



Medicinal chemistry, pharmacology, and therapeutic potential of α -conotoxins antagonizing the $\alpha 9\alpha 10$ nicotinic acetylcholine receptor

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ABSTRACT

α -Conotoxins are disulfide-rich and well-structured peptides, most of which can block nicotinic acetylcholine receptors (nAChRs) with exquisite selectivity and potency. There are various nAChR subtypes, of which the $\alpha 9\alpha 10$ nAChR functions as a heteromeric ionotropic receptor in the mammalian cochlea and mediates postsynaptic transmission from the medial olivocochlear. The $\alpha 9\alpha 10$ nAChR subtype has also been proposed as a target for the treatment of neuropathic pain and the suppression of breast cancer cell proliferation. Therefore, α -conotoxins targeting the $\alpha 9\alpha 10$ nAChR are potentially useful in the development of specific therapeutic drugs and pharmacological tools. Despite dissimilarities in their amino acid sequence and structures, these conopeptides are potent antagonists of the $\alpha 9\alpha 10$ nAChR subtype. Consequently, the activity and stability of these peptides have been subjected to chemical modifications. The resulting synthetic analogues have not only functioned as molecular probes to explore ligand binding sites of the $\alpha 9\alpha 10$ nAChR, but also have the potential to become candidates for drug development. From the perspectives of medicinal chemistry and pharmacology, we highlight the structure and function of the $\alpha 9\alpha 10$ nAChR and review studies of α -conotoxins targeting it, including their three-dimensional structures, structure optimization strategies, and binding modes at the $\alpha 9\alpha 10$ nAChR, as well as their therapeutic potential.

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1. Nicotinic acetylcholine receptors

Nicotinic acetylcholine receptors (nAChRs) are pentameric ligand-gated cation-selective channels that were initially shown to participate

in synaptic transmission at the neuromuscular junction (Hogg, Ragganbass, & Bertrand, 2003; Unwin, 2013) and are broadly distributed throughout both central and peripheral nervous systems (Bertrand & Terry, 2018; Zoli, Pucci, Vilella, & Gotti, 2018). To date, 17 subunits ($\alpha 1$ – $\alpha 10$, $\beta 1$ – $\beta 4$, γ , δ , and ϵ) have been identified and they assemble into distinct nAChR subtypes (Albuquerque, Pereira, Alkondon, & Rogers, 2009). Individual subunits contain a large N-terminal extracellular domain (ECD), an ion conducting transmembrane domain (TMD), and an

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Abbreviations

ACh	acetylcholine;
CCI	chronic constriction nerve injury;
ECD	extracellular domain;
ICD	intracellular domain;
IC ₅₀	half-maximal inhibitory concentration;
KO	knock out;
nAChR	nicotinic acetylcholine receptor;
NMR	nuclear magnetic resonance;
PDB	protein data bank;
PNL	partial sciatic nerve ligation;
TMD	transmembrane domain

intracellular domain (ICD) that provides an interface for communication with the cellular milieu (Gharpure, Noviello, & Hibbs, 2020; Thompson, Lester, & Lummis, 2010) (Fig. 1). A series of nAChR subtypes are involved in vital physiological processes, such as neurotransmitter release, synaptic transmission and neuronal integration (Zoli et al., 2018).

Dysfunctional nAChRs associated with genetic and epigenetic factors, altered regulation of expression levels, or cell metabolism and cofactors are implicated in a variety of human diseases and health conditions (Bertrand & Terry, 2018; Dani & Bertrand, 2007; Dineley, Pandya, & Yakel, 2015; Zoli, Pistillo, & Gotti, 2015). These conditions include neuropathic pain (Hone & McIntosh, 2018; Hone, Servent, & McIntosh, 2017; Umana, Daniele, & McGehee, 2013), cognitive deficits in schizophrenia and Alzheimer's disease (Hurst, Rollema, & Bertrand, 2013; Parikh, Kutlu, & Gould, 2016), Parkinson's disease (Jurado-Coronel et al., 2016; Quik, Zhang, McGregor, & Bordia, 2015), epilepsy (Becchetti, Aracri, Meneghini, Brusco, & Amadeo, 2015), tobacco addiction (Benowitz, 2009; Hurst et al., 2013), and cancer (Chen, Cheuk, Shin, & Kwong, 2019; Dang, Meng, & Song, 2016).

1.1. The $\alpha 9\alpha 10$ nAChR

Phylogenetic analysis of the nAChR genes from a broad selection of vertebrate species shows that among the members of the nAChR family,

the subfamily comprised of the *CHRNA9* and *CHRNA10* genes forms the earliest branch, suggesting that the $\alpha 9$ and $\alpha 10$ subunits are evolutionarily distinct from other nAChR subunits (Franchini & Elgoyhen, 2006; Pedersen et al., 2019). The $\alpha 9\alpha 10$ nAChR is critical for mediating synaptic transmission from the medial olivocochlear to the cochlear hair cells (Elgoyhen & Katz, 2012) and has been implicated in a series of pathological conditions including, neuropathic pain and tumor proliferation (Chen et al., 2019; Hone et al., 2017).

Compared to other subtypes, the $\alpha 9\alpha 10$ nAChR has a number of unique biophysical and pharmacological characteristics. The relevant divalent to monovalent cation permeability of the rat $\alpha 9\alpha 10$ nAChR to Ca^{2+} , Ba^{2+} and Mg^{2+} is high (e.g. $P_{\text{Ca}}/P_{\text{Na}} \approx 9$) and ACh-evoked currents were blocked in a voltage-dependent manner by higher concentrations (>0.5 mM) of these cations (Gómez-Casati, Fuchs, Elgoyhen, & Katz, 2005; Weisstaub, Vetter, Elgoyhen, & Katz, 2002). Pharmacologically, nicotine, a classic agonist of neuronal nAChRs, is an antagonist of the $\alpha 9\alpha 10$ nAChR, with a half-maximal inhibitory concentration (IC₅₀) of 3.9 μM for the rat subtype (Verbitsky, Rothlin, Katz, & Elgoyhen, 2000). Similarly, nicotinic receptor agonists of other nAChR subtypes, such as cytisine and epibatine, are antagonists of the $\alpha 9\alpha 10$ nAChR (Verbitsky et al., 2000). Muscarine, a selective agonist of muscarinic AChRs, also inhibits rat $\alpha 9\alpha 10$ nAChRs with an IC₅₀ of 41 μM (Elgoyhen et al., 2001; Vincler & McIntosh, 2007). These unique pharmacological properties of $\alpha 9\alpha 10$ nAChR are intriguing but also bring challenges for understanding its function.

1.2. The $\alpha 9\alpha 10$ nAChR in hearing

Physiologically, the $\alpha 9\alpha 10$ nAChR is best known for mediating the inhibition of hair cell function within the auditory sensory organ (Elgoyhen et al., 2001; Elgoyhen, Katz, & Fuchs, 2009). The organ of Corti in the mammalian cochlea is responsible for the transmission of sound waves into electrical signals, via the outer and inner hair cells. Synapses of both hair cells are regulated by the $\alpha 9\alpha 10$ nAChR, which is functionally coupled to the activation of small-conductance, Ca^{2+} -dependent potassium channels (Elgoyhen & Katz, 2012; Glowatzki & Fuchs, 2000; Gómez-Casati et al., 2005; Katz et al., 2004; Wedemeyer et al., 2018). This is also important developmentally; a recent study using an $\alpha 9$ knock-in mouse model has highlighted that transient efferent innervation

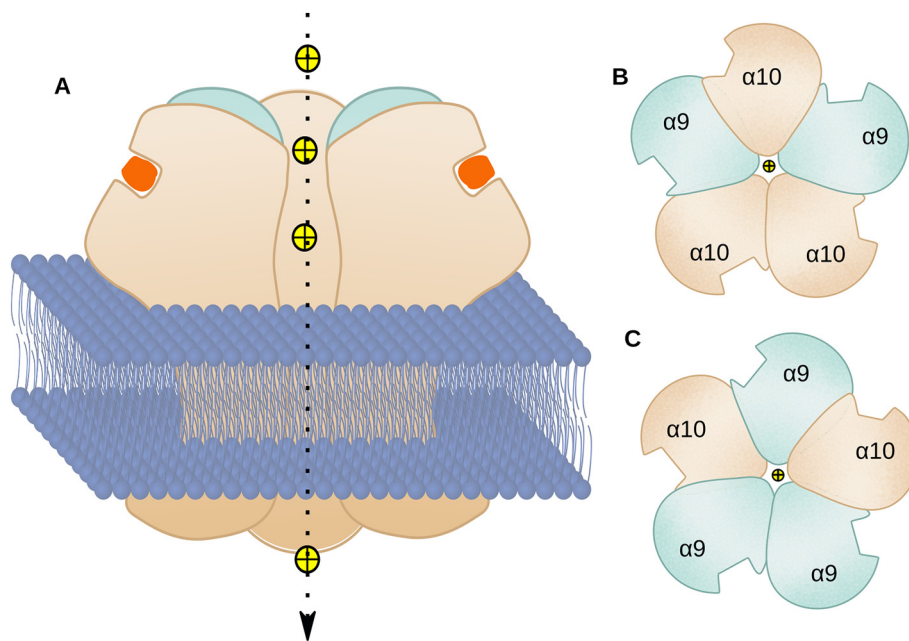


Fig. 1. Representative model of the $\alpha 9\alpha 10$ nAChR. (A) Side sectional view of the $\alpha 9\alpha 10$ nAChR (brown and teal) structure embedded in the cell membrane (blue). (B,C) Top view of the $\alpha 9\alpha 10$ nAChR structure in different stoichiometries. Binding of agonists (orange) to the binding sites located at the extracellular domain (ECD) opens the gate in the transmembrane domain (TMD), allowing cations (yellow) through the open channel.

to the cochlea is required for the correct establishment of the auditory system (Di Guilmi et al., 2019; Wedemeyer et al., 2018).

The outer hair cells of the adult rat cochlea express both $\alpha 9$ and $\alpha 10$ mRNAs; however, only $\alpha 9$ is detected in the inner cells after the onset of hearing and no ACh-mediated responses were observed in electrophysiological experiments (Katz et al., 2004; Morley & Simmons, 2002). It is also reported that cholinergic responses are insufficient to drive normal olivocochlear inhibition in $\alpha 10$ knockout (KO) rats (Vetter et al., 2007). The $\alpha 9$ subunit was initially suggested to form a homomeric pentamer (Elgoyhen, Johnson, Boulter, Vetter, & Heinemann, 1994) but the $\alpha 10$ subunit, which shares high sequence homology with the $\alpha 9$ subunit, has been functionally co-assembled *in vitro* with the $\alpha 9$ subunit to form $\alpha 9\alpha 10$ heteropentamers (Elgoyhen et al., 2001; Sgard et al., 2002). Co-injection of $\alpha 9$ and $\alpha 10$ mRNAs into *Xenopus laevis* oocytes boosts functional nAChR expression by ~100-fold compared to injection of $\alpha 9$ mRNA alone (Elgoyhen et al., 2001). These findings suggest that the $\alpha 10$ subunit is necessary in the formation of optimally functional receptors in the outer hair cells despite $\alpha 9$ alone being able to form a functional homomeric receptor *in vitro* (Elgoyhen et al., 1994). Moreover, the pharmacological properties of nAChRs expressed in hair cells closely match the $\alpha 9\alpha 10$ heteropentamer rather than the $\alpha 9$ homopentamer, suggesting that the native receptor is composed of $\alpha 9$ and $\alpha 10$ subunits (Gómez-Casati et al., 2005).

A functional role of $\alpha 9$ -containing nAChRs in auditory transmission is supported by studies on KO mice and use of heterologous receptor systems. The $\alpha 9$ subunit is implicated in selective attention, as suggested by poor performance of KO animals to visual stimuli in the presence of auditory distractors (Jorratt, Delano, Delgado, Dagnino-Subiabre, & Terreros, 2017). Additionally, heterologous $\alpha 9\alpha 10$ nAChRs have been proposed as a possible target mediating solvent-induced ototoxicity (van Kleef, Vijverberg, & Westerink, 2008). Taken together, the $\alpha 9\alpha 10$ nAChR plays an essential role in the efferent auditory system and may be considered as a potential therapeutic target for different hearing disorders, including noise-induced hearing loss, vertigo, and tinnitus (Lustig, 2006).

1.3. The $\alpha 9\alpha 10$ nAChR in inflammation, stress and regulation of neuropathic pain

Inflammation involves the recruitment of immune cells and release of mediators such as chemokines and cytokines in response to tissue injury, stress, and infection, and there is increasing evidence implicating inflammatory mechanisms in neuropathic pain. Neuropathic pain arises due to a lesion or disease of the somatosensory nervous system, which includes aberrant neuroinflammation in the peripheral and central nervous systems affected by autoimmune disorders. Additionally, traumatic neuropathy itself is associated with excessive inflammation, which may be involved in the development and persistence of neuropathic pain.

Anti-inflammatory efferent signals from the brain are mediated by the vagus nerve through the cholinergic anti-inflammatory pathway (Pavlov, Chavan, & Tracey, 2018). Activation of the vagal efferent fibers releases ACh that interacts with nAChRs of the immune cells, inhibiting pro-inflammatory cytokines release. Transcripts and proteins of the $\alpha 9$ and $\alpha 10$ subunits have been reported in a variety of immune cells (Lustig, Peng, Hiel, Yamamoto, & Fuchs, 2001; Peng et al., 2004), including purified populations of T-cells (CD3+, CD4+, CD8+ and the Jurkat, MT2 and CEM T-cell lines), B-cells (CD19+, CD80+ and EBV-immortalized B-cells), peripheral blood lymphocytes, monocytes, macrophages, dendritic cells, and microglia.

In mouse monocytes, $\alpha 9$ -containing receptors are postulated to mediate the effect of nicotine in attenuating both cell proliferation and production of pro-inflammatory cytokines (tumor necrosis factor (TNF)- α , interleukin (IL)-1 β and IL-12), while stimulating the production of the anti-inflammatory cytokine IL-10 (St-Pierre et al., 2016). Moreover, nicotine has been suggested to confer neural protection in a

mouse model of brain inflammation, possibly involving the $\alpha 9$ subunit (Simard et al., 2013), by reducing the infiltration of pro-inflammatory monocytes and neutrophils into the central nervous system (Jiang et al., 2016).

Additionally, in human monocyte-derived U937 cells, the $\alpha 9$ and/or $\alpha 10$ subunits are postulated to attenuate phosphocholine-induced release of IL-1 β , interestingly, via the metabotropic functions of the receptor, as phosphocholine itself failed to elicit ionotropic activities from both homo/heterologous $\alpha 9$ and $\alpha 9\alpha 10$ nAChRs (Richter et al., 2016; Zakrzewicz et al., 2017). In summary, $\alpha 9$ and/or $\alpha 10$ subunits may play an important role in regulating immune cell populations and cytokine production, and consequently, the manifestation of neuropathic pain.

The $\alpha 9\alpha 10$ nAChR is also expressed in adrenal and pituitary glands (Colomer et al., 2010; Sgard et al., 2002; Zemkova, Kucka, Bjelobaba, Tomic, & Stojilkovic, 2013), suggesting a potential role in the stress response. In cold-stressed rats, $\alpha 9\alpha 10$ nAChRs dominantly contribute to ACh-induced currents in adrenal chromaffin cells and expression levels of $\alpha 9$ nAChR transcript and protein are upregulated (Colomer et al., 2010). A role for the $\alpha 9\alpha 10$ -nAChR in behavioural and physiological stress responses, was also demonstrated by comparing the stress- and affect-related phenotypes of wild-type (WT) and $\alpha 9$ -nAChR KO mice (Mohammadi, Burton, & Christie, 2017). Naïve KO mice exhibited largely normal behaviour on standard tests of affective behaviour. However, after sub-chronic restraint stress $\alpha 9$ KO mice showed significantly decreased stress-induced arousal and increased anxiety-like behaviour when compared to WT animals. Physiologically, corticosterone responses were muted in KO mice after an acute stressor, but exaggerated in response to the same stressor after undergoing sub-chronic stress. Moreover, $\alpha 9$ KO mice exhibited unusual patterns of circadian activity and a dysfunction in reward seeking after a period of reduced access to reward (Mohammadi et al., 2017). These findings demonstrate a role of the $\alpha 9\alpha 10$ -nAChR in the regulation of stress responses, circadian activity and in reward-related affective behaviours.

Evidence to support the involvement of $\alpha 9\alpha 10$ nAChRs in pain comes primarily from *in vivo* pharmacological studies. The inhibition of $\alpha 9\alpha 10$ nAChRs by small molecules (e.g. tetrakis-quaternary ammonium compound ZZ-204G) and a class of α -conotoxins (e.g. Vc1.1, RglA, Pe1A and GeXIVA; see section 2) has been shown to alleviate the symptoms of pain (Del Bufalo, Cesario, Salinaro, Fini, & Russo, 2014; Di Cesare Mannelli et al., 2014; Holtman et al., 2011; Hone & McIntosh, 2018; McIntosh, Absalom, Chebib, Elgoyhen, & Vincler, 2009; Pacini et al., 2016). However, there is evidence that $\alpha 9\alpha 10$ nAChR inhibition is neither necessary nor sufficient for analgesia (Mohammadi & Christie, 2015). In a chronic constriction nerve injury (CCI) model of neuropathic pain, $\alpha 9$ -nAChR KO mice displayed normal responses to noxious mechanical and thermal stimuli, and chronic cold mechanical allodynia also developed normally. However, $\alpha 9$ KO mice exhibited a distinct phenotype in the development of mechanical hyperalgesia; WT mice continued to display elevated mechanical hyperalgesia 21 days after injury, whereas $\alpha 9$ KO mice showed substantially reduced hyperalgesia following CCI surgery (Mohammadi & Christie, 2014). In a separate study, conducted in the oxaliplatin model of peripheral neuropathy with a different strain of $\alpha 9$ KO mice, oxaliplatin produced robust cold allodynia in WT animals, but the expression of cold-allodynia in $\alpha 9$ KO mice was attenuated in both magnitude and symptom duration (Romero et al., 2017). Together, these studies suggest that germline deletion of $\alpha 9$ nAChRs *per se* can attenuate the development and progression of neuropathic pain and that there may not be a close phenotypic correlation between KO mice and pharmacological treatment in WT animals.

1.4. The $\alpha 9\alpha 10$ nAChR in cancer

Certain cancers are linked to selective overexpression of membrane receptors and ion channels, including nAChRs. Some nAChR subunits

are associated with the pathogenesis of cancers, such as $\alpha 5$, $\alpha 9$, and $\alpha 10$ which have been reported in various breast cancer cell lines and in human breast tumors, and $\alpha 9$ expression is significantly elevated in tumors compared to normal cells (Lee et al., 2010). Additionally, transcripts of $\alpha 9$ have also been reported in cervical and lung cancer cell lines and tumors (Liu, Qian, Sun, Zhangsun, & Luo, 2019; Mucchietto et al., 2018; Wang, Zhang, Gu, Bao, & Bao, 2014).

Contribution of the $\alpha 9$ subunit to cancer cell survival was critically shown by the failure of transiently *CHRNA9*-silenced human breast cancer cells to grow in cultures (Lee et al., 2010). Moreover, exposure to the primary active component of cigarettes, nicotine, promotes $\alpha 9$ -mediated oncogenesis of human breast epithelial cells possibly by stimulating cyclin D3 overexpression (Chen et al., 2011). Treatment of cultured breast cell lines with nicotine stimulates a cellular proliferation and migration signalling cascade involving protein kinase C and *cdc42* (cell division control protein 42 homolog), and consequently promotes cancer progression (Guo et al., 2008). Further research shows that long-term exposure to low-dose of nicotine and 4-(methylnitrosamino)-1-(3-pyridyl)-1-butanone (NNK) will cause non-malignant breast epithelial cell transformation through activation of the $\alpha 9$ -nAChR-mediated signalling pathway (Fararjeh et al., 2019). Although nicotine acts as an antagonist of the ionotropic $\alpha 9$ receptor (Verbitsky et al., 2000), the activation effects of nicotine have been postulated to be contributed by the metabotropic $\alpha 9$ nAChR as nicotine does not elicit current responses from homomeric $\alpha 9$ and/or $\alpha 9\alpha 10$ nAChRs (Richter et al., 2016). In addition to breast cancer, nicotine can also induce melanoma cell proliferation through stimulation of the $\alpha 9$ -nAChR-mediated AKT and ERK signalling pathways (Nguyen et al., 2019). In colorectal cancer, it has been suggested that parasympathetic nerves may promote the progression of tumors through $\alpha 9$ nAChR (Zhou et al., 2018). The role of the $\alpha 9$ subunit in the development of breast and lung cancers has been suggested (Chen et al., 2011; Huang et al., 2017; Lee et al., 2010; Mucchietto et al., 2018; Wang et al., 2014), whereby exposure of healthy and cancerous cells to nicotine modulates the expression and function of nAChRs, leading to tumor progression, invasion, metastasis, and resistance to apoptosis.

2. Conotoxins

Antagonists of the $\alpha 9\alpha 10$ nAChR can potentially be developed as therapeutic compounds for the treatment of physiological conditions associated with this subtype. A series of azaaromatic quaternary ammonium analogues have been proposed as possible agents for the treatment of neuropathic and tonic inflammatory pain (Wala, Crooks, McIntosh, & Holtman, 2012; Zheng et al., 2011). Moreover, potent anti-glioblastoma agents have been designed by hybridizing the anti-proliferative onium-alkyloxy-stilbene based structures of $\alpha 7$ and $\alpha 9$ nAChR antagonists with a pro-oxidant, mitocan (Bavo et al., 2018). However, these non-peptide, small molecular compounds have potential off-target effects, thus limiting their therapeutic applications. The discovery of highly potent and selective nAChR-targeting peptides in the venom of *Conus* marine snails (conotoxins) has opened up new opportunities for developing novel peptide therapeutics and molecular probes to study the structure and function of various nAChR subtypes (Clark, Fischer, Nevin, Adams, & Craik, 2006; Ellison et al., 2006; Luo et al., 2015). Molluscs of the genus *Conus* comprise more than 750 species (Jin et al., 2019) and these carnivorous cone snails hunt various prey types, ranging from worms to fish, and other molluscs, including cone snails (Luo et al., 2015; Olivera et al., 1985). Each cone snail venom contains a unique cocktail of hundreds to thousands of bioactive peptides called conotoxins (Akondi et al., 2014; Olivera et al., 1990). Conotoxins can be categorized into different subfamilies according to their signal peptide sequence, cysteine framework pattern, and biological target (Vetter & Lewis, 2012). Based on their signal peptide, the conotoxins have been grouped into different subfamilies such as

A-, D-, I-, J-, M-, O-, P-, S-, T and others (Kaas, Yu, Jin, Dutertre, & Craik, 2012; Robinson & Norton, 2014). In conotoxins, cysteine residues stabilize the secondary structure and facilitate the folding of the peptides (Gongora-Benitez, Tulla-Puche, & Albericio, 2014) and the unique arrangement of these residues is also used to group the peptides for which, to date, over 30 frameworks have been reported (Kaas et al., 2012). These bioactive peptides can be divided further into α -, δ -, γ -, κ -, μ -, ω -, ι -, ρ -, φ and other classes, depending on their pharmacological targets (Akondi et al., 2014; Kaas, Westermann, Halai, Wang, & Craik, 2008; Lewis, Dutertre, Vetter, & Christie, 2012), which include membrane receptors, ion channels, G protein-coupled receptors, transporters (Myers, Cruz, & Olivera, 1993; Nilsson et al., 2005; Sadeghi, McArthur, Finol-Urdaneta, & Adams, 2017; Sharpe et al., 2001), and enzymes (Pennington, Czerwinski, & Norton, 2018; Vetter & Lewis, 2012). This makes them valuable as novel drug leads for neuroscience research and disease treatment (Dutton & Craik, 2001; Halai & Craik, 2009).

Among the different classes of conotoxins, the α -conotoxins are the most studied due to their abundance and pharmacological importance (Abraham & Lewis, 2018; Giribaldi & Dutertre, 2018). The majority of these α -conotoxins act as competitive antagonists of muscle and neuronal nAChRs (Lewis et al., 2012). Classical α -conotoxins comprise 12–40 amino acids with four cysteine residues (C1 to C4) that adopt a CC–C–C framework. Depending on the disulfide bridge-contributing residues, there are three possible isomers, namely globular (C1–C3, C2–C4), ribbon (C1–C4, C2–C3) and bead (C1–C2, C3–C4) (Lebbe, Peigneur, Wijesekara, & Tytgat, 2014). The peptide segments between C2 and C3, and between C3 and C4 are referred to as loops, the length of which are used to sub-classify the α -conotoxins (Jin et al., 2019). Based on the number of amino acid residues in each loop, the α -conotoxins are further classified as 3/5, 4/3, 4/4, 4/6, 4/7, and 4/8 subtypes (Abraham & Lewis, 2018; Dutton & Craik, 2001).

2.1. Conotoxin antagonists of the $\alpha 9\alpha 10$ nAChR

To date, at least nine α -conotoxins that target the $\alpha 9\alpha 10$ nAChR have been described (Table 1) using proteomic analysis of crude cone snail venom or via transcriptomic screening of the venom duct. Interestingly, their structures are widely divergent, with different sequence lengths and various formations of disulfide bonds. The structures of typical α -conotoxins from four different *Conus* species are shown in Fig. 2.

α -PeIA that is isolated from the venom of *C. pergrandis*, consists of 16 amino acid residues and contains two disulfide bonds (McIntosh et al., 2005). It was determined to have a high potency for $\alpha 9\alpha 10$ nAChRs and has a 260-fold higher selectivity for rat $\alpha 9\alpha 10$ nAChR ($IC_{50} = 6.9$ nM) than rat $\alpha 7$ nAChR. Although PeIA can discriminate between $\alpha 7$ and $\alpha 9\alpha 10$ nAChRs, it also blocks rat $\alpha 3\beta 2$ and chimeric rat $\alpha 6/\alpha 3\beta 2\beta 3$ subtypes with relatively high potency (McIntosh et al., 2005).

The 16-residue Vc1.1 from the Australian molluscivorous cone snail, *C. victoriae* (Satkunanathan et al., 2005), has an amidated C-terminus, two disulfide bonds in a C1–C3 and C2–C4 arrangement, and a typical α -helical motif (Safavi-Hemami et al., 2011; Sandall et al., 2003) (Fig. 2). Vc1.1 has been reported to attenuate both mechanical hyperalgesia and allodynia in neuropathic pain models in rats (Napier et al., 2012; Satkunanathan et al., 2005) and it was reported that Vc1.1 accelerates functional recovery of injured neurons (Livett et al., 2006; Satkunanathan et al., 2005). Furthermore, previous studies also suggested that the analgesic potency of Vc1.1 is higher than that of ziconotide (Clark et al., 2006). However, *in vitro* studies showed that Vc1.1 is less potent at inhibiting human $\alpha 9\alpha 10$ nAChR ($IC_{50} = 1$ μ M) compared with rat $\alpha 9\alpha 10$ nAChRs ($IC_{50} = 20$ – 100 nM) (Table 1) and consequently its use was suspended after phase II human clinical trials (Del Bufalo et al., 2014).

To date, α -RglA from *C. regius* is the shortest conotoxin (13 amino acids) with potency at $\alpha 9\alpha 10$ nAChRs, with two disulfide bonds but devoid of C-terminus amidation (Ellison et al., 2006). Residues Arg9,

Table 1
Conotoxins targeting the $\alpha 9\alpha 10$ nAChR.

Conotoxin	Conus species	Sequence	IC ₅₀ (nM) at $\alpha 9\alpha 10$	
			Rat	Human
α -PeIA	<i>C. pergrandis</i>	GCCSHPACSVNHPELC*	6.9 (McIntosh et al., 2005) 33 (Hone et al., 2012)	22.2 (Yu et al., 2018)
α -Vc1.1	<i>C. victoriae</i>	GCCSDPRCNYDHPEIC*	19 (Clark et al., 2006) 64.2 (Nevin et al., 2007) 109 (Halai et al., 2009) 70 (Yu, Kompella, Adams, Craik, & Kaas, 2013) 28.3 (Cai et al., 2018) 5.2 (Vincler et al., 2006) 4 (Azam & McIntosh, 2012) 2.6 (Ren et al., 2019)	1,000 (Yu et al., 2018)
α -RgIA	<i>C. regius</i>	GCCSDPRCRYRCR	3900 [globular] >30,000 [ribbon] 1200 [bead] (Luo et al., 2013)	494 (Azam & McIntosh, 2012) 1,400 (Ren et al., 2019)
α B-VxXXIVA	<i>C. vexillum</i>	VRCLEKSGAQPNKLFPPCCQKGPSFARHSRCVYYTQSRE	22.7 [globular] 7 [ribbon] 4.6 [bead] (Luo et al., 2015)	ND
α O-GeXIVA	<i>C. generalis</i>	TCRSSGRYCRSPYDRRRRYCRITDACV*	198.6 [globular] 35.1 [ribbon] (Wu et al., 2017) 116 [globular] 20.3 [ribbon] 47.3 [bead] (Zhangsun et al., 2017)	ND
α S-GVIIIIB	<i>C. geographus</i>	SGSTCTCTFTSTNCQGSCELSPPGCYCSNNGIRQPQCSCTCPGTG*	9.8 (Christensen, Bandyopadhyay, Olivera, & McIntosh, 2015)	ND
α D-GeXXA	<i>C. generalis</i>	DVHRPCQSVRPGRVWVKCCLTRLCSTMCCARADCTCVYHTWRHGSCVM	1.2 (Xu et al., 2015)	28 (Xu et al., 2015)
α O-GeXXVIIA	<i>C. generalis</i>	ALMSTGTNYRLLKTCRSGRYCRSPYDCRRRYCRRISDACV*	ND	16.2 (Jiang et al., 2017)
α D-Lt28.1	<i>C. litteratus</i>	LHCHEISDLTPWILCSPEPLCGGKGCQAQEVDCSGPACTCPCL	3,092 (Lu et al., 2017)	ND

* = amidated C-terminal; C = cysteine residue; [] = disulfide bond isomer; IC₅₀ = half-maximal inhibitory concentration; ND = not determined

Tyr10, and Arg13 play important roles in the potency and selectivity for $\alpha 9\alpha 10$ nAChR (Ellison et al., 2008). Similar to Vc1.1, RgIA is reported as a potent analgesic in a CCI rat model and for nerve injury associated inflammation (Di Cesare Mannelli et al., 2014). Results from more recent studies also suggest that the administration of RgIA4 (an analogue of RgIA) can effectively reduce oxaliplatin-dependent hypersensitivity to mechanical and thermal noxious and non-noxious stimuli (Christensen et al., 2017). However, Vc1.1 and RgIA were also proposed to exert their effects by activating G protein-coupled γ -aminobutyric acid type B (GABA_B) receptors (Berecki, McArthur, Cuny, Clark, & Adams, 2014; Callaghan et al., 2008; Castro et al., 2017; Cuny et al., 2012; Huynh, Cuny, Slesinger, & Adams, 2015; Mohammadi & Christie, 2015; Sadeghi et al., 2017)

VxXXIVA is a member of the B-subfamily discovered in *C. vexillum*. Different from the majority of conotoxins whose precursor sequence is composed of a signal segment, a “pro” region and a mature sequence,

the precursor peptide of VxXXIVA lacks a “pro” region. The mature α B-VxXXIVA contains 40 amino acid residues and has a rare C-CC-C cysteine framework. The ribbon disulfide isomer shows the highest potency at rat $\alpha 9\alpha 10$ nAChRs, with an IC₅₀ of 1.2 μ M (Luo et al., 2013).

GeXIVA is a new O-superfamily α -conotoxin identified from *C. generalis* that consists of 28 amino acid residues. Unlike most O-superfamily conotoxins, which contain six cysteine residues, GeXIVA only has four cysteine residues, forming three possible disulfide isomers (Luo et al., 2015). The most active disulfide isomer is the bead isomer (Wu et al., 2017; Zhangsun et al., 2017) with an IC₅₀ of 4.6 nM at the rat $\alpha 9\alpha 10$ nAChR. The ribbon isomer is equipotent but has an additional helical motif from positions 12–18, which contributes to a more rigid structure that forms significant interactions with the $\alpha 9\alpha 10$ nAChR (Luo et al., 2015) (Fig. 2). Dissociation kinetics studies of GeXIVA at the $\alpha 9\alpha 10$ nAChR suggested that the binding site of GeXIVA does not overlap with that of RgIA, and a potential binding site is located at the principal $\alpha 9$ and complementary $\alpha 10$ subunit interface (Luo et al., 2015). Similar to RgIA and Vc1.1, GeXIVA also significantly reduces mechanical hyperalgesia in CCI rats and has no impact on the motor performance of the tested animals (Luo et al., 2015). Furthermore, GeXIVA can relieve and reverse oxaliplatin-induced mechanical and cold allodynia after single and repeated intramuscular injections in rats (Wang et al., 2019).

Most conotoxins targeting the $\alpha 9\alpha 10$ nAChR are extracted from mollusc- or worm-hunting cone snails. However, α S-GVIIIIB, which is composed of 45 amino acid residues and contains 10 cysteine residues, was isolated from the venom of the fish-hunting *C. geographus*. α S-GVIIIIB potently blocks the rat $\alpha 9\alpha 10$ nAChR, with an IC₅₀ of 9.8 nM and >100-fold selectivity over other subtypes. Both GVIIIIB and RgIA share a binding site contributed by the interface between the principal and complementary components of the $\alpha 10$ and $\alpha 9$ subunits, respectively (Christensen et al., 2015).

α D-conotoxins occur naturally as dimers with complex disulfide connections (Loughnan et al., 2006), including GeXXA from the venom of *C. generalis*, and each GeXXA monomer contains 50 residues, including 10 cysteines (Fig. 2). GeXXA inhibits various nAChR subtypes but it is most potent at the rat (IC₅₀ = 1.3 nM) and human

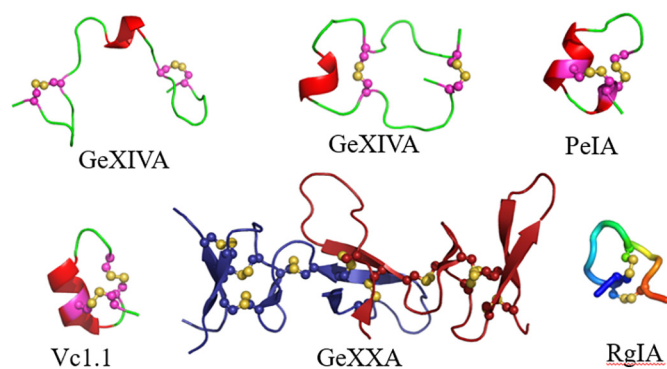


Fig. 2. Structures of typical $\alpha/\alpha O/\alpha D$ -conotoxins targeting the $\alpha 9\alpha 10$ nAChR. Nuclear magnetic resonance (NMR) structures of the bead and ribbon isomers of αO -GeXIVA (Luo et al., 2015). Crystal structures of α -PeIA (PDB code 5JME) and αD -GeXXA (PDB code 4X9Z), and NMR structures of α -Vc1.1 (PDB code 2H8S) and α -RgIA (PDB code 2JUT). GeXIVA and GeXXA were discovered in *C. generalis*. PDB, protein data bank.

($IC_{50} = 28$ nM) $\alpha 9\alpha 10$ nAChR. The species difference in potency is attributed to residue His7 of the rat $\alpha 10$ subunit and uniquely, GeXXA inhibition at the $\alpha 9\alpha 10$ nAChR is attained possibly via cooperative binding of the monomeric C-terminal domains to the top surface of the receptor (Xu et al., 2015).

In addition to GeXIA and GeXXA, the venom of *C. generalis* contains a third conotoxin, GeXXVIIA, with potent activity at the $\alpha 9\alpha 10$ nAChR. The precursor sequence of GeXXVIIA is similar to GeXIVA, and it also belongs to the O-superfamily. The native form of αO -GeXXVIIA is a disulfide-linked 5-cysteine-containing homodimer. In comparison to the folded monomer, the linear monomer of this toxin has the highest inhibitory activity at the human $\alpha 9\alpha 10$ nAChR, with an IC_{50} of 16.2 nM, indicating that the binding of the linear GeXXVIIA peptide to nAChR is only dependent on the sequence of the peptide, and the disulfide bonds have no contribution to its potency. GeXXVIIA is neither a competitive antagonist nor an open channel pore blocker by entering the membrane electric field of nAChR, thus representing a new class of nAChR allosteric inhibitor (Jiang et al., 2017).

The D-superfamily conotoxin Lt28.1 was cloned from *C. literatus* and comprises 45 amino acids with 10 cysteine residues (Lu et al., 2017). Lt28.1 selectively inhibits the rat $\alpha 9\alpha 10$ nAChR despite relatively low potency ($IC_{50} = 3$ μ M) (Lu et al., 2017).

3. Conotoxin optimization strategies

Although conotoxins possess favorable pharmacological activities, they also have a number of shortcomings, such as short half-life, instable

disulfide bonds, limited modes of administration and reduced potency at human nAChRs, and all of these hinder translational application of conotoxins as drug leads or pharmacological tools (Carstens et al., 2011; Romero et al., 2017; Tabassum et al., 2017). Therefore, in order to improve the activity, selectivity and stability of conotoxins, a series of strategies have been applied, including scanning mutation, disulfide bond modification, backbone cyclization and polymerization (Craik & Adams, 2007) (Fig. 3).

Among the α -conotoxins active at the $\alpha 9\alpha 10$ subtype, Vc1.1 and RglA have attracted significant research interest due to their short length and relatively stable structure. They share the same cysteine framework, in which loop 1 between C2 and C3 is crucial for binding whereas loop 2 between C3 and C4 is primarily responsible for subtype selectivity (Halai et al., 2009; Luo et al., 2015). Considering that inhibition of the $\alpha 9\alpha 10$ nAChR can effectively alleviate neuropathic and chronic visceral pain in animal pain models (Dutton & Craik, 2001; Giribaldi & Dutertre, 2018; Janes, 2005), as well as suppress tumor growth (Sun et al., 2020; Sun et al., 2020), structure-activity analysis of $\alpha 9\alpha 10$ nAChR-selective α -conotoxins is therefore critical for the development of therapeutic drug leads and pharmacological tools. Here, we summarize successful modification strategies applied to α -conotoxins targeting the $\alpha 9\alpha 10$ nAChR, which can provide guidance for future peptide optimization.

3.1. Amino acid sequence scanning

In the field of peptide research, alanine scanning mutagenesis is a well-known technique for identifying key residues for structural stability

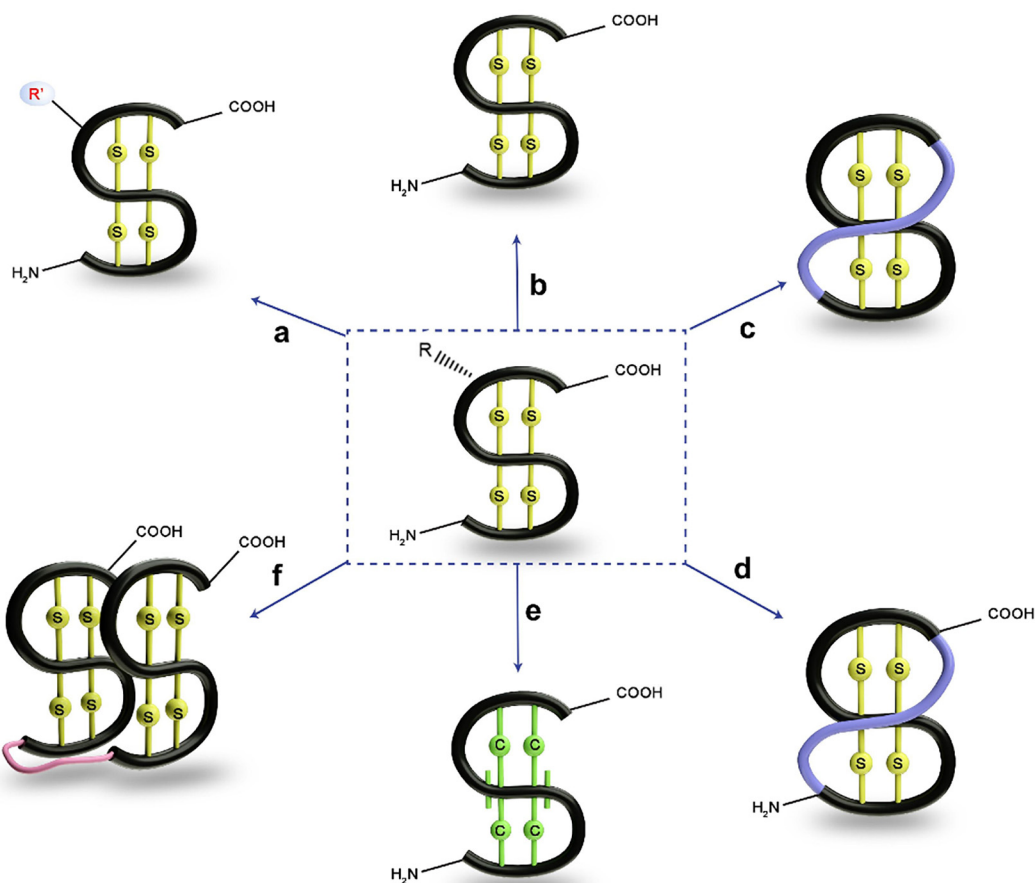


Fig. 3. Overview of the chemical modification strategies that have been applied to α -conotoxins inhibiting the $\alpha 9\alpha 10$ nAChR. a) Substitution or modification of side chain residues for activity and selectivity improvement. b) Replacement of L-amino acids with D-amino acids increases the enzyme stability of the peptide. c) Backbone cyclization increases the enzyme stability of the peptide. d) Side chain cyclization improves the stability of the peptide and maintains potency. e) A dicarba bridge substituted for the native cysteine framework improves peptide stability and tunes the selectivity of the peptide to certain receptors. f) Dimerization of the peptide improves the potency of α -conotoxins.

and bioactivity (Halai et al., 2009; Morrison & Weiss, 2001). Besides alanine scanning, researchers have also utilized aspartic and/or lysine scanning in order to explore the effects of side-chain charge on peptide-receptor interactions (Halai et al., 2009). In addition, D-type amino acid scanning in which L-amino acids are replaced with D-amino acids, has also been applied to facilitate the development of more stable analogues (Ren et al., 2019).

Halai et al. (2009) performed extensive Ala scanning in conjunction with Lys and Asp scanning to explore the effects of neutral, positive, and negative charge substitutions, respectively, at all non-cysteine residues of Vc1.1. Most analogues had a dramatic reduction in activity at the $\alpha 9\alpha 10$ nAChR, attributed to overall structural distortion and/or disruption in the interactions between amino acids of Vc1.1 and the receptor. In contrast, introduction of a positive charge at position 4 (Ser) and hydrophobic residues at position 9 (Asn), resulted in analogues with more potent activity at the $\alpha 9\alpha 10$ nAChR than the native peptide (Halai et al., 2009). Additionally, Pro residues of Vc1.1 are essential to maintain structural stability of the peptide. The Pro residue at position 6 is involved in defining both the ligand conformation and receptor binding affinity, whereas the Pro at position 13 facilitates the native folding of Vc1.1. Overall, residues at position 5 to 7 are crucial for Vc1.1 binding to the $\alpha 9\alpha 10$ nAChR, whereas residues at position 11 to 15 are required for receptor selectivity (Halai et al., 2009).

RglA is a member of the 4/3 family of α -conotoxins, as is Iml (Ellison et al., 2006; Quiram, Jones, & Sine, 1999). Interestingly, although they have a similar sequence and structure, their nAChR subtype targets are quite different. RglA is a selective antagonist of the human and rat $\alpha 9\alpha 10$ subtype, whereas Iml preferentially blocks the human $\alpha 7$ and $\alpha 3\beta 2$ subtypes. Despite this, the activity of both RglA and Iml at their respective nAChR subtypes is conferred by the conserved Asp-Pro-Arg (DPR) motif in loop1 (Ellison et al., 2006; Kennedy et al., 2020; Quiram & Sine, 1998). While loop 1 is responsible for latching the α -conotoxins to the receptor, residues at position 9 (Ala in Iml and Arg in RglA) are responsible for the nAChR subtype selectivity (Ellison et al., 2006).

Susceptibility to proteolytic degradation is an unfavorable property that greatly limits the clinical applications of α -conotoxins. Almost all naturally occurring peptides are built from L-amino acids, but D-amino acid-containing peptides have been described from a number of organisms (Quiram & Sine, 1998). Due to the limited prevalence of D-amino acids in nature, they are less prone to enzymatic degradation, thus D-amino acid scanning is a valuable strategy for prolonging the bioavailability and bioactivity of α -conotoxins and revealing the critical residues involved in conotoxin-target interactions. RglA is a potent selective antagonist of $\alpha 9\alpha 10$ nAChRs (Table 1), however, compared to other α -conotoxins, RglA is more susceptible to proteolysis due to the higher abundance of arginine residues (Ren et al., 2019). Thus, Ren et al. (2019) generated a series of RglA D-amino acid scanning analogues and tested their activity on $\alpha 9\alpha 10$ nAChR ACh-evoked currents and stability against enzymatic activity in serum. The change of amino acid chirality in RglA decreased its potency at $\alpha 9\alpha 10$ nAChRs, except for [D-Arg13]RglA, which was proposed to be located outside the binding site and with high mobility. Despite the reduced potency of other D-Arg analogues, the serum stability of these peptides including [D-Arg13]RglA was notably improved (Ren et al., 2019).

In a recent study, Huynh, Harvey, Gajewiak, Craik, and McIntosh (2020) implemented amino acid substitution to define the chemical properties of RglA that contribute to its activity against $\alpha 9\alpha 10$ nAChRs. The results indicated that the primary contribution to activity are the side chain properties of RglA residues, rather than backbone conformation. It was also found that replacement of Arg13 with Tyr significantly increased the potency of RglA for human $\alpha 9\alpha 10$ nAChRs by 243-fold and the discrepancy between human and rats was eliminated (Huynh et al., 2020).

3.2. Unnatural amino acid substitutions

Non-coded (unnatural) amino acids with unique side chain properties are commonly employed in structure-function studies of conotoxins. Recently, Chu et al. (2019) described unnatural 2,4-diamino butyric acid (Dab) analogues of Vc1.1 ([S4Dab, N9A]Vc1.1 and [S4Dab, N9W]Vc1.1) with ~20-fold increases of potency compared to unmodified Vc1.1 at the human $\alpha 9\alpha 10$ nAChR. Another example is RglA4, an analogue of RglA with two unnatural amino acids (citrulline at position 9 and 3-iodotyrosine at position 10), which has >300 fold higher potency at the human $\alpha 9\alpha 10$ nAChR compared to the parent peptide (RglA4 $IC_{50} = 1.5$ nM (Romero et al., 2017) vs RglA $IC_{50} = 500$ – 1400 nM) (Table 1). A unique highlight of RglA4 is essentially the absence of a species potency gap between human and rodent $\alpha 9\alpha 10$ nAChRs ($IC_{50} = \sim 1$ – 2 nM) (Christensen et al., 2017; Romero et al., 2017) in contrast to the native peptide. Most importantly, RglA4 has an analgesic effect without tolerance in a rat chemotherapy-induced neuropathic pain model (Christensen et al., 2017; Romero et al., 2017).

3.3. Peptide backbone cyclization

A major caveat to the potential of conotoxins as therapeutics is their susceptibility to *in vivo* degradation, which limits their effectiveness when delivered orally (Clark, Akcan, Kaas, Daly, & Craik, 2012; Clark et al., 2010). However, the discovery of natural cyclic peptides that are stable *in vivo* introduces a new dimension for improving the bioavailability of linear peptides (Clark et al., 2005; Franke et al., 2017).

Synthetic peptide cyclization can be achieved by performing an amidation reaction between the amino group of the N-terminus and the carboxyl group of C-terminus of the linear peptide. However, this technique may cause structural distortion that can result in reduced activity of the peptide. To resolve this issue, it is common to insert a linker consisting of amino acids between the two terminal ends of the peptide and optimization of the linker length is critical as it affects the properties of cyclic conotoxins (Armishaw, Dutton, Craik, & Alewood, 2010; Carstens et al., 2016; Clark et al., 2010; Halai et al., 2011). Cyclization of RglA generated peptides that are more stable in serum than the linear RglA, and constructs with 6- and 7-residue linkers consisting of glycine and alanines, were most stable. However, only the cyclic peptide with a 7-residue linker had comparable potency to linear RglA for inhibiting $\alpha 9\alpha 10$ nAChRs. An NMR structure study also suggested that a linker of three or four residues leads to perturbations in the peptide backbone fold, and a linker of five residues or more introduces negligible restraint on the flexibility of the peptides, which is necessary for binding to the receptor (Halai et al., 2011).

An orally active cyclized Vc1.1 (cVc1.1), with the connecting N- and C-termini linked via a GGAAGG-linker (4 glycines and 2 alanines), was ~10-fold less potent at $\alpha 9\alpha 10$ nAChRs than the linear Vc1.1 (Clark et al., 2010). Structurally, cVc1.1 has an α -helical region from residues Pro6 to Asn11, similar to the native Vc1.1. However, cVc1.1 also contains a new helix formed by residues Pro13 to Cys16 and a type I β -turn from residues Gly1 to Ser4, suggesting that cVc1.1 is somewhat more rigid than Vc1.1. This increased rigidity results in dramatically improved stability of cVc1.1 in human serum and simulated intestinal fluid. More importantly, cVc1.1 induced a strong analgesic effect in a rat CCI model when administered orally (Clark et al., 2010), and recent research also suggests that cVc1.1 inhibits colonic nociceptors from healthy mice (Castro et al., 2018). High stability, good activity and oral efficacy make cVc1.1 a significant milestone in the transformation of conotoxins into drugs. In another example, the ribbon isomer of GeXIVA was cyclized with a linker of two glycine residues (Wu et al., 2017). Compared to the linear peptide, the cyclic construct is equipotent at inhibiting the human $\alpha 9\alpha 10$ nAChR, with slightly improved serum stability. As a result of its high structural flexibility and Arg-rich sequence

(9 Arg in total), GeXIVA is highly susceptible to endoproteases and/or denaturation of side chains, which are hardly negated by backbone cyclization (Wu et al., 2017). Although cyclization did not improve the properties of the peptide, the introduction of the short linker resulted in selective yield of the ribbon disulfide isomer without the need for orthogonal protection during the chemical synthesis.

3.4. Peptide side-chain cyclization

Linear peptides can also be cyclized via amino acid side chain-to-side chain connectivity. Zheng et al. (2020) introduced a key lactam linkage at the termini through side chain cyclization and successfully developed an RglA4 analogue with improved serum stability while retaining potency at the human $\alpha 9\alpha 10$ nAChR (Zheng et al., 2020). The NMR structure of this analogue overlays well with that of RglA4, demonstrating that the cyclization does not perturb the overall conformation of backbone and key side-chain residues. Structurally, the extra lactam bond provides an additional conformational constraint to the bioactive conformation and suppresses disulfide scrambling, leading to considerable serum stability improvements. Furthermore, the analogue exhibited a strong analgesic effect in a chemotherapy-induced neuropathic pain model (Zheng et al., 2020).

3.5. Disulfide bond replacement

Disulfide bonds play a vital role in maintaining the stable structure and biological activity of conotoxins. However, multiple disulfide bonds are inherently susceptible to shuffling under reducing physiological environments, generating a heterogeneous peptide population. Disulfide bond isomers (globular, ribbon and bead) of α -conotoxins are shown to have different structural properties with a range of potencies that inhibit nAChRs (Gehrmann, Alewood, & Craik, 1998; Rabenstein & Weaver, 1996). Several disulfide bond replacement strategies have been applied to generate conotoxins with improved potential as drug leads, including the replacement of disulfide bonds with other cross-links and deletion by substitution of Cys with non-cross-linking residues (Green et al., 2014; MacRaild et al., 2009). A dicarba bridge was used as a substitute for the native cysteine framework of Vc1.1 and RglA in early research, and region-selective replacement of a disulfide bond with a dicarba bridge showed the potential to tune the innate biological activity of a peptide for one receptor over another (Kennedy et al., 2020). For instance, the [3,16]-dicarba Vc1.1 isomer retains activity at the $\alpha 9\alpha 10$ nAChR whereas the [2,8]-dicarba Vc1.1 isomer only acts on G protein-coupled GABA_B receptors. Similarly, the [3,12]-dicarba RglA analogue retains inhibition at the $\alpha 9\alpha 10$ nAChR but not at the N-type calcium channel, whereas [2,8]-dicarba analogues display opposite target selectivity. Use of dicarba-substituted Vc1.1 and RglA analogues demonstrated that the C1–C3 bridge is important for inhibiting the $\alpha 9\alpha 10$ nAChR, whereas the C2–C4 bridge is responsible for GABA_B receptor modulation (Chhabra et al., 2014; Van Lierop et al., 2013). Indeed, not only do these analogues provide more stable peptides, they are also valuable as probes for conotoxin structure-activity relationship studies at different targets.

Another strategy was to replace the C1–C3 disulfide bond of cVc1.1 with non-covalent bond residues in [C2H,C8F]cVc1.1 (Yu et al., 2015). Compared to cVc1.1, [C2H,C8F]cVc1.1 was marginally less potent at inhibiting the human $\alpha 9\alpha 10$ nAChR despite increased peptide hydrophobicity. The linear [C2H,C8F]Vc1.1 was unable to block the $\alpha 9\alpha 10$ nAChR although it is structurally similar to Vc1.1, thus suggesting that the C1–C3 disulfide bond of α -conotoxins plays a vital role in the inhibition of nAChRs, and that the linker of [C2H,C8F]cVc1.1 may inadvertently compensate for the activity loss resulting from disulfide bond deletion (Tabassum et al., 2017). Both cVc1.1 and [C2H,C8F]cVc1.1 also reduce nociception in a mouse model of chronic visceral pain, therefore, taking into account the structural simplicity and conformational stability of this cyclic Vc1.1 analogue, [C2H,C8F]cVc1.1 is a

candidate for the treatment of pain associated with gastrointestinal conditions (Castro et al., 2018; Yu et al., 2015).

Recently, Xu et al. (2020) explored the effect of replacing all or some of the disulfide bridges in GeXIVA with Ala or Ser residues. Interestingly, most analogues retained a potency similar to GeXIVA for inhibiting the human $\alpha 9\alpha 10$ nAChR. One analogue, [C2A,C9A,C20S,C27S]GeXIVA, was twice as active as the native peptide, suggesting that the disulfide bridges are not necessary for the activity of GeXIVA at $\alpha 9\alpha 10$ nAChR (Xu et al., 2020).

3.6. Multimerization of conotoxins

Multiple monomeric conotoxins attached to a single molecular scaffold may be more potent because they concomitantly occupy multiple binding sites at nAChRs. Wan et al. (2015) used a chain of 9 poly(ethylene glycol) molecules (PEG9) as a linker to synthesize dimer- and tetramer-ImI, which increased its potency at the human $\alpha 7$ nAChR by more than 100-fold (Wan et al., 2015). Recently, PEG9-dimeric constructs of PeIA, Vc1.1 and RglA# ([Δ R13]RglA) were designed and upon dimerization, all three constructs had significantly improved potency compared to their monomeric counterparts at the human $\alpha 9\alpha 10$ nAChR. Interestingly, dimeric RglA# also had significantly improved potency at the human $\alpha 7$ nAChR. Considering the $\alpha 7$ and $\alpha 9\alpha 10$ subtypes are involved in the development of tumors, dimeric RglA# may be valuable as a molecular probe in cancer research. Surprisingly, dimeric RglA# retains its activity at the $\alpha 9\alpha 10$ nAChR when either PEG6 or PEG13 is used as the linker, suggesting that PEG6 alone is sufficiently long for an α -conotoxin dimer to simultaneously bind two adjacent binding sites (Liang et al., 2020). This study provides a general method to dramatically increase the activity of conotoxins. In addition, it has been reported that the introduction of PEG is beneficial for the stability of peptides (Lawrence & Price, 2016).

Overall, various chemical modification strategies have been established to modify α -conotoxins targeting $\alpha 9\alpha 10$ nAChR in order to obtain analogues with higher activity and stability. These strategies may also promote exploration of the mechanism of action of conotoxins on $\alpha 9\alpha 10$ nAChR and enhance the versatility of these peptides as drug leads for analgesic therapy.

4. Binding sites and interactions at the $\alpha 9\alpha 10$ nAChR

The nAChR ligand binding site is located in the extracellular domain, contributed by the interface of adjacent subunits (Fig. 4A,B). Each binding site is composed of a principal (+) component formed by three highly conserved loops (loops A–C) from one subunit, and a complementary (–) component consisting of a β -sheet (loops D and E) and loop F from an adjacent subunit (Brejc et al., 2001; Dellisanti, Yao, Stroud, Wang, & Chen, 2007; Unwin, 2005). Owing to the lack of a crystal structure of the $\alpha 9\alpha 10$ nAChR pentameric extracellular domain, the stoichiometry and binding site of this receptor can only be explored by means of electrophysiology experiments and computational methods.

Due to their relatively simple, well-defined structure and similar pharmacological properties, Vc1.1 and RglA are often used to explore the binding pockets of $\alpha 9\alpha 10$ nAChR. Previous studies showed that RglA is a competitive antagonist and binds at the ACh-binding site, that is, the orthosteric site (Ellison et al., 2008; Kryukova et al., 2018). Using computational techniques, Perez, Cassels, and Zapata-Torres (2009) postulated that RglA binds to the human $\alpha 9(+)\alpha 10(-)$ interface, with residues Pro197 and Asp198 of the $\alpha 9$ subunit (+) component and Glu58 and Asp114 of the $\alpha 10$ subunit (–) component contributing to the interaction (Perez et al., 2009). However, this conclusion was challenged by an experimental study aimed at explaining the differential sensitivity to RglA by rat and human $\alpha 9\alpha 10$ nAChRs. It was proposed that RglA species differences could be attributed to the Thr residue at position 56 of the $\alpha 9$ subunit (–) component, therefore suggesting the $\alpha 10(+)\alpha 9(-)$ interface is more likely to be the binding

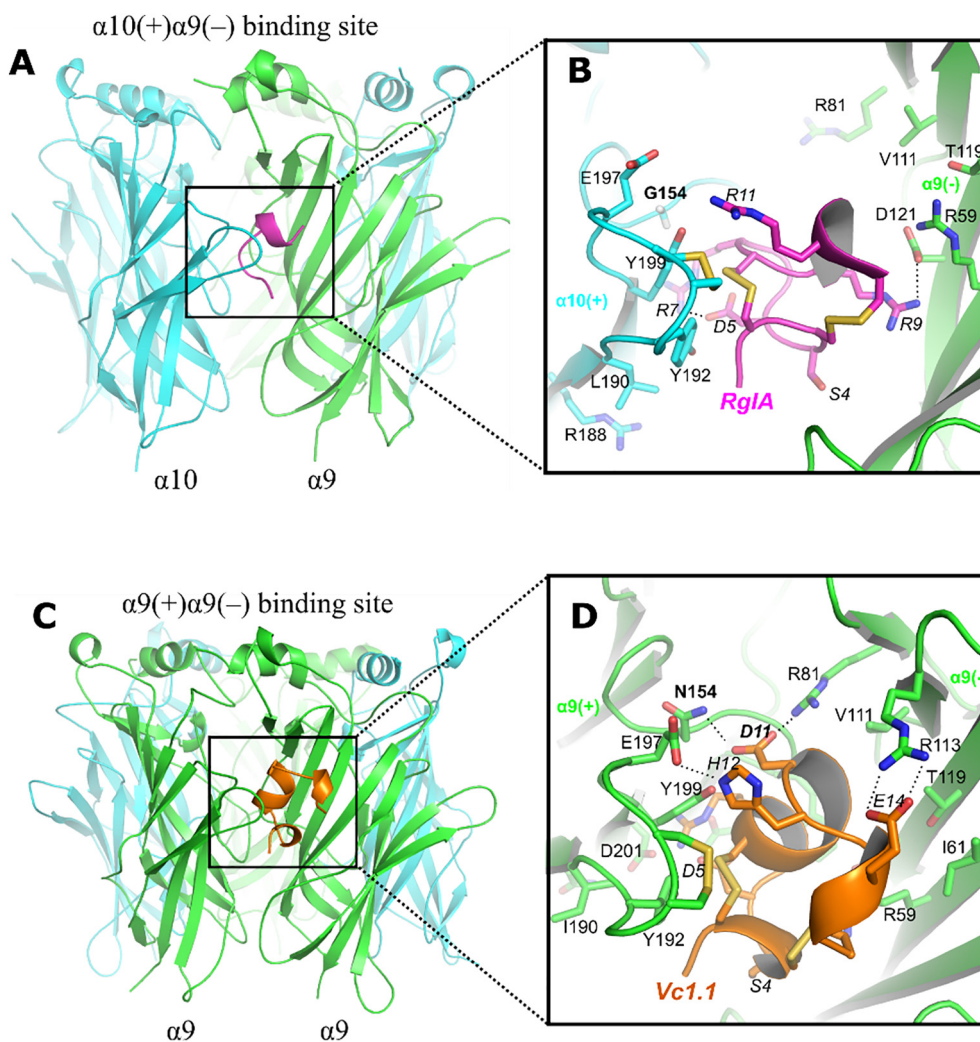


Fig. 4. Binding modes of α -conotoxins to the human $\alpha 9\alpha 10$ nAChR. (A) Binding of RglIA at the human $\alpha 10(+)\alpha 9(-)$ interface. (B) Expanded view of the interactions between RglIA and residues of the $\alpha 10(+)\alpha 9(-)$ binding site. (C) Binding of Vc1.1 at the human $\alpha 9(+)\alpha 9(-)$ interface. (D) Expanded view of the interactions between Vc1.1 and residues of the $\alpha 9(+)\alpha 9(-)$ binding site. Dashed lines indicate hydrogen bonds between the α -conotoxins and $\alpha 9\alpha 10$ nAChR residues. Residues from the RglIA and Vc1.1 are italicized. Modified and adapted with permission from Yu et al. (2018).

site of RglIA (Azam & McIntosh, 2012). A subsequent study demonstrated none of the residues predicted by Perez et al. (2009) are crucial for RglIA binding at the rat $\alpha 9(+)\alpha 10(-)$ site. However, mutations of homologous residues in opposing subunits resulted in a 19- to 1700-fold loss of RglIA potency (Azam et al., 2015). They also modeled the complexes of the rat $\alpha 9\alpha 10$ extracellular domain with RglIA and ACh using the crystal structure of the human $\alpha 9$ nAChR ECD (Zouridakis et al., 2014) and both experimental and computational methods provided additional support for the binding of RglIA at the $\alpha 10(+)\alpha 9(-)$ interface (Fig. 4C).

Using a combination of computational modeling and electrophysiology experiments, Yu et al. (2013) proposed the $\alpha 10(+)\alpha 9(-)$ interface as the binding site for Vc1.1 and that the Thr residue at position 59 of the $(-)$ site confers Vc1.1 preferential selectivity for rat over human $\alpha 9\alpha 10$ nAChRs.

Heteromeric nAChRs can assemble in two possible stoichiometries ($2\alpha, 3\alpha/\beta$ or $3\alpha, 2\alpha/\beta$) and stoichiometric variants of the $\alpha 4\beta 2$ subtype have been reported in the central nervous system (DeDominicis et al., 2017). Studies of $\alpha 4\beta 2$ nAChRs in native cells and heterologous systems suggest both stoichiometries have distinct functional and pharmacological properties (Carbone, Moroni, Groot-Kormelink, & Bermudez, 2009; DeDominicis et al., 2017; Mazzaferro et al., 2011). Initially for the

$\alpha 9\alpha 10$ nAChR, Plazas, Katz, Gómez-Casati, Bouzat, and Elgoyhen (2005) concluded that nAChRs expressed in *Xenopus* oocytes formed a stoichiometry consisting of two $\alpha 9$ and three $\alpha 10$ subunits ($(\alpha 9)_2(\alpha 10)_3$) (Plazas et al., 2005). However, using Vc1.1 to probe the function of $\alpha 9\alpha 10$ nAChRs assembled from biased $\alpha 9$ to $\alpha 10$ subunit ratios, Indurthi et al. (2014) proposed that heterologous rat receptors exist as a mixed population of $(\alpha 9)_2(\alpha 10)_3$ and $(\alpha 9)_3(\alpha 10)_2$ nAChRs (Fig. 4A, B). The biphasic concentration-response of Vc1.1 suggests the presence of a high-sensitivity $\alpha 9(+)\alpha 9(-)$ binding site in addition to low sensitivity $\alpha 10(+)\alpha 9(-)$ and/or $\alpha 9(+)\alpha 10(-)$ binding sites, which are present in both stoichiometries (Indurthi et al., 2014). Additionally, the authors inferred that Vc1.1 but not RglIA could act at the $\alpha 9(+)\alpha 9(-)$ interface.

Yu et al. (2018) explored the molecular determinants conferring binding preference of Vc1.1 at the human $\alpha 9\alpha 10$ nAChR. They demonstrated that the hydrogen bond between Asp11 of Vc1.1 and Asn154 in the $\alpha 9$ subunit $(+)$ component confers the stoichiometric-dependent activity of Vc1.1. By contrast, the corresponding Gly154 in the $\alpha 10(+)$ subunit is incapable of forming such interactions with Vc1.1. In addition, this work also demonstrated that the $\alpha 9(+)\alpha 9(-)$ interface is a high-affinity binding site for Vc1.1 (Yu et al., 2018) (Fig. 4D). Following this study, Chu et al. (2019) revealed in-depth details of Vc1.1 and $\alpha 9$

(+)α9(-) interactions. The Ser4 residue of Vc1.1 forms hydrogen bonds with two aspartic acid residues of the α9 subunit (Asp166 and Asp169), and the Vc1.1 Tyr10 residue forms hydrogen bonds with Asn107 and Asp119 in the binding pocket.

The binding site of GeXIVA has not as yet been identified, but competitive binding studies between GeXIVA and RgIA excluded the possibility of the α10(+)α9(-) site as a binding site of GeXIVA (Luo et al., 2015). Further study has indicated that the GeXIVA should act directly on the orthosteric site rather than the allosteric site or channel pore of the α9α10 nAChR (Kryukova et al., 2018). In a subsequent study, Xu et al. (2020) built computational models of disulfide-deficient analogues of GeXIVA for each probable orthosteric binding site, and all of the molecular models suggested a rational explanation for the limited effects of the two disulfide bonds on the affinity of GeXIVA. However, there were minor differences in the binding mode of the GeXIVA α-helix between the binding sites: for instance, the helix was tipped outward at the α9(+)α10(-) binding site, whereas at the α10(+)α10(-) binding site, Pro12 did not participate in the helix formation upon binding (Xu et al., 2020). Further investigations are required to clarify the exact binding site(s) for GeXIVA.

The high potency of GeXXVIIA for the human α9α10 nAChR and its unique structure also encouraged researchers to explore its mechanism of action (Jiang et al., 2017). Jiang et al. (2017) ruled out the possibility that the linear analogue of GeXXVIIA (GeXXVIIA-L) is a competitive antagonist or a channel pore blocker of the human α9α10 nAChR. Most likely, GeXXVIIA-L is a novel class of nAChR allosteric inhibitor and investigation of the mechanism of action may lead to the development of novel α9α10 nAChR-targeting drugs (Jiang et al., 2017).

A study by Boffi et al. (2017) explored the contribution of different subunit interfaces of α9α10 nAChRs. Mutations of Tyr190 and the disulfide bond in loop C comparably affected the function of both subunits, indicating that α9 and α10 subunits equally contribute to the (+) components of the α9α10 nAChR. However, the introduction of a W55T mutation in loop D impaired binding and function of the rat α9 subunit but not the α10 subunit, suggesting that the contribution of α9 and α10 subunits to the (-) components is non-equivalent (Boffi et al., 2017). Molecular dynamics simulation of RgIA binding to the α9α10 nAChR drew the same conclusion. Zouridakis et al. (2019) determined the crystal structure of the extracellular domain of monomeric α9 nAChR in complex with RgIA and further analyzed the binding modes of RgIA at α9(+)α9(-), α9(+)α10(-), and α10(+)α9(-) binding sites. The study supports favorable binding of RgIA at α9(+)/α9(-) or α10(+)/α9(-) sites rather than the α9(+)/α10(-) interface, in accordance with mutational data (Zouridakis et al., 2019). The results of these two studies may be helpful in designing improved α-conotoxin analogues targeting the α9α10 nAChR.

Although research on the interactions of Vc1.1 and RgIA at the α9α10 nAChR has made substantial progress, there is a burgeoning need to employ biophysical methods such as X-ray crystallography or cryo-electron microscopy to study them at an atomic level. Until then, computational techniques continue to play a dominant role in deciphering the mechanism of action of conotoxins at nAChRs.

5. Therapeutic potential of conotoxins targeting the α9α10 nAChR

5.1. Pain relief

Damage to the somatosensory nervous system may result in the induction of neuropathic pain (Bordet & Pruss, 2009), a complex and debilitating syndrome that affects millions of people worldwide. Conventional opioid analgesics lack analgesic potency for neuropathic pain, and opioid usage is restricted by tolerance, addiction, and unintentional overdose (Khademi, Kamangar, Brennan, & Malekzadeh, 2016). Thus, α-conotoxins Vc1.1, RgIA, and GeXIVA warrant attention not only because of their simple structures and capacity to alleviate

neuropathic pain in animal models, but, of particular interest, for their ability to produce enduring analgesia and accelerate the recovery of damaged nerves through immune-mediated mechanisms (Hone et al., 2017; Mohammadi & Christie, 2015).

Partial sciatic nerve ligation (PNL) and CCI models are typically used to evaluate the effectiveness of α-conotoxins in alleviating neuropathic pain (Bennett & Xie, 1988; McIntosh et al., 2009; Seltzer, Dubner, & Shir, 1990; Vincler & McIntosh, 2007). Subcutaneous administration of Vc1.1 in doses of 24, 80, 160, 240 or 800 μg/kg in rats with CCI dose-dependently alleviated mechanical allodynia by 54–80%, with a peak analgesic effect of 1 h, and the highest concentrations produced an extended effect lasting up to 24 h after administration (McIntosh et al., 2009; Vincler & McIntosh, 2007). In another experiment, Vc1.1 was administered daily for 7 days by intramuscular injection near the site of injury at doses of 0.036 μg, 0.36 μg and 3.6 μg to rats with CCI and at a dose of 0.36 μg in rats with PNL (Livett et al., 2009; Satkunathan et al., 2005). Vc1.1 significantly reversed mechanical hyperalgesia in both CCI and PNL rats at 1 h, 3 h and 24 h post-administration, and research on long-term effects showed that Vc1.1 attenuated mechanical hyperalgesia for up to a week following cessation of treatment, without tolerance (McIntosh et al., 2009; Satkunathan et al., 2005). More interestingly, administration of 0.36 μg and 3.6 μg Vc1.1 to the contralateral hind leg also reversed mechanical hyperalgesia, indicating that Vc1.1 is stable during systemic circulation (Satkunathan et al., 2005).

Vc1.1 has also been tested in a model of diabetic neuropathy induced by streptozotocin (Khan, Chen, & Pan, 2002). Subcutaneous administration of Vc1.1 at doses of 300 μg/kg significantly reduced mechanical allodynia for a prolonged period of at least 6 h but an acute analgesic effect was not observed on mechanical hyperalgesia at the same dose in this model. In addition, Vc1.1 was also shown to be an effective analgesic against pain resulting from an inflammatory injury. A dose of 2.4 mg/kg Vc1.1 significantly alleviated mechanical hyperalgesia induced by an intraplantar injection of complete Freund's adjuvant, with a peak analgesic effect at 1–1.5 h. Intramuscular injection of RgIA (2 and 10 nmol) to CCI rats also resulted in significant reduction of mechanical hyperalgesia, and repeated injection of RgIA reduced the development of pain even at 24 h after the last injection (Di Cesare Mannelli et al., 2014). A recently characterized αO-conotoxin, GeXIVA, also exhibited extremely strong activity in the CCI model. GeXIVA[1,2] or GeXIVA [1,4] at doses of 0.5 nmol, 1 nmol and 2 nmol per rat, was injected intramuscularly for one or two weeks. GeXIVA[1,2] at all doses dramatically reversed allodynia and persisted for up to 6 h after a single administration, whereas GeXIVA[1,4] only showed an analgesic effect at doses of 1 nmol and 2 nmol. Notably, both GeXIVA[1,2] and GeXIVA[1,4] at doses of 1 nmol produced an effect comparable to 500 nmol morphine but no addiction or motor side effects were observed during treatment. Analogous to Vc1.1, the short term effect of GeXIVA[1,2] and GeXIVA [1,4] was sustained for 24 h after injection, and the pain relief effect persisted for two weeks after the last injection (Li et al., 2016).

The analgesic effects of these α9α10 nAChR antagonists lasted for up to 24 h post-administration, which is longer than their half-life in serum. Moreover, when α-conotoxins were administered daily, analgesic effects remained for several days after the cessation of treatment and changes in the underlying disease pathology of nerve injury and repair were observed (Di Cesare Mannelli et al., 2014; Satkunathan et al., 2005). However, such extended and cumulative anti-nociceptive effects are inconsistent with the rapid off-rate kinetics for these conotoxins (Ellison et al., 2006; Luo et al., 2015), and thus some researchers have attributed the cumulative analgesic and restorative effects of these α9α10 nAChR antagonists to immunological effects, and histological analysis supported such a notion.

Rats subjected to CCI exhibit a number of morphological changes in the injured nerve including edema, axon demyelination, axon degeneration, and increased infiltration of immune cells into the site of injury (Basbaum, Gautron, Jazat, Mayes, & Guilbaud, 1991; Sommer, Lalonde,

Heckman, Rodriguez, & Myers, 1995). In addition, the cell bodies of these axons in the dorsal root ganglion (DRG) show signs of damage. RgIA increased the number of nerve fibers, myelin thickness and axon diameter while reducing edema in CCI rats, and prevented the activation of microglia and astrocytes in the dorsal horn of the spinal cord (Di Cesare Mannelli et al., 2014). Moreover, accumulating evidence indicates that immune cells play a crucial role in the development of neuropathic pain following nerve injury and $\alpha 9\alpha 10$ nAChRs have been reported to be expressed in a variety of immune cells (Grace, Hutchinson, Maier, & Watkins, 2014; Peng et al., 2004). Both Vc1.1 and RgIA have been demonstrated to reduce the number of immune cells infiltrating into sciatic nerves, including CD86+ macrophages and CD2+ lymphocytes (Di Cesare Mannelli et al., 2014; Satkunanathan et al., 2005). The possible analgesic mechanism of GeXIVA has also been considered to involve inhibiting infiltration of immune cells into injured nerves, although more definitive evidence is needed (Li et al., 2016). These observations highlight that antagonism of $\alpha 9\alpha 10$ nAChRs expressed in immune cells is a potential mechanism that accounts, in part, for the analgesic and anti-inflammatory properties of these $\alpha 9\alpha 10$ nAChR antagonists.

Although conotoxins targeting the $\alpha 9\alpha 10$ nAChR can exert certain analgesic and anti-inflammatory effects through immunomodulatory mechanisms, the precise analgesic target is still controversial. Nevin et al. (2007) showed that Vc1.1 analogues (vc1a and [P60] Vc1.1), which retained their potency at $\alpha 9\alpha 10$ nAChRs, produced no analgesia in PNL rats. Additionally, it was reported that $\alpha 9$ KO mice display a similar pain phenotype to wild-type mice and differences were detected only for chronic mechanical hyperalgesia (Mohammadi & Christie, 2014). These studies suggest that inhibition of $\alpha 9\alpha 10$ nAChR is insufficient for the analgesic activity of Vc1.1.

On this basis, conotoxin inhibition of the high voltage-activated calcium channels through activation of G protein-coupled GABA_B receptors has been proposed as the possible analgesic mechanism (Benke, 2020; Callaghan et al., 2008; Klimis et al., 2011; Sadeghi et al., 2017). The GABA_{B1} subunit is required for GABA_B receptor function and the GABA_{B1}-KO model was generated in order to elucidate the role that GABA_B receptors play in pain modulation (Goudet et al., 2009). GABA_{B1} KO mice exhibited hyperalgesia in several behavioral tests, including the hot plate, tail flick, and paw pressure tests (Schuler et al., 2001); however, there was no difference in neuropathic and chronic inflammatory pain between conditional mouse mutants lacking a functional GABA_{B(1)} subunit specifically in nociceptors (SNS-GABA_{B1}^{-/-} mice) and wild-type littermates in a spared nerve injury model or with intraplantar formalin injection (Gangadharan et al., 2009). Furthermore, in both radioligand binding and functional experiments, Vc1.1 and RgIA failed to interact with human GABA_B receptors expressed in *Xenopus* oocytes (McIntosh et al., 2009). In addition, use of the typical GABA_B agonist baclofen leads to tolerance to the anti-nociceptive effects and the analgesic effects appear to be centrally mediated (Enna & Bowery, 2004; Goudet et al., 2009; Kent, Park, & Lindsley, 2020), whereas the action of these analgesic peptides is almost entirely peripherally mediated and more importantly, without tolerance.

In summary, the α -conotoxins Vc1.1, RgIA and GeXIVA represent novel peptide compounds with unique pharmacological actions and analgesic effects. These $\alpha 9\alpha 10$ antagonists not only produce analgesia, but also accelerate the functional recovery of damaged nerves through immunological modulation, which makes them candidates for the treatment of neuropathic pain.

5.2. Treatment of inflammatory disorders

The $\alpha 9\alpha 10$ nAChR-selective α -conotoxin antagonists were shown to have analgesic effects in animal models of neuropathic and inflammatory pain, but knowledge of the role of $\alpha 9\alpha 10$ nAChRs in experimental colitis is limited. A recent study reported the role of $\alpha 9\alpha 10$ nAChRs in the dextran sodium sulfate (DSS) experimental animal colitis model (AlSharari, Toma, Mahmood, McIntosh, & Damaj, 2020). Compared to

the DSS-control group, a dose of RgIA of 0.2 nmol/mouse significantly reversed the disease activity index score, loss of body weight, and total histological damage score, as well as the colonic level of TNF- α . Moreover, RgIA dramatically rescued the shortening of colon length. These findings suggest a novel therapeutic application for RgIA and other $\alpha 9\alpha 10$ nAChR antagonists in the treatment of possibly other inflammatory disorders.

5.3. Antitumor activity

The nAChRs have attracted increased attention due to their major role in tumorigenesis and cancer progression (Dang et al., 2016). Breast cancer is the highest-incidence cancer among women worldwide (Bray et al., 2018), and the expression of $\alpha 9$ nAChR is closely correlated with the development of breast cancer (Lee et al., 2010). The $\alpha 9$ nAChR subunit is upregulated in various breast cancer cell lines compared with the normal epithelial cell line (Zhangsun, et al., 2020), and stimulation of the $\alpha 9$ nAChR led to cancer cell proliferation, angiogenesis and tumor metastasis (Ho, Lee, & Wu, 2011). Previous studies indicated that garcinol and green tea polyphenol(-)-epigallocatechin-3-gallate can inhibit nicotine-induced breast cancer cell proliferation through the downregulation of the $\alpha 9$ nAChR, further delaying the development of breast cancer cells *in vivo* (Chen et al., 2011; Tu et al., 2011). Luteolin and quercetin have also been shown to suppress tumor growth by downregulating the $\alpha 9$ nAChR subunit expressed on the human breast cancer cell surface (Shih et al., 2010). These results suggest that the regulation of $\alpha 9$ -containing nAChR expression plays an important role in the process of breast cancer development, and that inhibition of $\alpha 9$ -containing nAChRs could be a potential therapeutic strategy for cancer treatment.

The $\alpha 0$ -conotoxin GeXIVA has been used to investigate the effects of inhibiting $\alpha 9\alpha 10$ nAChR on different human breast cancer cell lines due to its high potency and selectivity for the receptor (Sun, Bao, et al., 2020). Recently, Sun, Zhangsun, et al. (2020) confirmed that the $\alpha 9$ nAChR subunit is overexpressed in different breast cancer cell lines and that GeXIVA concentration-dependently inhibited the growth of cancer cells, with IC₅₀ values ranging from 35 to 130 μ M (Sun, Bao, et al., 2020). GeXIVA was most effective on the MDA-MB-157 cell line (Sun, Bao, et al., 2020, Sun, Zhangsun, et al. (2020)), significantly suppressing the proliferation and migration of cells by downregulating the $\alpha 9$ -nAChR subunit. Moreover, flow cytometry analysis showed that GeXIVA promoted apoptosis of breast cancer cells (Sun, Bao, et al., 2020). Importantly, this study also showed growth inhibition of $\alpha 9$ -nAChR KO MDA-MB-157 cells, thus confirming the involvement of the $\alpha 9$ subunit in cancer cell proliferation (Sun, Bao, et al., 2020).

In addition to breast cancer cells, the effects of GeXIVA were also determined on SiHa and CaSki cervical cancer cell lines, in which the expression of both $\alpha 9$ and $\alpha 10$ subunits are upregulated. GeXIVA markedly inhibited the proliferation of SiHa and CaSki cell lines, while it was only mildly cytotoxic for normal cells (Liu et al., 2019). Given that targeted treatment of cervical cancer is still in the early stages of research, inhibition of $\alpha 9\alpha 10$ nAChR may be useful for cervical cancer-targeted therapy.

In addition, $\alpha 9\alpha 10$ nAChRs have also been shown to mediate nicotine-induced proliferation of A549 adenocarcinoma lung tumors cells and this effect can be inhibited using RgIA4 (Mucchiello et al., 2018). These results highlight the pathophysiological role of $\alpha 9\alpha 10$ nAChR in promoting non-small cell lung carcinoma cell growth and provides strong evidence for an antitumor effect of RgIA4.

The nAChRs are strongly implicated in the development of certain cancers, but there are currently few studies on the antitumor effects of conotoxins targeting the $\alpha 9\alpha 10$ nAChR (Ho et al., 2011; Lee et al., 2010; Mucchiello et al., 2018; Sun, Bao, et al., 2020, Sun, Zhangsun, et al. (2020)). In the treatment of breast, cervical and lung cancer, both the $\alpha 9\alpha 10$ nAChR and conotoxins that specifically target it present

an opportunity for further development and subsequent potential translation to the clinic.

6. Outlook

The $\alpha 9\alpha 10$ nAChR has attracted attention as a therapeutic target due to its involvement in key physiological and pathological conditions including hearing, inflammatory disorders, neuropathic pain, and cancer. However, the precise role of the $\alpha 9\alpha 10$ nAChR in some of these conditions remains to be explored. Moreover, structural determination of the intact $\alpha 9\alpha 10$ nAChR is long overdue and will assist in the development of therapeutics. Conotoxin antagonists of the $\alpha 9\alpha 10$ subtype represent a new class of therapeutics with high potency and selectivity, thus minimizing off-target effects, which is also possible due to the mainly peripheral distribution of the receptor. These peptides are effective analgesics in animal pain models and have anti-proliferative effects on cancer cells, warranting further development for future potential clinical translation.

Declaration of Competing Interest

The authors declare that there are no conflicts of interest.

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