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## Animal Toxins Influence Voltage-Gated Sodium Channel Function

**John Gilchrist,**

Department of Physiology, Johns Hopkins University, School of Medicine, Baltimore, MD 21205, USA

**Baldomero M. Olivera,** and

Department of Biology, University of Utah, Salt Lake City, UT 84112, USA

**Frank Bosmans**

Department of Physiology, Johns Hopkins University, School of Medicine, Baltimore, MD 21205, USA

Department of Neuroscience, Solomon H. Snyder, Johns Hopkins University, School of Medicine, Baltimore, MD 21205, USA

### Abstract

Voltage-gated sodium (Nav) channels are essential contributors to neuronal excitability, making them the most commonly targeted ion channel family by toxins found in animal venoms. These molecules can be used to probe the functional aspects of Nav channels on a molecular level and to explore their physiological role in normal and diseased tissues. This chapter summarizes our existing knowledge of the mechanisms by which animal toxins influence Nav channels as well as their potential application in designing therapeutic drugs.

### Keywords

Sodium channel; Animal toxin; Pore-blocker; Gating-modifier; Venom

## 1 Introduction

Voltage-gated sodium (Nav) channels regulate the Na<sup>+</sup> permeability of the cell membrane, thereby generating electrical signals that encode and propagate vital information across long distances (Catterall 2000; Hille 2001; Hodgkin and Huxley 1952; Ashcroft 1999).

Venomous animals and poisonous plants readily exploit this excitatory role by producing toxins that modify Nav channel opening or closing (e.g., gating) with the goal of incapacitating prey or as defense against predators (Bosmans and Swartz 2010; Catterall et al. 2007; Billen et al. 2008; Smith and Blumenthal 2007; Mebs 2002; Escoubas et al. 2002; de la Vega et al. 2005). Historically, toxins from spider, scorpion, sea anemone, cone snail, insect venoms, and plant extracts have been used to describe diverse receptor sites in

particular regions of the nine Nav channel isoforms that have been identified in various mammalian tissues (Nav1.1–Nav1.9) (Catterall 1980; Martin-Eauclaire and Couraud 1992; Catterall et al. 2005; Terlau and Olivera 2004; Honma and Shiomi 2006; Hanck and Sheets 2007). Based on their primary amino acid sequence, all Nav channel isoforms seem to be similarly configured and consist of four domains (I–IV) that each contains a voltage sensor and a portion of the structure that forms the Na<sup>+</sup>-selective pore which can open upon activation of the four voltage sensors in response to changes in membrane potential (Catterall 2000; Bosmans et al. 2008; Cha et al. 1999; Chanda and Bezanilla 2002; Horn et al. 2000; Sheets et al. 1999, 2000). The voltage sensors in domains I–III are essential for channel opening, whereas domain IV movement is crucial for terminating the Na<sup>+</sup> flux after the channel has opened by initiating fast inactivation (Billen et al. 2008; Cha et al. 1999; Chanda and Bezanilla 2002; Horn et al. 2000; Sheets et al. 1999, 2000; Campos et al. 2008; Capes et al. 2012). Similar to voltage-activated potassium (Kv) channels (Bosmans et al. 2008; Alabi et al. 2007; Jiang et al. 2003; Long et al. 2007; Phillips et al. 2005; Ruta and MacKinnon 2004; Swartz 2007; Swartz and MacKinnon 1997a, b; Xu et al. 2013), each Nav channel voltage sensor possesses a conserved S3b-S4 motif, or paddle motif, which drives activation of the voltage sensor in each domain and opening of the pore (Billen et al. 2008; Bosmans et al. 2011; Xiao et al. 2008; Campos et al. 2007, 2008). As is the case with Kv channels, each of the four Nav channel paddle motifs is a key pharmacological target for a range of animal toxins (Bosmans and Swartz 2010; Bosmans et al. 2008, 2011; Xiao et al. 2008; Rogers et al. 1996).

Overall, toxins that influence Nav channel function do so through two distinct mechanisms. Pore-blocking toxins inhibit the flow of Na<sup>+</sup> by binding to the outer vestibule or inside the ion conduction pore (Hille 2001; Terlau and Olivera 2004) whereas gating-modifier toxins interact with a region of the channel that changes conformation during channel opening to alter the gating mechanism (Cahalan 1975; Koppenhofer and Schmidt 1968a, b). Although certain gating-modifier toxins interact with the voltage-sensing domains as well as the pore region (Quandt and Narahashi 1982), their subsequent effect on Nav channel gating can usually be associated with their ability to stabilize a voltage sensor in a particular state. As such, in the next sections we will refer to the interaction site of animal toxins within mammalian Nav channels as either the voltage-sensing domains or the pore region and we will further refine this division using the primary functional effects of toxins on channel gating.

## 2 Toxins Influencing Nav Channel Function by Interacting with the Pore Region

### 2.1 Non-Peptidic Toxins

**2.1.1 Tetrodotoxin and Saxitoxin**—The naturally occurring marine toxins tetrodotoxin (TTX) and saxitoxin (STX) interact strongly with the Nav channel pore region to occlude the Na<sup>+</sup> permeation pathway (Fig. 1) (Hille 1975). Both toxins are of great historical and medical value and were originally isolated more than five decades ago from the Japanese Puffer fish (TTX) and marine dinoflagellates (STX) (Furukawa et al. 1959; Moore et al. 1967; Narahashi 1974; Narahashi et al. 1964). STX is perhaps most notorious for its role in

paralytic shellfish poisoning, caused by the consumption of toxic shellfish such as clams and mussels. TTX and STX have been used extensively in studying the structural and functional properties of Nav channels. Early work by Narahashi and others revealed that TTX affects neuronal Na<sup>+</sup> currents only when applied to the extracellular surface of the cell and not when perfused inside axons (Narahashi et al. 1964, 1967). After resolving the crystal structure of TTX in 1964 (Woodward 1964) and STX in 1975 (Schantz et al. 1975), this information was used by Hille to predict the diameter of the Nav channel pore (Hille 1975), thereby providing unique insights into the molecular structure of this ion channel family that resonate until this day (Payandeh et al. 2011, 2012; Zhang et al. 2012; McCusker et al. 2012). Later, the low-nanomolar affinity of [<sup>3</sup>H]TTX contributed to the isolation of the Nav channel pore-forming subunit from the electroplaque organ of the electric eel, *Electrophorus electricus* (Miller et al. 1983; Agnew et al. 1978). Similarly, [<sup>3</sup>H]STX played a vital role in the purification of the neuronal Nav channel from rat brain (Hartshorne and Catterall 1981) and skeletal muscle (Barchi et al. 1980), thereby also revealing the existence of two associated auxiliary subunits (Hartshorne et al. 1982). Nowadays, TTX sensitivity is extensively used to divide the Nav channel family into two groups; TTX-sensitive channels (Nav1.1–Nav1.4, Nav1.6–Nav1.7) are inhibited by nanomolar amounts (Fig. 1), whereas Nav1.8 and Nav1.9 require millimolar quantities to be fully blocked (Catterall 2000). Although Nav1.5 inhibition requires an intermediate micromolar concentration, TTX response can be markedly increased by substituting a cysteine in the domain I S5–S6 loop with a hydrophobic or aromatic residue such as a tryptophan or phenylalanine (Lipkind and Fozzard 1994; Leffler et al. 2005; Sivilotti et al. 1997). The latter amino acids support nanomolar blockade through the formation of a cation–pi interaction with TTX, possibly via an interaction with the charged guanidinium groups within the toxin (Lipkind and Fozzard 1994). These cationic groups also interact with anionic residues within the pore region of the channel to prevent Na<sup>+</sup> conductance. As such, experiments geared toward finding residues that diminished Nav channel TTX sensitivity aided in the discovery of amino acids that create the Nav channel selectivity filter (Terlau et al. 1991), namely an aspartate (DI S5–S6 loop), glutamate (DII S5–S6 loop), lysine (DIII S5–S6 loop), and alanine (DIV S5–S6 loop) (Lipkind and Fozzard 2008). Even though this region of the selectivity filter plays a role in STX interaction as well, other important extracellular residues have now been implicated in forming the STX receptor site (Fozzard and Lipkind 2010), most likely due to supplementary interactions with the additional guanidinium group present within the toxin.

Despite its potential toxicity, clinical trials in which TTX was used to treat various pain disorders have been conducted (Nieto et al. 2012). However, the results are ambiguous and further research is essential. Of note is the peculiar protein saxiphilin, a transferrin-like molecule that binds STX with nanomolar affinity (Morabito and Moczydlowski 1994). Saxiphilin is found across a variety of aquatic and terrestrial species, including fish, reptiles, amphibians, and even arthropods. Notwithstanding its ancient character and global distribution, the physiological role of saxiphilin is not fully understood. A possible contribution to neutralizing dietary or environmental STX seems most obvious, but many animals expressing saxiphilin do not occupy biomes in which they will encounter STX (Llewellyn et al. 1997). Regardless, saxiphilin may still find use as an alternative to animal testing or be incorporated into more efficient STX assays (Llewellyn et al. 1998).

**2.1.2 Ciguatoxin and Brevetoxin**—Aside from TTX and STX, the cyclic polyether ciguatoxins (Michio et al. 1989) and brevetoxins (Yong-Yeng et al. 1981) found in algae can also cause seafood poisoning. Produced by the dinoflagellates *Gambierdiscus toxicus* (Bagnis et al. 1980) and *Karenia brevis* (Yong-Yeng et al. 1981), respectively, these molecules can accumulate in the food chain in fish that are consumed by humans or marine mammals in which they disrupt Nav channel function (Lewis et al. 1991). Although ciguatoxins research has been hindered by the small quantities available from marine fauna (Legrand et al. 1989), this hurdle was recently overcome by Hirama et al. (2001) when they synthesized CTX3C, thereby permitting easier access to large quantities of purified toxin. Initial forays into algaetoxin pharmacology indicated that ciguatoxin (Bidard et al. 1984) as well as brevetoxin (Lombet et al. 1987), albeit with a much lower affinity (Lombet et al. 1987), can potentiate opening of multiple Nav channel isoforms in addition to altering their Na<sup>+</sup> permeability. As a result, both molecules are capable of inducing spontaneous firing in neurons which eventually leads to paralysis (Benoit et al. 1986). Interestingly, the Nav1.8 isoform found in the periphery seems particularly susceptible to CTX3C, resulting in the appearance of a large persistent current upon toxin exposure, an observation that may in part explain some of the neurological sequelae seen in ciguatera victims (Yamaoka et al. 2009). Although the exact working mechanism is unclear, photolabeling experiments on Nav channels indicate that the S6 segment within domain I and the S5 segment of domain IV are involved in brevetoxin binding (Trainer et al. 1994). Moreover, a study utilizing chimeric Nav1.4 and Nav1.8 channels in combination with CTX3C suggest an interaction site of this toxin within domains I and II (Yamaoka et al. 2009). Finally, it has been suggested that these ladder-like polyether toxins may partition in the membrane to complement a structural motif within the Nav channel (e.g.,  $\alpha$ -helix) by means of a hydrogen bond network, which may lead to their biological activity (Ujihara et al. 2008).

**2.1.3 Batrachotoxin**—Well known in popular culture is the image of the jungle cannibal dispatching his prey with poison-tipped darts launched from a blowgun. The poison used here is often found in the secretions of “poison dart frogs” (family *Dendrobatidae*) endemic to Central and South America. While all members of the *Dendrobatidae* secrete toxins, only the *Phyllobates* genus is known to produce batrachotoxin (BTX), a potent Nav channel toxin with an unusual steroidal alkaloid structure (Fig. 2) (Tokuyama et al. 1969). Frogs reared in captivity are not toxic, leading to the conclusion that they acquire and concentrate the toxin from their environment. Similarly, select species of birds from New Guinea (*Ifrita kowaldi* and members of the *Pitohui* genus) are found to secrete BTX onto their skin and feathers (Dumbacher et al. 2000). Dumbacher and coworkers propose that Melyrid beetles may be the dietary source of BTX for both poison-dart frogs and *Pitohui* birds; *Choresine* beetles are known to be rich sources of BTX alkaloids and related species are found in the New World (Dumbacher et al. 2004).

Although the exact working mechanism has yet to be elucidated, the Nav channel receptor site for BTX has been shown to involve a cluster of residues located in the S6 pore-segments of domains I (Wang and Wang 1998), III (Wang et al. 2000; Du et al. 2011), and IV (Linford et al. 1998) and may partially overlap with the binding site of local anesthetics (Wang et al. 1998). Unlike lidocaine, which blocks Na<sup>+</sup> currents, BTX may partially occlude the ion

permeation pathway, thereby leaving room for a fraction of Na<sup>+</sup> to pass through the pore. Although BTX may bind within the pore region, the toxin also (1) abolishes fast and slow inactivation (Huang et al. 1982) (Fig. 2) and (2) shifts Nav channel opening to voltages where it is normally closed (Quandt and Narahashi 1982; Bosmans et al. 2004), thereby leading to repeated depolarizations in vivo and eventual paralysis as muscles become insensitive to neuronal signals (Wang and Wang 1998; Linford et al. 1998; Bosmans et al. 2004; Wasserstrom et al. 1993; Catterall 1975).

Even though BTX is unsuitable for drug design, radioactive BTX has been used extensively for Nav channel identification in tissues and vesicles and in screening potential therapeutics (Cooper et al. 1987; Gill et al. 2003). A functional relative of BTX is veratridine, an alkaloid toxin found in *Liliaceae* plants, which causes persistent opening of Nav channels while reducing single-channel conductance (Ulbricht 1998). Although veratridine is thought to interact with the pore-forming S6 segments in open Nav channels, the exact mechanism by which the toxin causes persistent Nav channel opening remains uncertain. Nevertheless, due to its ability to open Nav channels, veratridine is used extensively in drug screening essays for which controlling the membrane voltage is impractical (Felix et al. 2004).

## 2.2 Peptidic Toxins

**2.2.1 Cone Snail Toxins**—The pore-blocking  $\mu$ -conotoxin peptides found in cone snail venom are among the best-characterized Nav channel antagonists. Identifying cone snail venoms likely to contain novel Nav channel pore-blocking peptide toxins was made possible by using the molecular phylogeny framework established for the 700 species of cone snails (Fig. 3). The biological rationale for the presence of these toxins in the venom of a specific subset of *Conus* species is presented here.

Cone snails (Fig. 4) are venomous predatory marine gastropods that are slow moving, unable to swim, and have little in the way of mechanical weaponry for catching their prey. As such, their successful adaptive radiation throughout tropical marine environments required the evolution of venoms that provide the only effective arsenal for capturing their victims. All pore-blocking Nav channel targeting conopeptides characterized to date are found in the venom of cone snail species that specialize in hunting fish as their primary prey (approximately 100 different species of cone snails are believed to be fish-hunting) (Olivera 1997). In order to block neuromuscular transmission, cone snails evolved groups of peptides that act coordinately (called “cabals”) but each on a different molecular target. Among those are the functionally linked signal components of the neuromuscular transmission circuitry, i.e., the nicotinic receptor at the postsynaptic terminus, the presynaptic voltage-gated calcium channels that control neurotransmitter release, and Nav channels that mediate action potential transmission on the muscle membrane (Terlau and Olivera 2004). The most abundantly expressed pore-blocking toxins within cone snail venoms, the  $\mu$ -conotoxins, primarily interact with Nav1.4, a Nav channel isoform found in skeletal muscle. Nonetheless, the affinity of each peptide for other Nav channel subtypes can vary considerably. By systematically investigating  $\mu$ -conotoxins from diverse clades of fish-hunting cone snails [see (Baldomero et al. 2014) for a discussion of different lineages of fish-hunting cone snails], a series of peptides with varying neuronal Nav channel selectivity

profiles has been obtained. To summarize this work,  $\mu$ -conotoxins from *Conus* species in five lineages are shown in Table 1 (Wilson et al. 2011) which demonstrates the striking affinity differences of a range of peptides for neuronal Nav channel subtypes.

The importance of  $\mu$ -conotoxins for the Nav channel field stems from the fact that at the present time, a sufficient diversity of toxins have been characterized to assemble a pharmacological kit for distinguishing various Nav channel isoforms. This toolkit takes advantage of individual  $\mu$ -conotoxin selectivity for the various neuronal Nav channel subtypes shown in Table 1 (Wilson et al. 2011; Bulaj et al. 2005; Leipold et al. 2011; Zhang et al. 2006). For example,  $\mu$ -conotoxin SxIIIa is highly selective for Nav1.4 while having at least a 50-fold lower affinity for all other subtypes, whereas  $\mu$ -conotoxin KIIIa and CnIIIa predominantly interact with neuronal Nav channel isoforms. Structure–function studies on KIIIa analogs (Bulaj et al. 2005; McArthur et al. 2011; Van Der Haegen et al. 2011; Zhang et al. 2007, 2009, 2010) demonstrate that the binding sites of the  $\mu$ -conotoxin and TTX overlap but not coincidence. Consequently, it was shown that KIIIa interacts with additional amino acid residues within the pore vestibule (McArthur et al. 2011; Van Der Haegen et al. 2011; Zhang et al. 2007). Thus, different  $\mu$ -conotoxins presumably interact with a particular subset of residues within the pore, thereby accounting for the diverse targeting selectivity for the various neuronal Nav channel isoforms. This diversity makes it possible to list which  $\mu$ -conotoxins are most effective for discriminating between any pair of Nav channel isoforms (see Table 2). Zhang et al. (2013a) employed  $\mu$ -conotoxins to identify particular Nav channel isoforms in native neuronal cell preparations and demonstrated that a combination of three  $\mu$ -conotoxins is sufficient to determine which TTX-sensitive Nav channel isoform contributes to the Na<sup>+</sup> current in the different neuronal subclasses present in the dorsal root ganglion. As such, the standard Nav channel classification into TTX-sensitive and TTX-resistant classes can be more finely parsed into the individual subtypes, using the appropriate combination of different  $\mu$ -conotoxins. Zhang and coworkers (Zhang et al. 2013b) also found that auxiliary  $\beta$ -subunits can influence the kinetics of toxin block thereby raising the possibility of employing  $\mu$ -conotoxins to discriminate different combinations of  $\alpha$ - and  $\beta$ -subunits present in native neurons.

**2.2.2 Spider Toxins**—Although a few spider toxins have been shown to inhibit Na<sup>+</sup> flux without altering channel gating, the mechanism through which they act remains elusive. For example, the binding site of Tx1 from the *Phoneutria nigriventer* spider may overlap with that of the  $\mu$ -conotoxin GIIIa, but not that of TTX (Silva et al. 2012). However, additional experiments are needed to clarify the state-dependent binding of Tx1, an observation that suggests an interaction with one or more Nav channel voltage-sensing domains. An additional example is Hainantoxin-I from the *Selenocosmia hainana* tarantula (Li et al. 2003), a toxin that weakly inhibits mammalian Nav channel currents without affecting channel opening or fast inactivation. However, a potential competition with cone snail toxins, TTX, or an interaction with the Nav channel pore region or its voltage sensors has not yet been investigated.



## 3 Toxins Influencing Nav Channel Gating by Interacting with the Voltage Sensors

### 3.1 Sea Anemone Toxins

Sea anemones are primitive aquatic animals that possess tentacles containing cells bearing a specialized structure called the nematocyst which, when triggered, injects a mix of toxins into the target. While this venom contains a diversity of chemical components, it is primarily the peptides that have been of great interest to neuroscientists. The majority of peptide toxins that target mammalian Nav channels have been isolated from the venom of the genus *Anemonia*, *Anthopleura*, and *Heteractis* (Kem et al. 1989). Despite this seemingly limited distribution, there are untold numbers of anemone species whose toxic components have not yet been explored, leaving open the possibility of many more bioactive peptides remaining to be discovered (Honma and Shiomi 2006). Sea anemone toxins that act on mammalian Nav channels are typically basic proteins, sharing a conserved arginine at position 14 (Khera and Blumenthal 1996) and a lysine residue around position 37 (Benzinger et al. 1998). The lysine is considered to be crucial for mammalian toxicity (Gallagher and Blumenthal 1994; Norton 2009; Barhanin et al. 1981) and flexibility of the loop containing this residue is important for Nav channel isoform discrimination by the toxin (Gooley et al. 1984; Seibert et al. 2003).

Due to their intimate interaction with the paddle motif in the domain IV voltage sensor (Rogers et al. 1996), sea anemone toxins can (1) inhibit Nav channel fast inactivation at nanomolar concentrations (Fig. 5) (Alsen et al. 1981; Romey et al. 1976; Catterall and Beress 1978), albeit with exceptionally slow on- and off-rates; and (2) enhance recovery from inactivation without affecting Nav channel activation, deactivation, or closed-state inactivation (Hanck and Sheets 2007; Sherif et al. 1992; Richard Benzing 1999). Although careful studies on various Nav channel isoforms with ATX-II and Ap-B (Fig. 5) reveal that sea anemone toxins exert their effect by delaying domain IV voltage sensor activation, Oliveira and colleagues observed that ATX-II is more potent on Nav1.2 when compared to Nav1.6 (Oliveira et al. 2004). Since the domain IV paddle motif in these two channel isoforms is very similar, their results suggest that ATX-II may interact with regions other than the domain IV voltage sensor. In contrast to Kv channels and acid-sensing ion channels for which sea anemone venoms have proven to be a valuable source of therapeutic leads (Chandy et al. 2004; Baron et al. 2013), a molecule with similar potential that targets Nav channels has yet to emerge.

### 3.2 Scorpion Toxins

Throughout some 400 million years of evolution, scorpions have perfected peptide toxins to specifically and potently target mammalian or insect ion channel families. As such, classic studies on scorpion venom recognized the presence of toxins capable of interfering with Nav channel voltage sensor function (Martin-Eauclaire and Couraud 1992; Cahalan 1975; Koppenhofer and Schmidt 1968a, b). In general, scorpion toxins interact with extracellular loops between S3 and S4 to stabilize the voltage sensors of Nav channels in particular states. Based on their functional effects, two classes of Nav channel scorpion toxins have been defined (Couraud et al. 1982).

First,  $\alpha$ -scorpion toxins act on Nav channels in a manner similar to sea anemone toxins and as such were found to compete for binding at the same location in the domain IV voltage sensor (Fig. 6) (Jover et al. 1978). Nonetheless, early antibody and photo-affinity-labeling studies indicated an interaction of LqTX (isolated from *Leiurus quinquestriatus* venom) with the S5–S6 loops of domains I (Tejedor and Catterall 1988) and IV (Thomsen and Catterall 1989) in rat neuronal Nav channels. Later, mutagenesis experiments revealed a strong interaction with the S3–S4 paddle motif within domain IV (Rogers et al. 1996), as well as with the domain I S5–S6 loop and domain IV S1–S2 loop (Wang et al. 2011). This secondary binding site in domain I may help to position the  $\alpha$ -scorpion toxin in such a way that the crucial hydrophobic residues within the toxin are positioned correctly for their interaction with the domain IV voltage sensor. Recently, a study by Campos et al. (2004) used Ts3 from *Tityus serrulatus* in concert with fluorescently labeled voltage-sensing domains demonstrating an inhibitory effect on voltage-sensing domain IV movement resulting in the inhibition of fast inactivation as well as speeding recovery from fast inactivation. Interestingly, Ts3 also affected the voltage-dependent gating of domain I suggesting the notion of an allosteric coupling between the adjacent domains I and IV.

A second class of Nav channel toxins present in scorpion venom are the  $\beta$ -scorpion toxins which promote subthreshold channel opening by shifting the voltage dependence of activation to more negative membrane potentials (Fig. 7). Distinct from  $\alpha$ -scorpion toxins and sea anemone toxins,  $\beta$ -scorpion toxins are thought to primarily target the paddle motif within the domain II voltage sensor and trap it in an activated state (Cestèle et al. 1998, 2006). With the voltage sensor trapped, further depolarizations require the transition of fewer voltage-sensing domains, resulting in the hyperpolarized voltage-dependent activation observed in toxin-bound channels (Fig. 7). A common practice to examine the functional effects of  $\beta$ -scorpion toxins is to apply a short depolarizing pre-pulse in order to initiate their effect on Nav channel gating (Cestèle et al. 1998; Leipold et al. 2012). Although it is conceivable that this pre-pulse facilitates an interaction with the activated domain II voltage sensor, not every  $\beta$ -scorpion toxin requires this additional depolarization. For example, TsVII from *Tityus serrulatus* (Marcotte et al. 1997) and Tz1 from the *Tityus zulianus* scorpion (Leipold et al. 2006) do not need such a pulse to influence Nav channel gating, possibly because these toxins are capable of influencing regions other than the one in domain II (Bosmans et al. 2008).

Despite the tedious nature of purifying scorpion toxins from complex venom mixtures, researchers have been successful in identifying peptides that show promise for designing drugs to treat disorders such as erectile dysfunction (Nunes et al. 2013), autoimmune diseases (Norton et al. 2004), and cancer (Stroud et al. 2011). The advent of advanced recombinant (Vita et al. 1995) and synthetic production techniques (M'Barek et al. 2004) in combination with genetic approaches may soon yield Nav channel drug leads as well.

### 3.3 Spider Toxins

In contrast to toxins from sea anemone, scorpion, and cone snail venoms, the exploration of the mechanism by which spider toxins interact with mammalian Nav channel voltage sensors has only recently begun. Structure–function studies on Magi 5 from the hexathelid



spider *Macrothele gigas* with Nav channels (Corzo et al. 2007) and the Kv channel toxin SGTx1 from the *Scodra griseipes* tarantula (Lee et al. 2004) reveal the functional importance of a hydrophobic residue cluster surrounded by charged amino acids. As a result of this ubiquitous amphipathic character, spider toxins may access their receptor site within Nav channel and Kv channel voltage-sensing domains after partitioning into the membrane (Bosmans and Swartz 2010; Milescu et al. 2007, 2009; Swartz 2008). Depending on which voltage sensors are targeted and how they couple to the overall Nav channel-gating process, spider toxins can have three diverse effects on Nav channel function. The most commonly observed is for the toxin to inhibit channel opening in response to membrane depolarization (Fig. 8) (Bosmans et al. 2008; Edgerton et al. 2008; Middleton et al. 2002; Smith et al. 2005, 2007; Sokolov et al. 2008). Another outcome is for the toxin to delay fast inactivation by impairing domain IV movement (Wang et al. 2008). Finally, as uniquely observed with Magi 5, the toxin can facilitate channel opening by shifting the activation voltage to more hyperpolarized values (Corzo et al. 2007). Recently, the identification of an S3b–S4 paddle motif within each of the four Nav channel voltage sensors significantly contributed to our understanding of the multifaceted working mechanism of spider toxins. As a result of this discovery, it was demonstrated that the paddle motif in each of the four Nav channel voltage sensors can interact with spider toxins and that multiple paddle motifs are often targeted by a single toxin (Bosmans et al. 2008). These novel insights also led to the identification of the first tarantula toxin (ProTx-I) active on Nav1.9, a Nav channel isoform predominantly expressed in nociceptive DRG neurons (Bosmans et al. 2011; Cummins et al. 1999). Interestingly, ProTx-I potentiates Nav1.9-mediated currents in rat DRG neurons, whereas the other TTX-resistant channel Nav1.8 is inhibited (Bosmans et al. 2011). The related tarantula toxin ProTx-II selectively targets Nav1.7, a Nav channel isoform implicated in various pain syndromes, with an affinity that is at least 100-fold higher when compared to other Nav channel isoforms that were examined (Schmalhofer et al. 2008). Although C-fiber compound action potential in de-sheathed cutaneous nerves can be completely inhibited, ProTx-II is not efficacious in rodent models of acute or inflammatory pain. As is the case with HWTX-IV from the Chinese bird spider *Selenocosmia huwena*, ProTx-II preferentially targets the Nav1.7 domain II voltage sensor (Xiao et al. 2010). Yet, ProTx-II also binds to the paddle motif in domain IV of this particular isoform, thereby resulting in a noticeable slowing of fast inactivation, a phenomenon that is not visible with Nav1.2 (Fig. 8) (Bosmans et al. 2008; Xiao et al. 2011). Several tarantula toxins have also been shown to possess a certain degree of selectivity toward Nav1.5, a Nav channel isoform known to be involved in cardiovascular function. For example, CcoTx3, JzTx-I, and JzTx-III modulate cardiac Na<sup>+</sup> currents; however, the isoform specificity of JzTx-I and JzTx-III has not yet been examined (Bosmans et al. 2006, 2009; Liao et al. 2007; Xiao et al. 2005). Overall, toxins isolated from spider venom have proven to be valuable tools to probe the structure and functional mechanisms of Nav channels. As such, future opportunities may arise for using these peptides as therapeutic drugs.

### 3.4 Wasp Toxins

The two wasp toxins that have been thoroughly examined so far,  $\alpha$ -pompilidotoxin from *Anoplius samariensis* and  $\beta$ -pompilidotoxin from *Batozonellus maculifrons* (Konno et al. 1998), are short peptides with no disulfide bonds or homology to toxins isolated from other

organisms (Sahara et al. 2000). Both peptides slow fast inactivation of neuronal Nav channels but not Nav1.4 and Nav1.5, doing so in a manner similar to  $\alpha$ -scorpion and sea anemone toxins (Fig. 9). Single amino acid mutagenesis of Nav1.2 has revealed an important role for a glutamate residue in the paddle motif of the domain IV voltage sensor in forming the toxin receptor site (Kinoshita et al. 2001). Moreover, similar to  $\alpha$ -scorpion and sea anemone toxins, cationic residues within these peptides were found to be critical for toxin activity (Konno et al. 2000). Mandaratoxin, a 19 kDa protein isolated from the hornet *Vespa mandarinia* venom, irreversibly reduces Na<sup>+</sup> current (Abe et al. 1982). Little else is known about this toxin, yet it serves as a reminder that many toxins in nature remain to be discovered, some of which with novel mechanisms of action that may be exploited for therapeutic or research use.

### 3.5 Cone Snail Toxins

Several distinct groups of cone snail toxins are thought to influence Nav channel gating by interacting with the voltage-sensing domains. The biological backdrop resulting in the evolution of these peptides is different from that of the cone snail pore-blocking toxins. In a number of fish-hunting cone snail clades, the ability to rapidly elicit muscle paralysis was insufficient for success. As a result, these snails have evolved to make prey capture even more efficient through a mechanism that is functionally equivalent to electrocuting their victims. In essence, at the venom injection site, a combination of peptides that block Kv channels but keep Nav channels open, elicits a massive depolarization of the axons first encountered by the venom. This causes the affected axons to fire action potentials uncontrollably, analogous to applying a Taser at the point of injection. The result is an almost immediate tetanic paralysis after a successful strike by the cone snail. The group of toxins that cause this very rapid prey immobilization is called the “lightning strike cabal.” The first characterized group of Nav channel targeting cone snail toxins that belong to this lightning strike cabal are called  $\delta$ -conopeptides and inhibit channel fast inactivation (Terlau et al. 1996) resulting in a continuous entry of Na<sup>+</sup> into the affected axons followed by a massive depolarization of the targeted plasma membranes. Consistent with their effect on Nav channel fast inactivation, it was shown that  $\delta$ -conotoxins target the paddle motif in the domain IV voltage sensor (Leipold et al. 2005).  $\delta$ -conotoxins are expressed in a wide range of cone snail venoms and are typically between 25 and 35 amino acids in length. Despite the fact that they are ubiquitous in cone snail venoms, the hydrophobic character of these peptides makes them a challenge to synthesize chemically thereby rendering them a less well-characterized family when compared to the  $\mu$ -conotoxins (Figs. 3 and 4).  $\delta$ -conotoxins belong to the O-superfamily, are genetically unrelated to the pore-blocking  $\mu$ -conotoxins (which belong to the M-superfamily), and are primarily found in several clades of fish-hunting cone snails (Barbier et al. 2004; Bulaj et al. 2001; West et al. 2005; Fainzilber et al. 1995; Shon et al. 1995), and in at least one clade of mollusc-hunting snails (Hasson et al. 1993; Hillyard et al. 1989; Shon et al. 1994; Sudarslal et al. 2003). Interestingly, the first  $\delta$ -conotoxin was discovered in the molluscivorous species *Conus textile* and was called the King Kong peptide because injection of the toxin into lobsters caused the animal to continuously assume a dominant posture (Hillyard et al. 1989).

A second group of cone snail toxins that contribute to the lightning strike cabal are the  $\nu$ -conotoxins, which shift Nav channel activation to more hyperpolarized potentials thereby causing these channels to open at voltages where they are normally closed. These peptides differ from the  $\mu$ -conotoxins and the  $\delta$ -conotoxins in their mechanism of action, the gene superfamily to which they belong, and the presence of unusual posttranslational modifications. So far, these peptides have been found in only one species of fish-hunting cone snail, *Conus radiatus*, and belong to the I<sub>1</sub> gene superfamily which is typically defined by four disulfide crosslinks and a length of about 40–50 amino acids. A most unusual feature of many native  $\nu$ -conotoxins is the presence of a single posttranslationally modified D-amino acid toward the C-terminal end. The first biochemically characterized  $\nu$ -conotoxin, r11a was found to contain a single D-Phe<sup>44</sup> (Buczek et al. 2005a). The NMR structure of this peptide revealed that three of the disulfide linkages are consistent with an inhibitory cysteine knot (ICK) motif, with one additional disulfide linkage. The modified D-Phe residue is present beyond the last disulfide crosslink in the C-terminal region, and the NMR structure suggests that this region of the peptide is disordered in solution. Functionally, r11a target selectivity with respect to Nav channel isoforms expressed in *Xenopus* oocytes is Nav1.6 > Nav1.2 > Nav1.7, whereas other channel subtypes tested are insensitive to the toxin (Fiedler et al. 2008). Substitution of L-Phe for D-Phe has two major functional consequences: (1) a twofold lower affinity and twofold faster off-rate can be observed for the Nav1.6 subtype and (2) the L-Phe analog is inactive on Nav1.2. So far, four  $\nu$ -toxins have been purified from *Conus radiatus* and chemically synthesized, whereas only one peptide (r11a) has been identified and characterized from the worm-hunting cone snail, *Conus arenatus* (Buczek et al. 2005a, b, 2008; Jimenez et al. 2003). While all of the  $\nu$ -conotoxins from the fish-hunting species *Conus radiatus* cause severe excitotoxic symptoms when injected into mice, the *Conus arenatus*  $\nu$ -conotoxin only causes mild symptoms even at high doses. Furthermore, it was demonstrated that three of the peptides from *Conus radiatus* (r11a, r11b, and r11c) have a posttranslationally modified amino acid at the predicted site as opposed to only one peptide from *Conus radiatus* (r11d) and one from *Conus arenatus* (r11a) in which all amino acids are in the L configuration. Despite their unique characteristics, the receptor site to which  $\nu$ -conotoxins bind remains to be determined, yet it seems likely that one of the three voltage sensors involved in channel opening may be stabilized in an activated state.

Similar to a variety of other polypeptide toxins, the  $\mu$ O-conotoxins target Nav channel voltage sensors, yet they have distinctive properties (Daly et al. 2004; Leipold et al. 2007; Zorn et al. 2006). Unlike other conotoxins, the  $\mu$ O-conotoxins have not been found in fish-hunting cone snails. Instead, they were discovered in the molluscivorous *Conus marmoreus*. After this *Conus* species stings other snails, their envenomated prey become progressively more flaccid; thus, like fish-hunting cone snails, some molluscivorous *Conus* may have the equivalent of a “motor cabal” to block neuromuscular transmission and would likely have evolved Nav channel antagonists. In contrast to the  $\mu$ -conotoxins that physically occlude the pore region, the  $\mu$ O-conotoxins are gating modifiers capable of antagonizing Nav channel opening (Leipold et al. 2007; Zorn et al. 2006). It has been hypothesized that they inhibit conductance by preventing the domain II voltage sensor from activating, a feature known to prevent channel opening. The two  $\mu$ O-conotoxins that have been characterized thus far,  $\mu$ O-

MrVIA and MrVIB (Fainzilber et al. 1995; Daly et al. 2004; McIntosh et al. 1995), were shown to inhibit Na channel conductance without competing with the pore-blocking  $\mu$ -conotoxins (Terlau et al. 1996). The analysis carried out by Heinemann and collaborators (Leipold et al. 2007; Zorn et al. 2006) demonstrates that the peptide interacts with both domains II and III, and competition with the  $\beta$ -scorpion toxin Ts1 suggests that the receptor site of  $\mu$ O-conotoxins may overlap with that of  $\beta$ -scorpion toxins (Leipold et al. 2006). Part of the intense interest in  $\mu$ O-conotoxins (Bulaj et al. 2006; Ekberg et al. 2006) stems from their ability to inhibit TTX-resistant Nav channel isoforms, some of which are thought to be involved in nociception (Gilchrist et al. 2012; Knapp et al. 2012). Subsequently,  $\mu$ O-conotoxins have been assessed for analgesic activity and were shown to be anti-nociceptive in various animal models of pain (Teichert et al. 2012).

## Conclusions

Notwithstanding their limited availability, animal toxins have been successfully employed for many decades to investigate Nav channel function. Now more than ever, the ability to construct cDNA libraries from animal venom glands in concert with recombinant and synthetic production techniques will allow researchers to fully exploit animal peptides and probe the functional aspects of various Nav channel isoforms on a molecular level as well as investigate their physiological role in healthy and diseased tissues. Moreover, novel synthetic methods such as minimization, cyclization, and the use of diselenide bridges (Bulaj 2008) can address the challenges that may exist between the initial drug discovery phase and the clinical application of animal toxins, which will expand the use of these peptides as therapeutic drugs.

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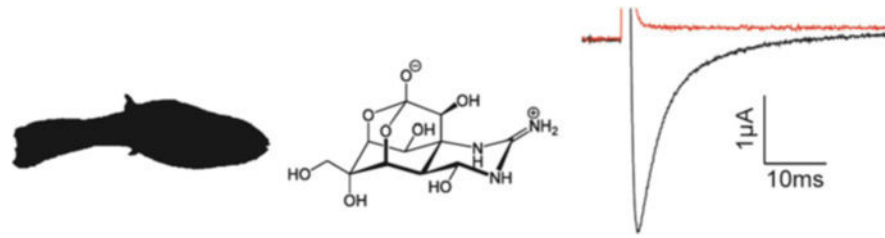
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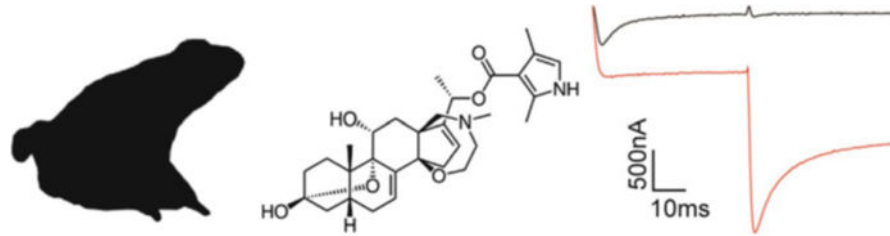


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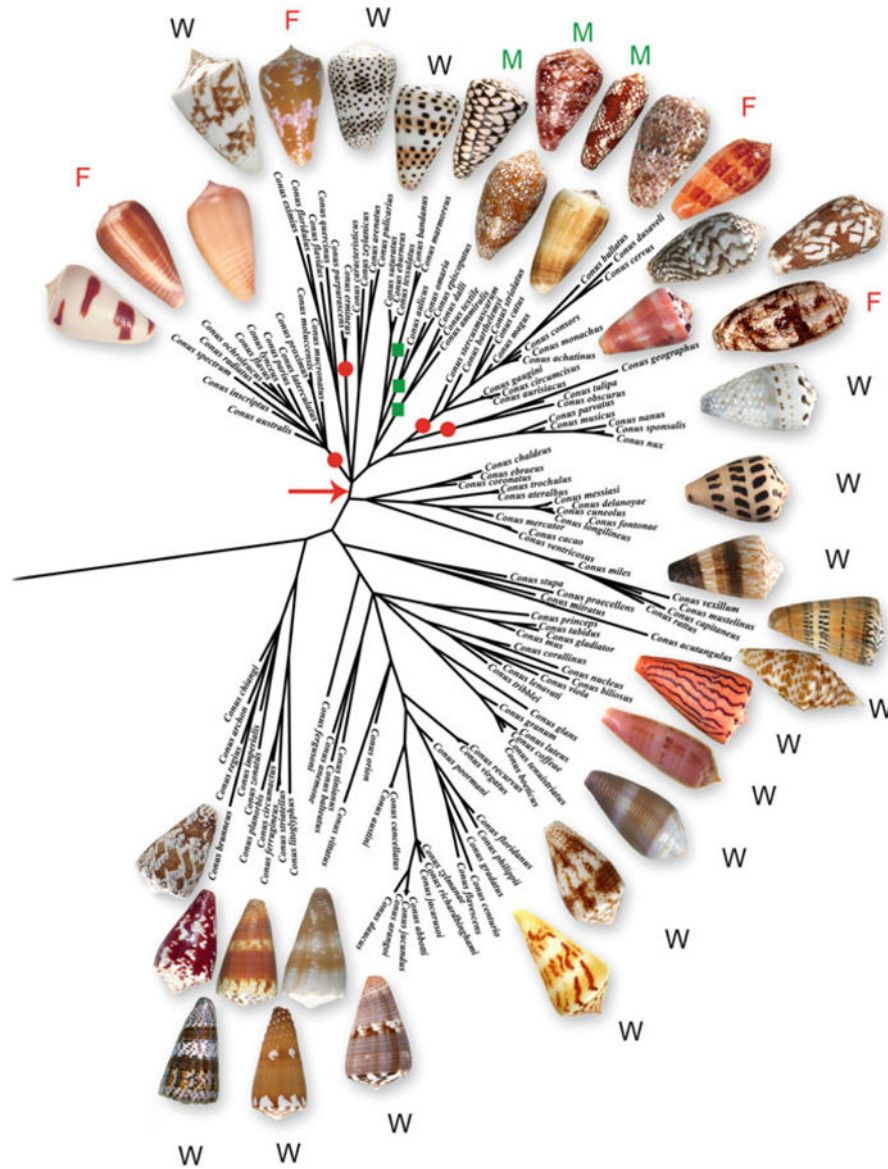
**Fig. 1.**

Tetrodotoxin inhibits Nav channel opening. TTX is found in the Japanese puffer fish (silhouette of *Takifugu rupripes* on the *left*) and has a complex molecular structure (*middle*). At 10 nM, TTX inhibits rNav1.2a currents evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of 10 nM TTX (*right*)



**Fig. 2.**

Batrachotoxin disrupts Nav channel gating. BTX is found in particular frog species (silhouette of *Phylllobates bicolor* on the left) and has a complex molecular structure (middle). At 5  $\mu\text{M}$ , BTX completely inhibits fast inactivation of rNav1.8 currents evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. During the second voltage step to  $-30$  mV, channels normally close; however, BTX-bound channels are still deactivating. *Black* is control and *red* is after addition of TTX (right)

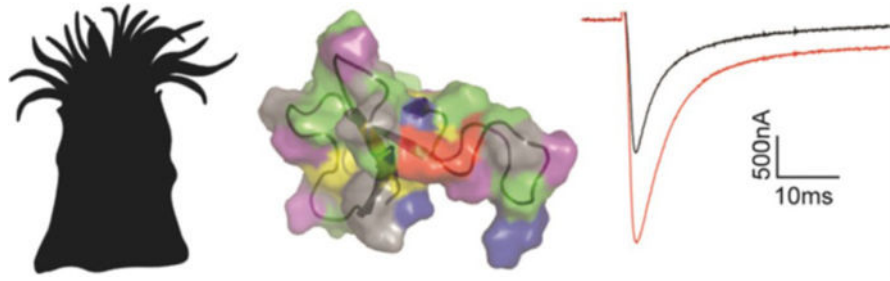


**Fig. 3.** Phylogenetic tree of a variety of *Conus* species. Fish-hunting clades are labeled with a red dot, mollusc-hunting clades with a green square; others are labeled “W” and are believed to be worm-hunting *Conus*.  $\mu$ -conotoxins are derived from venoms of fish-hunting clades, whereas the  $\mu$ O-conotoxins are from the venom of a snail-hunting species. The tree is based on 12S mitochondrial rRNA markers; data generated by M. Watkins; tree constructed by J. P. Ownby



**Fig. 4.**

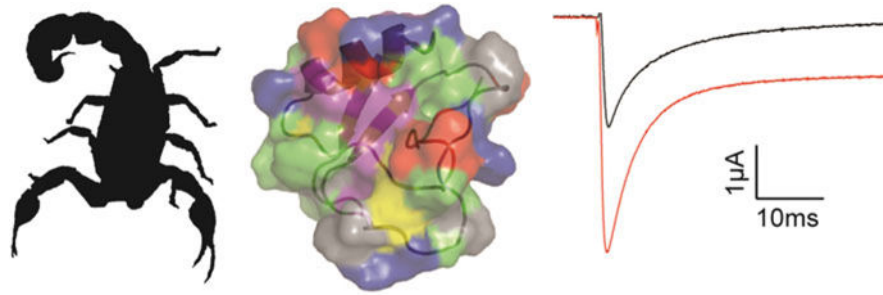
*Conus* shells are remarkably diverse. Shells of fish-hunting *Conus* species listed in Table 1. *Top row, left to right: C. consors; C. magus; C. tulipa; C. aurisiacus; C. geographus; and C. striatus. Bottom row, left to right: C. bullatus; C. stercusmuscarum; C. purpurascens; and C. striolatus.* Different clades of fish-hunting *Conus* are represented. *Conus purpurascens* belongs to the subgenus *Textilia*, *Conus tulipa* and *Conus geographus* to the subgenus *Gastridium*, and all other species shown to the subgenus *Pionoconus*. Figure prepared by My Hyunh



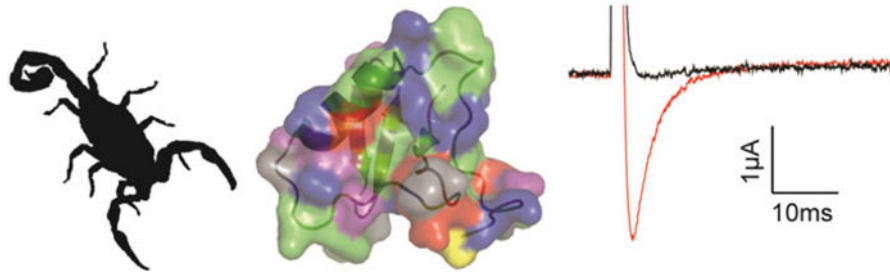
**Fig. 5.**

ATX-II inhibits Nav channel fast inactivation. ATX-II is found in the *Anemonia sulcata* sea anemone and amino acids important to toxin functionality have been identified throughout the related peptide Ap-a (*middle figure*: protein backbone is shown together with the electrostatic surface of the protein. *Blue* are basic residues, *red* acidic, *green* hydrophobic, *yellow* cysteine, and *purple* polar.). At 500 nM, ATX-II inhibits fast inactivation of rNav1.2a currents evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of 500 nM ATX-II (*right*)



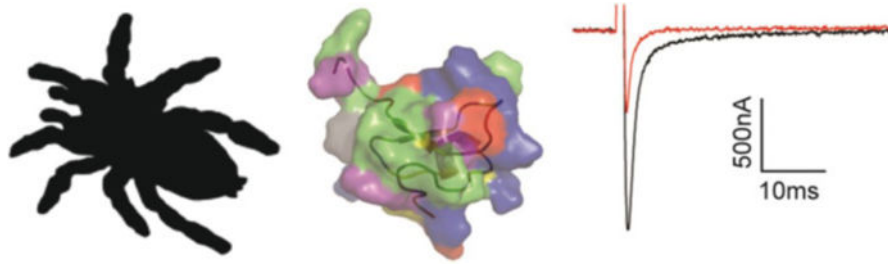


**Fig. 6.**  $\alpha$ -scorpion toxins hamper Nav channel fast inactivation. The  $\alpha$ -scorpion toxin AaHII is produced by the *Androctonus australis* Hector scorpion (silhouette on the *left*) and amino acids important to toxin functionality have been identified in both the hydrophobic patch as well as charged residues surrounding it (*middle figure*: protein backbone is shown together with the electrostatic surface of the protein). At 100 nM, AaHII inhibits fast inactivation of rNav1.2a currents evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of 100 nM AaHII (*right*)



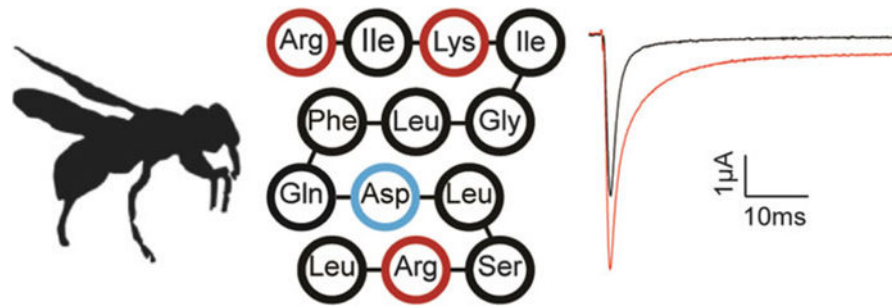
**Fig. 7.**

$\beta$ -scorpion toxins promote Nav channel opening. The  $\beta$ -scorpion toxin CssIV is found in the venom of the *Centruroides suffusus suffusus* scorpion (silhouette on the *left*) and amino acids important to toxin functionality have been identified in both the hydrophobic region and a ring of charged residues a (*middle figure*: protein backbone of the related  $\beta$ -scorpion toxin TsVII is shown together with the electrostatic surface of the protein). At 1  $\mu$ M, CssIV opens rNav1.2a at voltages where the channel is normally closed. Current trace shown was evoked from a holding potential of  $-90$  mV to a voltage of  $-40$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of 1  $\mu$ M CssIV (*right*)



**Fig. 8.**

Hanatoxin is a tarantula toxin that inhibits Nav channel opening. HaTx is found in the venom of the Chilean Rose tarantula (*Grammostola spatulata*) (silhouette of the related tarantula *Brachypelma smithi* is shown on the *left*) and amino acids important to toxin functionality have been identified in both the hydrophobic dimple as well as the ring of charged residues surrounding it (*middle*: protein backbone is shown together with the electrostatic surface of the protein). At 100 nM, HaTx inhibits rNav1.2a opening when currents are evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of 100 nM HaTx (*right*)



**Fig. 9.** Pompilidotoxins inhibit Nav channel fast inactivation.  $\beta$ -pompilidotoxin from *Batozonellus maculifrons* (silhouette of related wasp *Vespula germanica* on the *left*—peptide sequence in the *middle*) inhibits rNav1.2a fast inactivation when currents are evoked from a holding potential of  $-90$  mV to a voltage of  $-20$  mV when expressed in *Xenopus* oocytes. *Black* is control and *red* is after addition of  $1 \mu\text{M}$  toxin (*right*)

**Table 1**

Affinities of m-conopeptides (nM) for Nav channel subtypes

Peptide	Conus species (Fish-hunting clade)	1.1	1.2	1.3	1.4	1.5	1.6	1.7	1.8
SmIIIA	<i>C. stercusmuscarum</i> (1)	0.0038	0.0013	0.035	0.00022	1.3 <sup>aa</sup>	0.16 <sup>a</sup>	1.3 <sup>a</sup>	>100 <sup>a</sup> West et al. (2002)
KIIIA	<i>C. kinoshitai</i> (2)	0.29	0.005	8 <sup>a</sup>	0.09 <sup>a</sup>	287 <sup>a</sup>	0.24 <sup>a</sup>	0.29	>100 <sup>a</sup> Bulaj et al. (2005)
SIIIA	<i>C. striatus</i> (1)	11 <sup>a</sup>	0.05	11 <sup>a</sup>	0.13 <sup>a</sup>	251 <sup>a</sup>	0.76 <sup>a</sup>	65 <sup>a</sup>	>100 <sup>a</sup> Bulaj et al. (2005)
CnIIIA	<i>C. consors</i> (1)	14.2 <sup>a</sup>	0.25	11 <sup>a</sup>	0.27 <sup>a</sup>	7.4 <sup>a</sup>	7.1 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Zhang et al. (2006)
MIIIA	<i>C. magus</i> (1)	22.6 <sup>a</sup>	0.45	7.7	0.33	>100 <sup>a</sup>	21.6 <sup>a</sup>	97 <sup>a</sup>	>100 <sup>a</sup> Zhang et al. (2006)
GIIIA	<i>C. geographus</i> (3)	0.26	17.8 <sup>a</sup>	>100 <sup>a</sup>	0.019 <sup>a</sup>	>100 <sup>a</sup>	0.68 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Cruz et al. (1985)
PIIIA	<i>C. purpurascens</i> (4)	0.12 <sup>a</sup>	0.62 <sup>a</sup>	3.2 <sup>a</sup>	0.036 <sup>a</sup>	>100 <sup>a</sup>	0.1 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Shon et al. (1998)
SxIIIA	<i>C. striolatus</i> (1)	0.37 <sup>a</sup>	1 <sup>a</sup>	>100 <sup>a</sup>	0.007 <sup>a</sup>	>100 <sup>a</sup>	0.57 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Walewska et al. (2008)
BullIIA	<i>C. bullatus</i> (5)	0.35	0.012	0.35	0.013	13.8 <sup>a</sup>	4.4 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Holford et al. (2009)
BullIIB	<i>C. bullatus</i> (5)	0.36	0.013	0.2	0.0036	9 <sup>a</sup>	1.8 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Kuang et al. (2013)
TIIIA	<i>C. tulipa</i> (2)	0.9 <sup>a</sup>	0.045	7.9 <sup>a</sup>	0.005	>100 <sup>a</sup>	25 <sup>a</sup>	>100 <sup>a</sup>	>100 <sup>a</sup> Lewis et al. (2007)

Fish-hunting clades: (1) *Pionoconus*, (2) *Alfonsoconus*, (3) *Gastridium*, (4) *Cheleconus*, (5) *Textilia*

<sup>a</sup>IC50 values; all other values are KDs. All Nav channel clones were from rat except Nav1.6, which is from mouse

m-Conopeptide activity matrix: peptides that best discriminate between given pairs of Nav1-isoforms, as revealed by their discrimination index (DI) values

**Table 2**

Nav	1.1	1.2	1.3	1.4	1.5	1.6	1.7
1.1	SIIA	MIIA	TIIA	CmIIA	SIIA	KIIA	
	2.3	0.5	2.3	0.3	1.2	0.0	
1.2	GIIA	PIIA	GIIA	GIIA	GIIA	GIIA	
	1.8	-0.7	3.0	-0.8	1.4	-0.8	
1.3	GIIA	KIIA	SxIIA	CmIIA	SxIIA	KIIA	
	2.6	3.2	4.2	0.2	2.2	1.4	
1.4	KIIA	KIIA	MIIA	CmIIA	KIIA	KIIA	
	-0.5	1.3	-1.4	-1.4	-0.4	-0.5	
1.5	KIIA	KIIA	BuIIIB	TIIA	KIIA	KIIA	
	3.0	4.8	1.7	4.3	3.1	3.0	
1.6	SmIIA	TIIA	BuIIA	TIIA	CmIIA	KIIA	
	1.6	2.7	1.1	3.7	0.0	-0.1	
1.7	PIIA	BuIIIB	BuIIIB	BuIIIB	CmIIA	PIIA	
	2.9	3.9	2.7	4.4	1.1	3.0	