of the structural basis for the nAChR subtype selectivity of \(\alpha\)-conotoxins (Celie et al., 2005; McIntosh et al., 2005; Ulens et al., 2006; Dutertre et al., 2007). We were surprised to find that the three conotoxins (\(\alpha\)-ImI, and variants of \(\alpha\)-PnIA and \(\alpha\)-TxIA) that have been cocryrstallized with AChBP showed a similar orientation within the ACh binding pocket despite divergent primary sequences. All three structures show a strong contribution of hydrophobic contacts between a conserved proline and several hydrophobic residues of the \(\alpha\)-conotoxins and several residues in the aromatic cage of AChBP (Fig. 7). Therefore, the different nAChR selectivity profiles arise from specific electrostatic interactions and hydrogen bonds formed between \(\alpha\)-conotoxin and nAChR subunits. For instance, \(\alpha\)-conotoxin TxIA uses a unique electrostatic pairing between Arg5 and AChBP-Asp195 to achieve its high-affinity binding (Dutertre et al., 2007). In addition, a tilt in the orientation of the \(\alpha\)-conotoxin TxIA structure within the ACh binding pocket was found to correlate with nAChR subtype selectivity. Clearly, additional \(\alpha\)-conotoxin-AChBP crystal structures and new models of \(\alpha\)-conotoxin-nAChR interactions are expected to emerge, which should further expand our understanding of subtype-selectivity at nAChR. The structures of the 4/7 \(\alpha\)-conotoxin A10L-TxIA and the smaller 4/3 \(\alpha\)-conotoxin ImI and their interactions with the AChBP are shown in Fig. 7.

Compared with the \(\alpha\)-conotoxins, the other conotoxin families targeting nAChRs are less well understood, both in their mode of action and pharmacophore. These nontraditional \(\alpha\)-conotoxins are often named with a letter to designate their superfamil families. For example, the first member of the \(\alpha\)-C-conotoxin family, PrXA, was isolated from the venom of Conus spurius (Jimenez et al., 2007). This 32-amino acid peptide induced paralysis when injected into mice and fish and was shown to potently inhibit the muscle nAChR in vitro in a competitive manner. The primary structure of this peptide seems very different from that of \(\alpha\)-conotoxins, with only one disulfide bond and three hydroxyprolines. A second family comprises \(\alpha\)-S-Conotoxin RVIIIA, which is also unique, with a broad selectivity profile against nAChR subtypes and the presence of \(\gamma\)-carboxyl glutamates, a post-translational modification not otherwise found in conotoxins targeting nAChRs (Teichert et al., 2005a). RVIIIA is also paralytic to mice and fish but elicits seizures in mice upon intracranial injection. Electrophysiological recordings of recombinantly expressed nAChR in oocytes revealed it competitively inhibited several neuronal subtypes in addition to the muscle nAChR. Within the same family is \(\alpha\)-GVIIIA, a peptide that targets another ligand-gated ion channel, the serotonin receptor (see section IV.B). Conotoxin It14a belongs to yet another family \(\alpha\)-L-conotoxin and was discovered using a cDNA library from the venom gland of C. litteratus (Peng et al.,...
The sequence showed no homology to other families, but the cysteine arrangement is reminiscent of that of the \( \alpha \)-conotoxins. A synthetic version was tested on frog nerve preparations and PC12 cells, assuming the \( \alpha \)-conotoxin cysteine connectivity (1–3; 2–4), and it was found to block the response of ACh-evoked currents. It is noteworthy that although this peptide has not been tested across the various subtypes of nAChRs, lt14a produced dose-dependent analgesia in a hot-plate assay in mice, suggesting that it may target therapeutically relevant nAChRs. Further atypical \( \alpha \)-conotoxins include the \( \alpha \)J-pl14a, which was recently identified with an unusual dual activity at two different classes of ion channels (Imperial et al., 2006). Indeed, this 25-amino acid peptide inhibits both K\(_{\text{L}}\) and muscle \( \alpha 3\beta 2 \) nAChRs (see section III.D). Its well defined structure, comprising an \( \alpha \)-helix and two short \( 3_{10} \)-helices, may allow future struc-
ture–activity relationship studies to reveal whether this peptide uses the same or different pharmacophores to interact with both receptors.

An unusually large family of conopeptides found only in one clade of worm-hunting cone snails also inhibit nAChRs (Loughnan et al., 2006, 2009; Kauferstein et al., 2009). These αD-conotoxins have a molecular mass of ~11 kDa, with Edman degradation, mass spectrometric, and NMR data revealing they assemble as a pseudo-homodimer comprising two 47–50-residue peptides. So far, data revealing they assemble as a pseudo-homodimer comprise species of cone snails where traditional conotoxins have been isolated only from worm-hunting targets this important physiological target, providing Conus subtypes (Lluisma et al., 2008). Thus, it seems that nAChR, with a preference for the adult over the fetal showed that binding assays and two-electrode voltage-clamp analyses revealed that these αD-conotoxins are potent inhibitors of several nAChRs, including α7, α3β2, and α4β2 subtypes. Finally, several noncompetitive conotoxins have also been discovered (Shon et al., 1997). These ψ-conotoxins show homology to the μ-conotoxins, which are Nα-channel pore blockers. PIIIIE was originally shown to block muscle nAChR, but targets a different binding site compared with α-bungarotoxin. PIIIIE was also shown to potently inhibit muscle nAChR with a preference for the adult over the fetal subtype (Lluisma et al., 2008). Thus, it seems that Conus spp. have devised many original solutions to target this important physiological target, providing us with as many templates for nAChR subtype-selective tools and drugs.

B. α-Conotoxin Inhibitors of Serotonin 5-HT₃ Receptors

One family of conotoxins targets the 5-HT₃ receptor, pentameric, cation-selective channels that open in response to the binding of the neurotransmitter serotonin (Hoyer et al., 1994) and share overall topology with nictinic receptors. Five human subtypes (5-HT₃A, 5-HT₃B, 5-HT₃C, 5-HT₃D, and 5-HT₃E) have been cloned (Karovský et al., 2003; Niesler et al., 2003) but only homomorphic 5-HT₃A and heteromorphic combinations of 5-HT₃A and 5-HT₃B have been pharmacologically characterized in detail. To date, only the large α-conotoxin GVIIIA has been identified to target 5-HT₃ receptors (England et al., 1998). GVIIIA inhibits 5-HT₃ receptors expressed in Xenopus laevis oocytes in a competitive manner. This 41-amino acid peptide contains 10 cysteines (five disulfide bonds), an amidated C terminus, and the unusual post-translational modification 6-bromoptryphan. Unfortunately, this complicated structure precluded chemical synthesis and any structure-activity relationship studies at the receptor.

C. Ikot-Ikot Conopeptide Enhancers of α-Amino-3-hydroxy-5-methyl-4-isoxazolepropionic acid Receptors

A novel polypeptide isolated from C. striatus venom has been shown to selectively target AMPA receptors (Walker et al., 2009). This toxin, named con-ikot-ikot (referring to the Filipino word for “spinning around” in reference to the swimming phenotype observed in fish injected with this toxin), is 86 amino acids long with 13 cysteines, corresponding to a molecular mass of 9432 Da. It is noteworthy that the active form of con-ikot-ikot is a dimer of dimers, as evidenced by a band corresponding to a molecular mass of 38 kDa on an electrophoresis gel. This peptide achieves its biological effect through block of AMPA desensitization, greatly increasing the current magnitude. AMPA receptors belong to the ionotropic glutamate receptors, and together with NMDA and kainate receptors, mediate excitatory neurotransmission in the central nervous system (Dingledine et al., 1999). Native AMPA receptors assemble as heterotetramers (dimer of dimers) to form a functional channel. Each subunit (GluA1–4) consists of four domains: the N-terminal domain, the ligand binding domain, the pore forming transmembrane domain, and finally a small C-terminal domain (Chen and Wyllie, 2006). The structure of intact AMPA receptors was solved by Sobolevsky et al. (2009), revealing a dimer of dimers arrangement of four subunits. This structure is expected to help identify the binding site of con-ikot-ikot and guide further structure-activity studies for this novel class of conotoxin.

<table>
<thead>
<tr>
<th>Conantokins inhibiting NMDA glutamate receptors</th>
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<tbody>
<tr>
<td><strong>Species</strong></td>
</tr>
<tr>
<td>C. characteristicus</td>
</tr>
<tr>
<td>C. ermineus</td>
</tr>
<tr>
<td>C. geographus</td>
</tr>
<tr>
<td>C. gloriamaris</td>
</tr>
<tr>
<td>C. lyncus</td>
</tr>
<tr>
<td>C. purpurascens</td>
</tr>
<tr>
<td>C. ochroleucus</td>
</tr>
<tr>
<td>C. parius</td>
</tr>
<tr>
<td>C. quercinus</td>
</tr>
<tr>
<td>C. radiaus</td>
</tr>
<tr>
<td>C. sulcatus (brettinghami)</td>
</tr>
<tr>
<td>C. tulipa</td>
</tr>
</tbody>
</table>

P, fish; M, molluscs; V, worms; γ, γ-carboxyglutamate; *, C-terminal amidation; N.D., not determined.
D. Conantokin Inhibitors of N-Methyl-D-aspartate Receptors

Conantokins are small peptides (17–22 amino acids) isolated from the venom of various Conus species that selectively and potently inhibit NMDA receptors. The first conantokin isolated was Con-G; more recent members have been isolated from another 11 species (see Table 9). Conantokins have therapeutic potential as analgesics (Malmberg et al., 2003) and anticonvulsants (Jimenez et al., 2002). As opposed to the vast majority of conopeptides, conantokins do not contain cysteines but instead have a high content of \( \gamma \)-carboxyglutamic acid residues that when correctly spaced, induce \( \alpha \)-helicity in the presence of divalent cations. Structure-activity studies of conantokins (Nielsen et al., 1999b) have revealed a number of important residues for binding, and a docking model showed that Con-G can fit into the agonist binding cleft of the NR2 subunit (see Fig. 8) (Wittekindt et al., 2001), revealing interactions between Glu386/Asp689 and Asn662 from NR2 subunit and Asn17/Lys15 and Glu2 of Con-G, respectively.

NMDA receptors are tetrameric ligand-gated ion channels with high Ca\(^{2+}\) permeability that mediate fast excitatory neurotransmission in the CNS (Dingledine et al., 1999). They are composed mainly of two NR1 and two NR2 subunits, with an NR3 subunit potentially coassembling with NR1 and NR2 to modify NMDA receptor-mediated responses, reducing calcium permeability and single-channel conductance (Ciabarra et al., 1995). The topology of each subunit comprises an extracellular N-terminal domain, an agonist binding core, three transmembrane domains (domains 1 and 2 are separated by a “P-loop”), and a cytoplasmic tail of a variable length (Mayer and Armstrong, 2004). For the proper functioning and gating of NMDA receptors, the binding of both the agonist glutamate...
mate (on the NR2 subunit) and the coagonist glycine (on the NR1 subunit) is required at the same time. Differential expression of isoforms (i.e., NR2A–D) occurs in the central nervous system, where they mediate fast excitatory neurotransmission. NMDA receptors have also been implicated in a number of chronic and acute neurological disorders, and significant research efforts are currently directed toward the development of specific drugs that can inhibit these targets (Loftis and Janowsky, 2003). Atomic resolution structures of the NMDA extracellular binding domains bound to agonists, partial agonists, and antagonists have been determined that might open the way to the rational development of NMDA receptor antagonists (Furukawa and Gouaux, 2003; Furukawa et al., 2005). Based on the docking model shown in Fig. 8, it is conceivable that conantokin analogs might be rationally designed to have selectivity for subunit combinations of clinical interest.

E. Ligand-Gated Ion Channels Inhibitors in Pain Management

A number of ligand-gated ion channels have been implicated in pain modulation and chronic pain states but this discussion will focus on the two families of channels with evidence for application of conopeptides. Conopeptides targeting subtypes of nAChR subtypes (α-conotoxins) and NMDA receptors (several conantokins) have shown good efficacy in preclinical pain models and have reached different stages of development for use in humans. Their pharmacological characteristics underlying their analgesic effects are discussed below.

The involvement of nAChR subtypes in pain modulation is complex, and the mechanisms of action of α-conotoxins in pain relief remains controversial. Much of the difficulty in resolving the actual targets of these toxins arises from the complexity of physiologically and pathologically relevant nAChR subtypes found in vivo, together with limited knowledge of expression and role of subunits in pain pathways (Olivera et al., 2008). For example, nicotinic agonists selective for α4β2 subtypes of nAChRs produce analgesic actions in neuropathic pain models (Bannon et al., 1998; Rashid and Ueda, 2002), probably as a result of stimulation of α4β2 nAChRs on inhibitory interneurons in the dorsal horn of the spinal cord (Genzen and McGehee, 2005). By contrast, analgesic α-conotoxins are selective antagonists of different neuronal nAChR subtypes (and agonists at GABA receptors, see below) but avoid muscle or α4β2 nAChRs.

Synthetic Vc1.1 (ACV1) identified from cDNA was the first α-conotoxin shown to exhibit efficacy in pain models (Sandall et al., 2003; Satkunanathan et al., 2005). The peptide was potent and peripherally active after intramuscular injection, producing partial reversal of mechanical allodynia in several neuropathic pain models. The findings that the effectiveness of the peptide escalated with repeated daily injections and seemed to allow functional recovery of injured nerves (Satkunanathan et al., 2005) suggested that it had clinical potential in treatment of neuropathic pain. Vc1.1 was initially selected for testing in pain models on the basis of its potent block of neuronal (bovine adrenal chromaffin cells) versus muscle nAChRs (Livett et al., 2006; see Table 10). Bovine adrenal chromaffin cells express α3-, α5-, a7-, and β4-nAChR subunits (Salà et al., 2008). Accordingly, the main nAChR subtypes expressed on nociceptive peripheral fibers and their central terminations are composed of α3, α5, β4, and β2 subunits (Khan et al., 2003; Lang et al., 2003; Rau et al., 2005). Vc1.1 also inhibited peripheral nerve-mediated vascular responses in rats (Satkunanathan et al., 2005) and, at low concentrations (100 nM), inhibited excitatory responses of

<table>
<thead>
<tr>
<th>α-Conotoxins</th>
<th>Efficacy</th>
<th>nAChR selectivity</th>
<th>Nanomolar GABA&lt;sub&gt;Gy&lt;/sub&gt;:Ca&lt;sub&gt;s&lt;/sub&gt; Activity</th>
<th>References</th>
</tr>
</thead>
<tbody>
<tr>
<td>Vc1.1</td>
<td>Partially reverses mechanical alldynia in several neuronal models after intramuscular dosing. Escalating actions and recovery of nerve function.</td>
<td>α9α10 ⇒ α6α3β2β3 &gt; α6α3β4 &gt; α3β4 ~ a3β2</td>
<td>Yes</td>
<td>Sandall et al., 2003; Satkunanathan et al., 2005; Vincler et al., 2006; Klimis et al., 2011</td>
</tr>
<tr>
<td>CyclizedVc1.1</td>
<td>Partially reverses mechanical alldynia in several neuronal models after oral dosing.</td>
<td>Very weak α9α10</td>
<td>Yes</td>
<td>Clark et al., 2010</td>
</tr>
<tr>
<td>Vc1a</td>
<td>No reversal of alldynia in a neuropathic pain model. Recovery of nerve function retained.</td>
<td>α9α10 ⇒ α3β4 ~ a3β2</td>
<td>No</td>
<td>Nevin et al., 2007</td>
</tr>
<tr>
<td>Rg1A</td>
<td>Partially reverses mechanical alldynia in several neuronal models after intramuscular dosing.</td>
<td>α9α10 ⇒ α7 ⇒ α3β4 ~ a3β2</td>
<td>Yes</td>
<td>Vincler et al., 2006</td>
</tr>
<tr>
<td>AuIB</td>
<td>Partially reverses mechanical alldynia in several neuronal models after intramuscular dosing.</td>
<td>α3β4 &gt; α3β2 ⇒ α9α10</td>
<td>Yes</td>
<td>Klimis et al., 2011</td>
</tr>
<tr>
<td>MII</td>
<td>Partially reverses mechanical alldynia in several neuronal models after intramuscular dosing.</td>
<td>α3β2 &gt; α3β4 ⇒ α9α10</td>
<td>No</td>
<td>Klimis et al., 2011</td>
</tr>
<tr>
<td>Lt14a</td>
<td>Acute thermal antinociception (hotplate test) after intraperitoneal administration.</td>
<td>Unknown but inhibits PC12 cell nAChR (α3-, α6-, α7-, β2-, β3-, and β4-subunits)</td>
<td>Unknown</td>
<td>Sun et al., 2011</td>
</tr>
</tbody>
</table>
human sural nerve to nicotine (Lang et al., 2005). Vc1.1 has relatively low affinity for α3β2 and α3β4 nAChRs (Clark et al., 2006; Vincler and McIntosh, 2007) but may have higher affinity for more complex subunit combinations; e.g., its affinity for α6/α3α2β2β3 nAChRs is 140 nM (Vincler and McIntosh, 2007). It was therefore suggested that Vc1.1 might produce pain relief via inhibition of α3 and/or α5 nAChR channels on sensory nerves. It is noteworthy that the analgesic α-AuIB has relatively low affinity for α3β4 but MII has very high affinity for α3β2 nAChRs (~1 nM). It therefore remains possible that pain relief may be achieved in the periphery by antagonism of nAChRs, potentially contributing to its analgesic effects in neuropathic pain models (Vincler et al., 2006). However, another potential target for the pain-relieving actions of Vc1.1 and other analgesic α-conotoxins is summarized in Table 10 and discussed below.

Vc1.1 was also shown to be a potent antagonist at α9α10 nAChRs, potentially contributing to its analgesic effects (Vincler et al., 2006). Another potential target for the pain-relieving actions of Vc1.1 and other analgesic α-conotoxins is summarized in Table 10 and discussed below.

In summary, several α-conotoxins seem to be potential candidates for development of treatments for neuropathic pain. Although the mechanism(s) of action remain controversial, they produce partial relief from the signs of neuropathic pain and seem to accelerate functional recovery of sensory nerve function. The α-conotoxins are also relatively small peptides, and the recent development of a cyclized analog of Vc1.1 (Clark et al., 2010) revealed that the peptide could relieve signs of neuropathic pain when administered orally. ACV1 (Vc1.1) was taken through a phase I clinical trials by Metabolic Pharmaceuticals (Melbourne, VIC, Australia) but subsequently dropped after completion of a phase 2A trial over potential concerns over efficacy and its reduced efficacy at human versus rat α9α10 nAChRs.

Finally, NMDA receptors, particularly those in the dorsal spinal cord that include the NR2B subunit, have long been recognized as candidates for development of pain therapeutics (Parsons, 2001), with small-molecule NR2B-selective antagonists selectively inhibiting signs of chronic pain in animal models (Boyce et al., 1999).
Several conantokins, including conantokin-G, selectively inhibit NMDA receptors composed of NR1 and NR2B subunits (Layer et al., 2004) and inhibit signs of neuropathic pain intrathecally. Unfortunately, Con-G produced motor side effects in a similar dose range in nerve injury models (Malmberg et al., 2003), and the utility of intrathecal conantokins targeting NR2B for pain management remains to be established.

V. Conotoxins Interacting with G Protein-Coupled Receptors and Neurotransmitter Transporters

Two novel classes of conopeptide (\(\rho\)- and \(\chi\)-conopeptides) were discovered that inhibit noradrenaline activation of \(\alpha1\)-adrenoceptors or its transport via the noradrenaline transporter (Sharpe et al., 2001). It is noteworthy that both noncompetitively (allosterically) inhibited noradrenaline, making them useful new probes of allosteric sites on these physiologically and pathologically important membrane proteins. In contrast, competitive (isosteric) agonists of the vasopressin and neurotensin receptors have also been discovered that are closely related to the endogenous peptides for these targets. Sequences of known conopeptides belonging to these four classes are shown in Table 11, and their structures are compared in Fig. 9.

A. \(\rho\)-Conopeptide Inhibitors of \(\alpha1\)-Adrenoceptors

The conopeptide \(\rho\)-TIA is a 19-amino acid peptide with two disulfide bonds isolated from the venom of Conus tulipa (Sharpe et al., 2001). This peptide was originally discovered after reduction of the noradrenergic component of the electrically evoked contraction of the rat vas deferens. Competition experiments with radiolabeled ligands revealed TIA was a selective and negative allosteric modulator of hamster \(\alpha1\)B (Sharpe et al., 2003b). Additional radioligand displacement studies showed that TIA is also 10-fold selective for human \(\alpha1\)B over \(\alpha1\)A and \(\alpha1\)D (Chen et al., 2004). An alanine walk identified Asn2, Trp3, Arg4, Leu7, and Ile8 as the major binding determinants on TIA (Sharpe et al., 2003b). It is noteworthy that the first four residues in the N-terminal “tail” are key determinants of binding, despite being outside the disulfide bonds and relatively unconstrained in solution (Sharpe et al., 2003b). F18A (and F18N) analogs of TIA had increased selectivity for \(\alpha1\)B, whereas the I8A analog had slightly reduced af-
finity for α₁B- and its mode of action was switched to become a competitive antagonist (Chen et al., 2004).

High-resolution crystal structures of the closely related β-ARs have been determined in both the resting and activated states, as well as in complex with various ligands (Cherezov et al., 2007; Rasmussen et al., 2007, 2011a, 2011b; Warne et al., 2008; Rosenbaum et al., 2011; Warne et al., 2011). Although these structures confirmed the location of the orthosteric binding site for competitive ligands that had been mapped previously using affinity labeling, site-directed mutagenesis, and substituted-cysteine accessibility methods, the site of allosteric compounds remains rather elusive. Allosteric ligands are of particular interest to both fundamental science and the pharmaceutical industry, because they can achieve greater selectivity and act only where the endogenous agonist exerts its physiological effect (Conn et al., 2009). Using the recent crystal structure of β-adrenoceptors, modeling of the interaction between TIA and α₁B-AR should provide a clearer view of this allosteric binding site and potentially allow the development of more selective inhibitors.

It is worthwhile to consider the therapeutic potential of peptide inhibitors of α₁-adrenoceptors, a traditional small-molecule GPCR drug target. These receptors belong to the family A of GPCRs, and therefore share the common topology comprising a core composed of seven transmembrane helices connected by three extracellular and three intracellular loops. Adrenoceptors regulate critical aspects of blood pressure control, myocardial contractility, pulmonary function, metabolism, and activities in the CNS (Koch et al., 1995). They are broadly divided in α₁-α₂, and β-adrenoceptors based on anatomical localization; then, each group is further separated into three subtypes based on pharmacological and molecular strategies (α₁A, α₁B, and α₁D; α₂A, α₂B, and α₂C; β₁, β₂, and β₃) (Bylund et al., 1994; Graham et al., 1996). The α₁-ARs are located on postsynaptic membranes, whereas α₂-ARs are found on presynaptic nerve terminals (Langer, 1974). In particular, α₁-ARs are crucial for the stimulation of smooth muscle contraction (Bylund et al., 1994). Agonists at the α₁-ARs may be associated with an alerting or antidepressant action, whereas antagonists are being used and refined for the treatment of benign prostatic hypertrophy (Hieble and Ruffolo, 1996). Peptides with improved selectivity and restricted to peripheral compartments have the potential to treat diseases such as benign prostatic hypertrophy.

B. χ-Conopeptide Inhibitors of the Noradrenaline Transporter

χ-Conopeptides are small hydrophobic peptides that selectively inhibit the transport of noradrenaline by NET, an important target for drugs treating a range of neurological diseases, including depression, anxiety, obsessive-compulsive disorder, and attention deficit hyperactivity disorder (Goddard et al., 2010). χ-MrIA and χ-MrIB noncompetitively inhibit NET (Sharpe et al., 2001), providing opportunities to regulate NET efficiently, irrespective of the concentration of noradrenaline present. χ-MrIA seems to be specific for NET, with no effect on the function of a diverse range of targets (Sharpe et al., 2001), including other monoamine neurotransmitter transporters (Sharpe et al., 2001). The solution structure of MrIA revealed that χ-conopeptides have a rigid framework stabilized by two disulfide bonds and two antiparallel strands connected by an inverse γ-turn (Sharpe et al., 2001; Nilsson et al., 2005). Although the cysteine spacings in the linear sequence are reminiscent of small α-conotoxins, χ-conopeptides have an alternative cysteine-stabilized scaffold, with cysteines bonded 1 to 4 and 2 to 3 (see Table 11), that allows a γ-turn to form in an optimized conformation for high-affinity interactions with NET. Residues in this γ turn (Gly6, Tyr7, Lys8, and Leu9), plus His11 in loop 2, have been identified as critical for high-affinity interactions at NET through alanine-scanning mutagenesis, but only mutations to Gly6 affect structure (Sharpe et al., 2003a). To define the χ-conopeptide pharmacophore, an expanded series of analogs was synthesized, revealing that χ-conopeptides interact with NET mainly through interaction of Tyr7 with NET via aromatic and/or H-bond acceptors, Lys8 contributing an essential basic residue for NET binding, Leu9 interacting with a large hydrophobic patch on NET, and His11 and hydroxyproline 12 contributing weaker interactions through aromatic and basic interactions (Brust et al., 2009).

Based on its mode of action to inhibit NET, intrathecal administration of MrIA was evaluated in rodent models of acute, inflammatory, and neuropathic pain, where it was able to produce significant reversal of the signs of acute and neuropathic pain in mice and rats, respectively, without significant side effects (McIntosh et al., 2000; Nielsen et al., 2005). To consider χ-MrIA as a therapeutic lead, its chemically unstable N-terminal asparagine needed to be replaced or removed to allow long-term human use in implanted pumps. Extensive replacements and truncations/extensions at the N-termini revealed that replacing asparagine with a pyroglutamate significantly improved chemical stability without compromising the side-effect profile observed for MrIA (Brust et al., 2009). Pyroglutamate1-MrIA (Xen2174), produced few side effects even at high doses, and an extended duration of action after a single bolus intrathecal dose in the rat model of neuropathic pain (Nielsen et al., 2005). Xen2174 was recently a phase IIa intrathecal study in patients with cancer pain. This open label, dose-escalating study was conducted in 37 cancer patients suffering severe chronic pain that was poorly controlled using conventional therapies. It is noteworthy that Xen2174 reportedly provided pain relief rapidly and for a sustained period across a wide range of tolerated intrathecal bolus doses from 0.1 to 30...
mg. Xen2174 is presently being prepared for a phase IIb double-blind study to establish whether Xen2174 is safe and efficacious in a bunionectomy setting of postsurgical pain. Further details on the discovery and development of Xen2174 are reported in a review by Lewis (2011).

C. Conopeptides Modulating Vasopressin/Oxytocin Receptors

Conopressins were first discovered in the venom of fish-hunting cone snails based on the “scratching effect” induced in mice upon intracerebral injection (Cruz et al., 1987). The sequences of both conopressin-G and conopressin-T were very similar to vasopressin itself, with only an additional positive charge in position 4. It is noteworthy that conopressin-G was later isolated from a worm-hunting cone snail species, Conus imperialis, as well as from the nonvenomous snails Lymnea stagnalis and Aplysia californica and the leech Erpobdella octoculata (McMaster et al., 1992; Salz et al., 1993; Nielsen et al., 1994; Van Kesteren et al., 1995). Therefore, conopressin-G was proposed to represent the endogenous vasopressin homolog in these invertebrates. However, novel conopressins have since been discovered from other cone snail species, supporting a role in envenomation (Möller and Mari, 2007; Dutertre et al., 2008; Ueberheide et al., 2009). We were surprised that conopressin-T acted as a V₁-vasopressin receptor-selective antagonist, with partial agonist activity at the oxytocin receptor and replacing Gly9 with Val9 also switched the activity of vasopressin and oxytocin from agonist to antagonist (Dutertre et al., 2008). Therefore, new conopressins may serve as templates for the design of novel ligands with tailored pharmacological profiles.

Vasopressin and oxytocin receptors belong to the GPCR family A and apparently bind vasopressins and conopressins in a pocket formed by the arrangement of the seven transmembrane domains (Mouillac et al., 1995; Dutertre et al., 2008). On the basis of extracellular domain exchanges between and oxytocin receptor, it has been proposed that the three extracellular loops are also important for agonist binding (Postina et al., 1996). Models of the interaction of vasopressin with V₁ and V₃ developed using a rhodopsin structural template were consistent with most experimental data and supported by follow-up site-directed mutagenesis (Rodrigo et al., 2007). At least three different subpopulations of vasopressin receptors have been recognized: V₁ (or V₁A), V₂, and V₃ (or V₁B) (Birnbauer, 2000). V₁ regulates blood pressure and vasconstriction, whereas activation of V₂ produces an antidiuretic effect on the kidney, and stimulation of V₃ is responsible for corticotrophin release from the pituitary gland. Only one oxytocin receptor has been characterized, and its activation stimulates the contraction of uterine and mammary myocytes during parturition and lactation, respectively (Pettersson, 2002). Using such models, it may be possible to rationally develop vasopressin/oxytocin receptor antagonists with tailored selectivity.

D. Neurotensin Receptor Agonists

Contulakin-G (also known as CGX-1160) was isolated from the venom of Conus geographus and was shown to possess agonist activity at neurotensin receptors 1 (NTSR1) and 2 (NTSR2) (Craig et al., 1999). The primary sequence of contulakin-G (ZSEEGGSNATKKPYIL) closely resembles neurotensin (ZLYENKPRRPYIL), yet contulakin-G is approximately 150-fold less potent at NTSR2 and NTSR1 receptors compared with the endogenous ligand, which contains a glycosylation at Thr10 (Craig et al., 1999, 2001). It is noteworthy that the native peptide was more biologically active than the synthetic nonglycosylated peptide (Craig et al., 1999).

Neurotensin plays important roles in neurotransmission and neuromodulation in the nervous system (Hermans and Maloteaux, 1998) by activating NTSR1 and NTSR2, which belong to G protein-coupled receptor family A (Tanaka et al., 1990; Vita et al., 1993). Both subtypes exhibit distinct pharmacological properties, NTSR1 showing high affinity for levocabastine, whereas NTSR2 has much lower affinity (Vita et al., 1998). Docking of neurotensin in the NTSR1 binding pocket was modeled based on rhodopsin structure (Härterich et al., 2008). Neurotensin has since been shown also to interact with D2 dopamine receptor (Fuxe et al., 1995; the recent crystal structure of D3 dopamine receptor may provide a more appropriate template to model these interactions (Chien et al., 2010).

Because neurotensin is analgesic, contulakin-G was assessed for its antinociceptive activity in formalin models of acute and inflammatory pain in rats and dogs (Allen et al., 2007). Contulakin-G showed an antinociceptive effect greater than morphine, without motor deficits, prompting preclinical development and progression to phase I clinical trials. However, the mechanism by which contulakin-G induces analgesia remains unclear, because the antinociceptive effect is realized at a concentration 100-fold lower than its NTSR1 binding affinity.

VI. Conclusions and Outlook

In addition to their well recognized value as pharmacological tools to dissect the physiological and pathophysiological roles of ion channels, receptors, and transporters in a vast range of disease pathways, cone snail venom peptides are attracting growing interest as potential therapeutic leads because of their high potency and specificity at mammalian targets. With only a fraction of the conopeptides identified and characterized to date, the natural product space of cone snail venom peptides represents a vast untapped biological resource. Given this potential, accelerated discovery platforms are becoming increasingly important to unravel conotoxin diversity. In particular, high-throughput and high-content approaches promise to accelerate the discovery of novel bioactives as well as the potential to provide unique insight into the effects and mechanisms of action of conopeptides even on heterogeneous cell populations such as DRG neurons. In addition,
Recent technological advances and improved bioinformatic tools have led to the successful application of transcriptomic and proteomic approaches to Conus spp. venom peptide discovery. These approaches are likely to lead to the rapid identification of novel conotoxins belonging to known pharmacological classes and to accelerate the identification and characterization of conopeptides with new sequences and potential novel biological activities.

Naturally occurring conotoxins are ideal scaffolds for the interrogation of specific pharmacophores using alanine-scanning mutagenesis approaches, and these structure-activity relationships can help guide molecular docking studies to define new allosteric sites on membrane proteins. Detailed studies of the interaction of conotoxins with their respective pharmacological targets have already provided invaluable insight into the pharmacology of ion channels, receptors and transporters. Exemplifying this are Na, interactions with naturally derived compounds, including μ-, μO-, and δ-conotoxins, which have contributed significantly to our understanding of this channel's structure and function. As crystal structures of these membrane protein targets become available, such as the recently reported sodium channel structure (Payandeh et al., 2011), further refinement of our understanding of toxin-target interactions will without doubt lead to improved conotoxin-derived compounds with exceptional affinity and subtype selectivity. It is noteworthy that non-native disulfide bond isomers of conopeptides can also provide useful membrane protein probes, further expanding on the pharmacology of conopeptides. For example, the two isomers of α-AuIB differ in their inhibitory mechanisms, with the AuIB (ribbon) form competitively inhibiting only α3β4 nAChRs containing an α3 subunit in the fifth position, an effect distinct from the native AuIB (globular) form, which inhibited α3β4 nAChRs independent of the fifth subunit, primarily through a noncompetitive mechanism (Grishin et al., 2010). Furthermore, a structural isomer of ρ-TIA named NMB-1 was found to preferentially inhibit the sustained component of mechanically evoked current in DRG neurons, providing a novel diagnostic tool for the molecular definition of channels involved in hearing and pressure-evoked pain (Drew et al., 2007).

In recent years, an increasing emphasis has been placed on genetic ablation or knockdown of pharmacological targets to dissect their role in physiology and the pathophysiology of disease. However, an inherent flaw of this approach is that heteromultimeric ion channels composed of several subunits, such as nAChR or K, channels, cannot be targeted selectively. This has profound implications for our understanding of the composition and identity of receptor subtypes expressed in native tissues, as well as their physiological roles. The high selectivity and subtype specificity of conopeptides can yield novel insights especially for such targets and can help unravel the physiologic and pathophysiological roles of specific subunit combinations of these ion channels. Here, the α-conotoxins have proved especially valuable for chemically dissecting the role of a wide range of physiologically and pathologically relevant nAChR subunit combinations.

In addition, the importance of conotoxins as therapeutics in their own right is becoming increasingly apparent. Both naturally occurring conotoxins such as synthetic ω-MVIIA (ziconotide) or the sequence-optimized χ-conopeptide Xen2174 have become either novel pharmaceutics or promising drug leads. Although conotoxins acting at peripheral targets can be delivered by systemic routes, central targets still require direct delivery to the site of action (e.g., intrathecal injection) because of the limited permeability of the blood-brain barrier to peptides. However, our understanding of conotoxin structure-activity relationships is now being applied to the design of smaller, orally active conotoxin peptidomimetics, with the hope of engineering novel therapeutic molecules based on the unique pharmacological properties of conotoxins. The growing realization of the many limitations inherent to small molecules, as well as improved peptide dosage form design and drug delivery strategies, such as liposomal packaging, pro-drug approaches, conjugation to carrier molecules, and microinjection devices (Malik et al., 2007), promise to refocus drug development efforts beyond traditional approaches to more fully embrace the potential of peptide therapeutics. The favorable characteristics of conotoxins as peptide therapeutics in particular arise from their small size, relative ease of synthesis and high structural stability as a result of their disulfide connectivity and compact, relatively rigid structures. These properties of conotoxins also impart a low immunogenic potential and perhaps advantageous pharmacodynamic and pharmacokinetic behavior allowing compartmentalized delivery that can reduce side effects. For example, delivery of conotoxins to the intrathecal space could, in principle (on the basis of limited redistribution because of their peptidic nature), avoid side effects resulting from on-target effects at different sites. In addition, once delivered to these compartments, it seems that many conotoxins are surprisingly stable, with half-lives of hours or more, rather than minutes (Wermeling et al., 2003; Kern et al., 2007). For example, a relatively long half-life in cerebrospinal fluid may also account for the extended duration of action observed after intrathecal dosing of Xen2174 (Lewis, 2011). In addition, it is now possible to engineer potentially more stable N-C-cyclized forms as exemplified by using α-conotoxin Vc1.1, which retained analgesic activity even after oral dosing (Clark et al., 2010). Thus, it is now possible to extend the broadly evolved bioactivity of cone snail venom-derived peptides to novel uses that will further expand the potential and unique source of new research tools and potential therapeutic agents.

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Dr. Anderson Wang prepared the homology models of Na_{1.2} and Ca_{2.2} and performed the docking simulations shown in Fig. 3.
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