

Research Paper

Multiple Sodium Channel Variants in the Mosquito *Culex quinquefasciatus*

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Abstract

Voltage-gated sodium channels are the target sites of both DDT and pyrethroid insecticides. The importance of alternative splicing as a key mechanism governing the structural and functional diversity of sodium channels and the resulting development of insecticide and acaricide resistance is widely recognized, as shown by the extensive research on characterizing alternative splicing and variants of sodium channels in medically and agriculturally important insect species. Here we present the first comparative study of multiple variants of the sodium channel transcripts in the mosquito *Culex quinquefasciatus*. The variants were classified into two categories, CxNa-L and CxNa-S based on their distinguishing sequence sizes of ~6.5 kb and ~4.0 kb, respectively, and generated via major extensive alternative splicing with minor small deletions/ insertions in susceptible S-Lab, low resistant HAmCq^{G0}, and highly resistant HAmCq^{G8} *Culex* strains. Four alternative Cx-Na-L splice variants were identified, including three full length variants with three optional exons (2, 5, and 21i) and one with in-frame-stop codons. Large, multi-exon-alternative splices were identified in the CxNa-S category. All CxNa-S splicing variants in the S-Lab and HAmCq^{G0} strains contained in-frame stop codons, suggesting that any resulting proteins would be truncated. The ~1000 to ~3000-fold lower expression of these splice variants with stop codons compared with the CxNa-L splicing variants may support the lower importance of these variants in S-Lab and HAmCq^{G0}. Interestingly, two alternative splicing variants of CxNa-S in HAmCq^{G8} included entire ORFs but lacked exons 5 to 18 and these two variants had much higher expression levels in HAmCq^{G8} than in S-Lab and HAmCq^{G0}. These results provide a functional basis for further characterizing how alternative splicing of a voltage-gated sodium channel contributes to diversity in neuronal signaling in mosquitoes in response to pyrethroids, and possibly indicates the role of these variants in the development of pyrethroid resistance.

Key words: Sodium channel, transcript variants, alternative splicing, insecticide resistance, *Culex quinquefasciatus*.

INTRODUCTION

The insects' voltage-gated sodium channels are the targets for insecticides, such as DDT and pyrethroids [1-4], which are responsible for the rising phase of action potentials in the membranes of neurons and most electrically excitable cells [5]. Pyre-

throids and DDT deliver their toxic, insecticidal effects primarily by binding to the sodium channel, thus altering its gating properties and keeping the sodium channel open for unusual long time, thereby causing a prolonged flow of sodium current that initiates repet-

itive discharges and prevents the repolarization phase of action potentials [5-7]. The common feature found in sodium channels is that relatively small changes, such as point mutations or substitutions [3, 8-14], short sequence insertions or deletions, or alternative splicing [15-23] in the structure of these channels significantly affect their behavior and are sufficient to change neuronal firing, resulting in different phenotypes. Modifications of the insect sodium channel structure can cause insensitivity of the channels to DDT and pyrethroids via a reduction in or an elimination of the binding affinity of the insecticides to proteins [6-7], and hence result in the development of insecticide resistance.

In mammalian systems, molecular characterization of voltage-gated sodium channel genes has revealed the existence of multiple genes [5, 24-26]: ten paralogous voltage-gated sodium channel genes have been identified in humans [25]; 8 in zebra fish [27]; and 6 in electric fish [28]. Several invertebrate species have also been found to include multiple sodium channel genes in their genome; for example, 4 sodium channel genes have been characterized in *Hirudo medicinalis* (leech) [29] and 2 in *Halocynthia roretzi* (ascidia) [30-31]. Compared to the fairly well defined multiple vertebrate sodium channel genes, it appears that a single sodium channel gene that has been well characterized in many insect species, homologous to *para* (currently *DmNav*) of *Drosophila melanogaster* [32-33] encodes the equivalent of the α -subunit of the mammalian sodium channels. While mammals rely on the selective expression of at least ten different sodium channel genes in various tissues to achieve sodium channel diversity [25], insects may produce a range of diverse sodium channels with different functional and pharmacological properties from a single sodium channel by extensive alternative splicing [16-23, 34].

Because of the importance of alternative splicing as a key mechanism for generating structural and functional diversity in sodium channels [19], following the first discovery of the existence of alternative splicing of the *para* sodium channel gene from *Drosophila melanogaster* [32], alternative splicing events were subsequently characterized in many medically or agriculturally important insect and arachnid pest species [17, 19-23, 34-36]. As yet, however, there have been no reports of alternative splicing in *Culex quinquefasciatus*, an important mosquito vector of human pathogens such as St. Louis encephalitis virus (SLEV), West Nile virus (WNV), and the parasitic *Wuchereria bancrofti* nematode in many urban settings throughout the tropical and temperate regions of the world [37-39]. Here we present the first comparative study

of full length sequences of the para-orthologue sodium channel transcripts from the *Culex quinquefasciatus* mosquito and examine multiple variants obtained through the mechanism of alternative splicing.

MATERIALS AND METHODS

Mosquito strains

Three strains of mosquito *Cx. quinquefasciatus* were studied. S-Lab is an insecticide susceptible strain provided by Dr. Laura Harrington (Cornell University). HAmCq^{G0} is a low insecticide resistant strain with a 10-fold level of resistance to permethrin compared with the laboratory susceptible S-Lab strain [40]. It was originally collected from Huntsville, Alabama, in 2002 and established in our laboratory without further exposure to insecticides [41]. The HAmCq^{G8} strain is the 8th generation of permethrin-selected HAmCq^{G0} offspring and has a 2,700-fold level of resistance [40]. All mosquitoes were reared at 25±2°C under a photoperiod of 12:12 (L:D) h.

Amplification of the full length of sodium channel transcripts in *Cx. quinquefasciatus*

For each of the three mosquito populations, total RNA was extracted from the 4th instar larvae, and different tissues (head + thorax, and abdomen) from 2-3 day-old adult females before blood feeding using the acidic guanidine thiocyanate-phenol-chloroform method [42]. Messenger RNAs (mRNAs) were isolated using Oligotex-dT suspension (QIAGEN). The full length cDNA of the *Cx. quinquefasciatus* sodium channel gene was subsequently isolated from each of the mosquitoes populations by RT-PCR using the Expand Long Range, dNTPack kit (Roche) with a specific primer pair, KDR S16 (TGTTGGCCATATAGACAATGACCGA) /KDR AS09 (GCTTCTGAATCTGAATCAGAGGGAG), synthesized based on the respective 5' and 3' end sequences of the putative sodium channel cDNAs [43], accession numbers: JN695777, JN695778, and JN695779]. The PCR reaction was conducted following a PCR cycle of 92°C for 2 min, 10 cycles of 92°C for 10 s, 55°C for 15 s, and 68°C for 6 min, and 35 cycles of 92°C for 10 s, 55°C for 15 s, and 68°C for 8 min, with a final extension of 68°C for 10 min. All PCR products were cloned into PCRTM 2.1 Original TA cloning vector (Invitrogen) and sequenced. Cloning and sequence analyses of sodium channel cDNA fragments were repeated at least two times for each mosquito strain with different preparations of RNAs and mRNAs. The inserts of *Culex* sodium channel clones were sequenced and analyzed.

Quantitative real-time PCR (qRT-PCR)

The total RNA (0.5 µg/sample) from each mosquito sample was reverse-transcribed using SuperScript II reverse transcriptase (Stratagene) in a total volume of 20 µl. The quantity of cDNAs was measured using a spectrophotometer prior to qRT-PCR, which was performed with the SYBR Green master mix Kit and ABI 7500 Real Time PCR system (Applied Biosystems). Each qRT-PCR reaction (25 µl final volume) contained 1x SYBR Green master mix, 1 µl of cDNA, and a sodium channel transcript specific primer pair designed according to each of the sodium channel transcript or allele sequences (Table 1 shows the accession number for each of the sodium channel transcripts or alleles) at a final concentration of 3-5 µM. All samples, including the A 'no-template' negative control, were performed in triplicate. The reaction cycle consisted of a melting step of 50°C for 2 min then 95°C for 10 min, followed by 40 cycles of 95°C for 15 sec and 60°C for 1 min. Specificity of the PCR reactions was assessed via a melting curve analysis for

each PCR reaction using Dissociation Curves software [44]. Relative expression levels for the sodium channel transcripts were calculated by the $2^{-\Delta\Delta CT}$ method using SDS RQ software [45]. The 18S ribosome RNA, an endogenous control, was used to normalize the expression of targets [46-49]. Preliminary qRT-PCR experiments with a primer pair (Table 1) designed according to the sequences of the 18S ribosome RNA had revealed that the expression of this gene remained constant among all 3 mosquito strains, so the 18S ribosome RNA was used for internal normalization in the qRT-PCR assays. Each experiment was repeated three to four times with different preparations of RNA samples. The statistical significance of the gene expressions was calculated using a Student's *t*-test for all 2-sample comparisons and a one-way analysis of variance (ANOVA) for multiple sample comparisons (SAS v9.1 software); a value of $P \leq 0.05$ was considered statistically significant. Significant overexpression was determined using a cut-off value of a ≥ 2 -fold change in expression [50].

Table 1. Oligonucleotide primers used in qRT-PCR reactions for amplifying sodium channel variants.

Mosquito population	Variants	Forward Primer	Reverse Primer
S-Lab	CxNa _v -Lv1	5' AATCAGCTGTAAAAGTGATGGCGC 3'	5' AGCTCGTAGTACCCTGAATGTTCT 3'
	CxNa _v -Lv2	5' CACTGCAAAAAGCCCGTAAAGTGAG 3'	5' ATAGTATACTGGAACGATGATTGCA 3'
	CxNa _v -Lv3	5' ACAAGGGCAAGAAGAACAAGCAGC 3'	5' CTTTATACTGGCAGTGTTCATCGTC 3'
	CxNa _v -Sv1	5' ATCGATATCTGAGAGAACGTAGTT 3'	5' TTCATCCTCGTCCTCATCGTCGTA 3'
HAmCq ^{G0}	CxNa _v -Lv4	5' GGTCGGAAGAAAAAGAAAAAGAGA 3'	5' TATCCTTTCTTTACTAATACTACTA 3'
	CxNa _v -Lv5	5' GCCAAAAAAGTACTACAACGCAA 3'	5' TCCCGTCGCTTGTAGTGAT 3'
	CxNa _v -Lv6	5' AGCACAACCATCTCAGTTGGATAT 3'	5' TCGTCGTCGAGTTCTTCGTCGAATT 3'
	CxNa _v -Sv2	5' CAAAAGTTCGACATGATCATCATG 3'	5' TGAAGAACGACATCCCGAAGATG 3'
	CxNa _v -Sv3	5' TACTACATGGACAGGATATTCAC 3'	5' CAGGTTTATGAGCGAGAGCATCA 3'
HAmCq ^{G8}	CxNa _v -Lv7	5' TCGAGTGTTCAAGCTAGCAAA 3'	5' AATGCAGAGCACAAACGTCAG 3'
	CxNa _v -Lv8	5' TTCCAGTATACTATGCTAATTTAG 3'	5' TTGGTGTCGACGTAGGACATGTT 3'
	CxNa _v -Sv4	5' TCCAAGGTGATAGGCAATTCATT 3'	5' TCAATTCCTAGGTCTCTCTTGCT 3'
	CxNa _v -Sv5	5' ACTACTACGAATGTCTTAATGTTT 3'	5' TGTACTAAAATATAAATAGCTACG 3'

Results

Generation of sodium channel transcripts in *Cx. quinquefasciatus*

To examine the number of transcripts of the para-type sodium channel gene in the genome of *Culex* mosquitoes, RNAs isolated from S-Lab, HAmCq^{G0} and HAmCq^{G8} were subjected to PCR amplification using a primer pair: KDR S16 (TGTTGGCCATA TAGACAATGACCGA)/KDR AS09 (GCTTCTGAAT CTGAATCAGAGGGAG), synthesized based on the

respective 5' and 3' end sequences of the putative sodium channel cDNAs (Table 1, 43). Two distinct molecular sizes of sodium channel cDNAs with ~6.5 and ~4 kb were generated by PCR amplification from each of the three mosquito strains, namely susceptible (S-Lab), intermediate (HAmCq^{G0}), and highly resistant (HAmCq^{G8}), when only a single primer pair, KDR S16/ KDR AS09 was used (Fig. 1). The PCR products of both the ~6.5 and ~4.0 kb fragments from each strain were then cloned and sequenced. Sequence analysis of insertions of clones (3, 3, and 2 clones for S-lab, HAmCq^{G0}, and HAmCq^{G8}, respec-

tively) with ~6.5 kb and clones (2, 7, and 2 clones for S-lab, HAmCq^{G0}, and HAmCq^{G8}, respectively) with ~4.0 kb PCR amplified products from each strain indicated that all the cDNA clones were indeed the sodium channel transcripts. Interestingly, nucleotide sequence analysis of these sodium channel transcripts revealed the existence of multiple variants in each of ~6.5 and ~4.0 kb PCR amplification products in each mosquito strains. These variants were then assigned to two categories, CxNa-L and CxNa-S, based on their sizes of ~6.5 and ~4.0 kb, respectively.

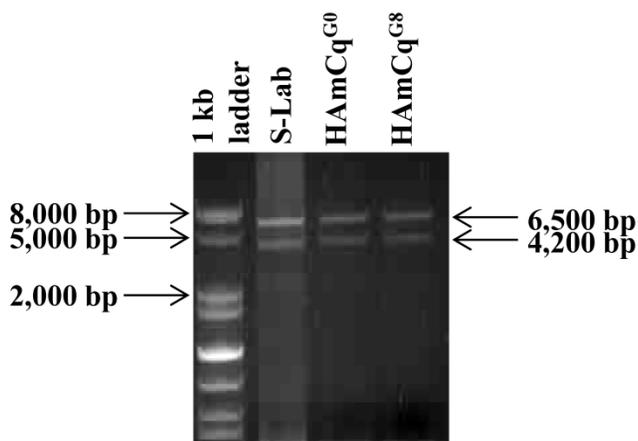


Figure 1. Polymerase chain reaction (PCR) amplification of *para*-type sodium channel transcripts from genomic RNAs of *Culex* mosquitoes. Sodium channel cDNA transcripts amplified from RNAs isolated from S-Lab, HAmCq^{G0} and HAmCq^{G8} mosquito strains were subjected to PCR amplification using a primer pair: KDR S16 (TGTTGGCCATATAGACAATGACCGA)/KDR AS09 (GCTTCTGAATCTGAATCAGAGGGAG), synthesized based on the respective 5' and 3' end sequences of the putative sodium channel genes [43].

The CxNa-L PCR products included three cDNA sequences of the sodium channel, CxNa-L_{v1}, CxNa-L_{v2}, and CxNa-L_{v3}, in the S-Lab strain, with molecular sequence sizes of 6246, 6273, and 6234 bps, respectively (Fig. 2); three sodium channel cDNA sequences, CxNa-L_{v4}, and CxNa-L_{v5} and CxNa-L_{v6}, in the HAmCq^{G0} strain, with 6276, 6285, and 6063 bps, respectively (Fig. 3); and two cDNA sequences, CxNa-L_{v7} and CxNa-L_{v8}, in the HAmCq^{G8} strain, with 6267 and 6273 bps, respectively (Fig. 4). In contrast, the CxNa-S PCR products contained only one cDNA sequence of the sodium channel in S-Lab, CxNa-S_{v1}, with a molecular size of 3891 bps (Fig. 2); two cDNA sequences in HAmCq^{G0}, CxNa-S_{v2} and CxNa-S_{v3}, with molecular sizes of 3615 and 3417 bps, respectively (Fig. 3); and two sodium channel cDNA sequences in HAmCq^{G8}, CxNa-S_{v4} and CxNa-S_{v5}, with 4068 and

3987 bps, respectively, (Fig. 4). This discovery provides strong evidence supporting the existence of multiple transcripts of the sodium channel gene in the mosquito *Cx. quinquefasciatus*, as we previously suggested [51].

Structural analysis of deduced sodium channel protein sequences within each strain and/or among different strains of *Culex* mosquitoes

The putative amino acid sequences for the CxNa-L and the CxNa-S transcript sequences were compared for each of the three mosquito strains studied. In the S-Lab strain, of the three transcripts identified in the CxNa-L category, two, CxNa-L_{v1} and CxNa-L_{v2} (Accession numbers: JN695777 and JX424546), consisted of full length sodium channel sequences encoding the entire ORFs of the sodium channel proteins with 2082 and 2091 amino acid residues, respectively. These exons were numbered 1 through 33 (Fig. 5), based on the silkworm *Bombyx mori* sodium channel *BmNav* [35] and house fly sodium channel sequences [11, 52-53]. However, the *Culex* mosquito sodium channel lacked the exon 12 present in both the *BmNav* and *DmNav* sodium channel sequences. CxNa-L_{v1} and CxNa-L_{v2} shared very high sequence similarity (96%), except for a missing exon 5 as a result of the alternative splicing (Figs. 2 and 5) and several short insertions identified in the CxNa-L_{v2} sequence (Figs. 2 and 5). The remaining transcript, CxNa-L_{v3}, incorporated several in-frame premature stop codons, with the first occurring at domain I segment 2 (IS2) (Figs. 2 and 5). Short deletions and insertions were also identified in CxNa-L_{v3} compared with CxNa-L_{v1} and CxNa-L_{v2}.

Similar length transcripts/variants were identified in the CxNa-L transcripts of the HAmCq^{G0} mosquitoes (Figs. 3 and 5), in which two of the three transcripts identified, CxNa-L_{v4} and CxNa-L_{v5} (Accession numbers: JN695778 and JX424547), were entire sodium channel ORFs, encoding 2092 and 2095 amino acid residues, respectively, and sharing 99% sequence similarity. Comparing the transcript sequences of CxNa-L_{v4} and CxNa-L_{v5} revealed that an alternative splicing exon 2, a short in-frame insertion in exon 12, and a short in-frame deletion in exon 21ii were present in CxNa-L_{v5} (Figs. 3 and 5). The third CxNa-L transcript, CxNa-L_{v6}, in the HAmCq^{G0} mosquitoes was again the exception, incorporating several in-frame premature stop codons, with the first occurred in the linker between IIS6 and IIIS1, in addition to short insertions and deletions (Figs. 4 and 5). CxNa-L_{v6} also exhibited an alternative splicing of exon 2 compared to that identified in CxNa-L_{v5}. The two CxNa-L transcripts, CxNa-L_{v7} and CxNa-L_{v8}

(Accession numbers: JN695779 and JX424548), identified in HAmCq^{G8} were both full length sodium channel transcripts encoding entire ORFs of sodium channels proteins (Figs. 4 and 5). CxNa-L_{v7} and CxNa-L_{v8} shared very high sequence similarity (99%), except for an alternative splicing of exon 21i present in CxNa-L_{v8} (Figs. 4 and 5). The above results indicate that multiple ~full length transcripts presented in the mosquitoes, with at least two transcripts in each mosquito strain, had entire ORFs. The other transcripts found in both S-Lab and HAmCq^{G0} incorporated in-frame premature stop codons and, as such, any resulting proteins would be truncated from those regions onward and thus less likely to be functional transcripts.

The sequences of the CxNa-S transcripts with the ~4.0 kb sized sodium channels in each of the mosquito strains were found to be similar to those of the full length CxNa-L sequences; i.e., one or more transcripts were present in each of the mosquito strains. The main difference in the CxNa-S transcripts compared with those of the full length sequences were the internal exons missing through the alternative splicing, along with some minor short deletions or insertions. In the S-Lab strain, only one transcript was observed, CxNa-S_{v1}, containing a single in-frame stop codon at the IIS6 region in the sequence (Fig. 2). However, the CxNa-S_{v1} transcript also lacked exons 2, 5 to18, 21i, and 22 as a result of the alternative splicing, and thus had a short sodium channel sequence. Two transcripts, CxNa-S_{v2} and CxNa-S_{v3}, were identified in the HAmCq^{G0} strain (Fig. 3). Both of these sequences exhibited alternative splicing of exons, in-frame stop codons, and short deletions and insertions. The CxNa-S_{v2} sequences were found to have alternative splicing of exons 2, 12-26, whereas the CxNa-S_{v3} sequences lacked exons 2-15, and parts of exons 21 and 22 (Fig. 3) due to the alternative splicing, once again resulting in a short sodium channel sequence. The HAmCq^{G8} strain contained 2 transcripts, CxNa-S_{v4} and CxNa-S_{v5}, with entire ORFs, encoding 1356 and 1329 amino acid residues (Accession numbers: JX424549 and JX424550), respectively, and sharing 98% sequence similarity (Fig. 4). Compared with the PRFs of the CxNa-L transcripts, these two CxNa-S transcripts lacked exons 5-18 as a result of the exon alternative splicing (Figs. 4 and 5). Thus, among all the CxNa-S transcripts identified in the tested mosquitoes, only CxNa-S_{v4} and CxNa-S_{v5} in the highly resistant HAmCq^{G8} mosquitoes contained the entire ORFs of the sodium channels.

Expression analysis of sodium channel transcripts in *Culex* mosquitoes

The extent of the variation in alternative transcript expression was also addressed by determining the levels of expression of individual sodium channel transcripts in the 4th instar larvae and different tissues from the adult mosquitoes in each strain using qRT-PCR. Characterizing the developmental and regional expression of the sodium channel transcripts in mosquitoes is critical to our understanding of their relative biological importance. We therefore determined the relative expression levels of sodium channel RNAs for all the transcripts identified in all three mosquito strains, S-Lab, HAmCq^{G0} and HAmCq^{G8}. Total RNAs were extracted from whole bodies of 4th instar larvae, as well as the head+thorax, and abdomen tissues of 2-3 day old adults. The expression levels were determined using qRT-PCR and the expression ratios for the head + thorax and larval samples were then calculated relative to the quantity of the transcript expression in the corresponding abdomen samples for each strain (Fig. 6). The results show that the sodium channel expression in all three strains shared a number of common features. The expression levels were relatively high in the head + thorax tissues compared to the abdomen tissues; the full length sodium channel transcripts of CxNa-L with an ORF of ~6.5 kb had abundant expression compared with those of CxNa-S ~4.0 kb transcripts, the transcripts with in-frame-stop codons, and CxNa-L_{v5} with in-frame-stop codons (Fig. 6). Comparing the transcripts with the full length ORFs in each of the three strains, even though the transcripts had undergone alternative splicing events the expression levels were similar, suggesting that the variants may have equivalent functional importance in the tissues and the mosquitoes. Indeed, the transcripts with in-frame stop codons were detected in both the S-Lab and HAmCq^{G0} mosquitoes, but at extremely low levels. The difference in the sodium channel expression between the CxNa-L and CxNa-S transcripts was particularly pronounced for S-Lab and HAmCq^{G0}, where the CxNa-S transcripts were expressed at levels more than 1000-fold lower than the CxNa-L sodium channel transcripts (Fig. 6a, b). In contrast, only about a 10-fold difference in expression between the CxNa-L and CxNa-S transcripts was identified in HAmCq^{G8} (Fig. 6c). This feature, plus the markedly higher expression in HAmCq^{G8}, might reflect their function in HAmCq^{G8}.

CxNa-L _v 1	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETGFGRKKKKKE	60
CxNa-L _v 2	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETVPGRKKKKKE	60
CxNa-L _v 3	MTDDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETGFGRKKKKKE	60
CxNa-S _v 1	MTDDLDRYLRE-RSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGE-----	48
exon3		
CxNa-L _v 1	IRYDDEDEDEGQPDPSTLEQGVPFVVRMQGSFPPELASTPLEDIDAFYANIKTFVVVSKG	120
CxNa-L _v 2	IRYDDEDEDEGQPDPSTLEQGVPFVVRMQGSFPPELASTPLEDIDAFYANIKTFVVVSKG	120
CxNa-L _v 3	IRYDDEDEDEGQPDPSTLEQGVPFVVRMQGSFPPELASTPLEDIDAFYANIKTFVVVSKG	120
CxNa-S _v 1	IRYDDEDEDEGQPDPSTLEQGVPFVVRMQGSFPPELASTPLEDIDAFYANIKTFVVVSKG	108
exon4 IS1		
CxNa-L _v 1	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTLGNCILMIMPSTPTVEST	180
CxNa-L _v 2	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTLGNCILMIMPSTPTVEST	180
CxNa-L _v 3	KDIFRFSATNASYVLDPFNPIRRVAIYILVHPLFSFFIITTLGNCILMIMPSTPTVEST	180
CxNa-S _v 1	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTLGNCILMIIPSTPTVEST	168
IS2 exon5 IS3		
CxNa-L _v 1	EVI FTGIYTFESAVKVMARGFILQPFTYLRLDAWNWLDVVI ALAYVTMGIDLGNL AALRT	240
CxNa-L _v 2	E-----YVTMGIDLGNL AALRT	197
CxNa-L _v 3	EVI FTGIYTFDQL*SDGARFHI TTVYLS*-RCMELVGLRSNSISICNYGYRFG*SRCIEN	239
CxNa-S _v 1	E-----	169
exon6 IS4 IS5		
CxNa-L _v 1	FRVLRAPKTVAIVPGLKTI VGAVIESVKNL RDVI I LTMFSLSVFALMGLQIYMGVLTQKC	300
CxNa-L _v 2	FRVLRALKTVAIVPGLKTI VGAVIESVKNL RDVI I LTMFSLSAFALMGLQIYMGVLTQKC	257
CxNa-L _v 3	TQGTSSQNSGHRSRSDHRRRCHRVRKESQRCDNFNNVFVVGVCFN GAADLHGRADAKV	299
CxNa-S _v 1	-----	
exon7 exon8		
CxNa-L _v 1	IKEFPTDGSWGNL THENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEEGYVCLQGF	360
CxNa-L _v 2	IKEFPTDGSWGNL THENWERHHSNDSNWYFSETGDTPVCGNSSGAGQCEEGYVCLQGF	317
CxNa-L _v 3	HQGVFDGRLVGDPPRELGAAPFERFQLVLFNRGHAPLR-QFVGCWPM*GRICMFTFRWR	359
CxNa-S _v 1	-----	
exon9 IP IS6		
CxNa-L _v 1	NPNYGYTSFDTFGWAFLSAFLRMTQDYWENLYQLVLR SAGPWHMLFFIV IIFLGSFYLVN	420
CxNa-L _v 2	NPNYGYTSFDTFGWAFLSAFLRMTQDYWENLYQLVLR SAGPWHMLFFIV IIFLGSFYLVN	377
CxNa-L _v 3	*SKLRVYKF*YFRMGIL ICLSSHDPGLLGDLYQLVLR SAGPWHMLFFIV IIFLGSFYLVN	419
CxNa-S _v 1	-----	
exon10		
CxNa-L _v 1	LILAIVAMSYDELQKRAEEEEAAEEEEALREAEAAAAAKQAKLEAHAAAAAAAAANPEIAKS	480
CxNa-L _v 2	LILAIVAMSYDELQKRAEEEEAAEEEEALREAEAAAAAKQAKLEAHAAAAAAAAANPEIAKS	437
CxNa-L _v 3	LILAIVAMSYDELQKRAEEEEAAEEEEALREAEAAAAAKQAKLEAHAAAAAAAAANPEIAKS	479
CxNa-S _v 1	-----	178
exon11		
CxNa-L _v 1	PSDFSCHSCEL FVGQEKGNDDNNKEKMSIRSEGLASLSLPGSPFNLRGRGRGSHQFTI	540
CxNa-L _v 2	PSDFSCHSYEL FVGQEKGNDDNNKEKMSIRSEGLASLSLPGSPFNLRGRGRGSHQFTI	522
CxNa-L _v 3	PSDFSCHSYEL FVGQEKGNDDNNKEKMSIRSEGLASLSLPGSPFNLRGRGRGSHQFTI	539
CxNa-S _v 1	-----	
exon12		
CxNa-L _v 1	RNGRGRFVGVP GSDRKLVLSTYLDAQEHLPYADDSNAVTPMSEENGSRHSSYTSHQSRI	600
CxNa-L _v 2	RNGRGRFVGVP GSDRKLVLSTYLDAQEHLPYADDSNAVTPMSEENGSRHSSYTSHQSRI	594
CxNa-L _v 3	RNGRGRFVGVP GSDRKLVLSTYLDAQEHLPYADDSNAVTPMSEENGSRHSSYTSHQSRI	599
CxNa-S _v 1	-----	
exon13		
CxNa-L _v 1	SYTSHGDLGGMTKESRLRSRTQRNTNHSIVPPANMAASAASVTGAGSGAPNMPYVDTNP	660
CxNa-L _v 2	SYTSHGDLGGMTKESRLRSRTQRNTDHSIVPPANMAASAASVTGAGSGAPNMSYVDTNH	654
CxNa-L _v 3	SYTSHGDLGGMTKESRLRSRTQRNTNHSIVPPARTWRPRRRR*RVPARAR-PTCPTSTP	658
CxNa-S _v 1	-----	
exon14 exon15		
CxNa-L _v 1	KGQQRDFDQSQDYTD DAKIKHNDNPFIEPSQTQTVVDMKDVMVLNDIEQAAGRHSRAS	720
CxNa-L _v 2	KGQQRDFDQSQDYTDHAGTIKHNDNPFIEPSQTQTVVDMKDVMVLNDIEQAAGRHSRAS	714
CxNa-L _v 3	TTRASSATLISPKTQIMLVK*NTTTLSSSLKPKP**KT*WC*NDIEQAAGRHSRAS	720
CxNa-S _v 1	-----	
exon16 IIS1		
CxNa-L _v 1	DHGEDDDEDGPTFKHKAAEFGMRMIDIFCVWDCWVWLKFQEWVSFIVDFPFVELFITLC	780
CxNa-L _v 2	DHGEDDDEDGPTFKDKAVEFGMRMIDIFCVWDCWVWLKFQEWVSFIVDFPFVELFITLC	782
CxNa-L _v 3	DHGEDDDEDGPTFKDKAVEFGMRMIDIFCVWDCWVWLKFQEWVSFIVDFPFVELFITLC	780

CxNa-L _v 3	IYMYLYFVFFIIIFGSFFTLNLFIVGVIIDNFNQKKKAGGSLEMFMTEQKKYINAMKKMG	1576
CxNa-S _v 1	IYMYLYFVFFIIIFGSFFTLNLFIVGVIIDNFNQKKKAGGSLEMFMTEQKKYINAMKKMG	775
	IVS1 exon30	
CxNa-L _v 1	SKKPLKAI PRPKWRPQAI VFEICTNKKFDMIIMLFMGNMLTMTLDHYKQTETFSAVLDY	1620
CxNa-L _v 2	SKKPLKAI PRPKWRPQAI VFEICTNKKFDMIIMLFMGNMLTMTLDHYKQTETFSAVLDY	1627
CxNa-L _v 3	SKKPLKAI PRPKWRPQAI VFEICTNKKFDMIIMLFMGNMLTMTLDHYKQTETFSAVLDY	1636
CxNa-S _v 1	SKKPLKAI PRPKWRPQAI VFEICTNKKFDMISMLFMGNMLTMTLDHYKQTETFSAVLDY	835
	IVS2 IVS3	
CxNa-L _v 1	LNMI FICIFSSSECLMKI FALRYHYFIEPWNLFDFVWVILSILGLVLSDLIEKYFVSPPTLL	1680
CxNa-L _v 2	LNMI FICIFSSSECLMKI FALRYHYFIEPWNLFDFVWVILSILGLVLSDLIEKYFVSPPTLL	1687
CxNa-L _v 3	LNMI FICIFSSSECLMKI FALRYHYFIEPWNLFDFVWVILSILGLVLSDLIESTSSRRCV	1697
CxNa-S _v 1	LNMI FICIFSSSECLMKI FALRYHYFIEPWNLFDFVWVILSILGLVLSDLIEKYFVSPPTLL	895
	IVS4 exon31 IVS5	
CxNa-L _v 1	RVVRVAKVGRVLRRLVKGAKGIR TLLFALAMSLPALFNICLLFLVMFIFAIFGMSFFMHV	1740
CxNa-L _v 2	RVVRVAKVGRVLRRLVQGPASG TLLFALAMSLPALFNICLLFLVMFIFAIFGMSFFMHV	1748
CxNa-L _v 3	WCAWPRSVGCCVSSRAP ^{Δ14} SGRCLRWPCRCRCSTSVCCSW*CSSSPSSECRSSCT*--	1756
CxNa-S _v 1	RVVRVAKVGRVLRRLVKGAKGIR TLLFALAMSLPALFNICLLFLVMFIFAIFGMSFFMHV	955
	IVP exon32	
CxNa-L _v 1	KDKSGLDDVYNFKTFGQSMILLFQMSTSAGWDGVL DGI INEEDCLPPDDDKGYPGNCGSA	1800
CxNa-L _v 2	KDKSGLDDVYNFKTFGQSMILLFQMSTSAGWDGVL DGI INEEDCLPPDNDKGYPGNCGSA	1808
CxNa-L _v 3	RTRAGWTTCTTSRRSARA*SCCFRCQRLRGGTVRWMVSSTRRTACRRI TTRVTPGTAGSA	1819
CxNa-S _v 1	KDKSGLGDVYNFKTFGQSMILLFQMSTSAGWDGVL DGI INEEDCLPPDNDKGYPGNCGSA	1015
	IVS6 exon33	
CxNa-L _v 1	TIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYIEIWQQFDPDG	1860
CxNa-L _v 2	TIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYIEIWQQFDPDG	1868
CxNa-L _v 3	SRTCWHIWSSVS*SLSTCTSLSFRI TRRPRRTCRV*--RTTRSTTCTTRLWQQFDPDG	1877
CxNa-S _v 1	TIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYIEIWQQFDPDG	1075
CxNa-L _v 1	TQYIRYDQLSDFLDVLEPPLQIHKPNKYKIISMDIPICRGDMMFCVDIILDALTKDFFARK	1920
CxNa-L _v 2	TQYIRYDQLSDLLERAGTAC ^{Δ17} FTNPNKYKIISMDIPICRGDMMFCVDIILDALAKDFFARK	1929
CxNa-L _v 3	TQYEVV ^{Δ16} RPVAVGLFRRAGTA ^{Δ18} ADSQTERVQDHL DGHSDLR-----RHDVLRGHSGRA	1930
CxNa-S _v 1	TQYIRYDQLSDFLDVLEPPLQIHKPNKYKIISMDIPICRGDMMFCVDIILDALTKDFFARK	1135
CxNa-L _v 1	GNPIEDSAEMGEVQQRPEVGYEPVSS TLWRQREEYCARLIQHAYRNFKERGGVGGGGGG	1980
CxNa-L _v 2	GNPIEDSAEMGEVQQRPEVGYEPVSS TLWRQREEYCARLIQHAYRNFKERGGVGGGGGG	1989
CxNa-L _v 3	DEGLLRAEGPPDRGQCRDG*--GFAAAGRRLRAVDVVAPTGFVLRVAVDTARVPEL*GT	1989
CxNa-S _v 1	GNPIEDSAEMGEVQQRPEVGYEPVSS TLWRQREEYCARLIQHAYRNFKERGGVGGGGGG	1195
CxNa-L _v 1	GGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGS IAGGGSQANLGPPSPKESPDG	2040
CxNa-L _v 2	GGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGS IAGGGSQANLGAPPKESPDG	2049
CxNa-L _v 3	RRCWWR ^{Δ19} RRRWRWRRRWR ^{Δ19} RRR*HRRRCL**RARDRESRRG---QRRWPQHRGRRLP--	2044
CxNa-S _v 1	GGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGS IAGGGSQANLGPPSPKESPDG	1255
CxNa-L _v 1	NNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2082
CxNa-L _v 2	NNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2091
CxNa-L _v 3	--GSPRAAVTQRIARWQSSRSNGR----PSRK*WICN*	2078
CxNa-S _v 1	NNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	1297

Figure 2. Alignment of deduced amino acid transcript sequences of the *para*-type sodium channel transcripts (Cx-Na) in S-Lab *Culex* mosquitoes. Transmembrane segments are indicated on the line over the sequence. Exons are indicated above the sequence with solid triangle symbols to indicate the boundaries between exons. The differences in the aa sequences are indicated by shading. A stop codon is marked by an asterisk (*). -- indicates deletions. Δ indicates insertions with the sequences of Δ1: P; Δ2: VSEITRTTAPTATAAGTAKARKVSA; Δ3: GAIIVPVYYANL; Δ4: *I; Δ5: VSVYYFPT; Δ6: GPFR; Δ7: E; Δ8: *; Δ9: **SSR**VR; Δ10: *HCQY; Δ11: *; Δ12: G; Δ13: R; Δ14: R; Δ15: RRR; Δ16: T; Δ17: R; Δ18: A; Δ19: G; Δ20: **

	exon1	
CxNa-L _v ,4	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETGFGRKKKKRE	60
CxNa-L _v ,5	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGE-----	49
CxNa-L _v ,6	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGE-----	49
CxNa-S _v ,2	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGE-----	49
CxNa-S _v ,3	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGE-----	49
	exon3	
CxNa-L _v ,4	IRYDDEDEDEGPPRADSTLEQGVPIPVVMQGSFPPELASTPLEDIDAFYSNIKTFVVVSKG	120
CxNa-L _v ,5	IRYDDEDEDEGPPADSTLEQGVPIPVVMQGSFPPELASTPLEDIDAFYSNIKTFVVVSKG	109
CxNa-L _v ,6	IRYDDEDEDEGPPADSTLEQGVPIPVVMQGSFPPELASTPLEDIDAFYSNIKTFVVVSKG	109
CxNa-S _v ,2	IRYDDEDEDEGPPADSTLEQGVPIPVVMQGSFPPELASTPLEDIDAFYSNIKTFVVVSKG	109
CxNa-S _v ,3	-----	
	exon4	IS1
CxNa-L _v ,4	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTTILGNCILMIMPSTPTVEST	180
CxNa-L _v ,5	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTTIRGNCILMIMPSTPTVEST	169
CxNa-L _v ,6	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTTILGNCILMIMPSTPTVEST	169
CxNa-S _v ,2	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIITTTILGNCILMIMPSTPTVEST	169
CxNa-S _v ,3	-----	
	IS2	exon5
	IS3	
CxNa-L _v ,4	EVIFTGIYTFESAVKVMARGFIIQPFYYLRDAWNWLDVVI ALAYVTMGIDLGNLAALRT	240
CxNa-L _v ,5	EVIFTGIYTFESAVKVMARGFIIQPFYYLRDAWNWLDVVI ALAYVTMGIDLGNLAALRT	229
CxNa-L _v ,6	EVIFTGIYTFESAVKVMARGFIIQPFYYLRDAWNWLDVVI ALAYVTMGIDLGNLAALRT	229
CxNa-S _v ,2	EVIFTGIYTFESAVKVMARGFIIQPFYYLRDAWNWLDVVI ALAYVTMGIDLGNLAALRT	229
CxNa-S _v ,3	-----	
	IS4 exon6	IS5
CxNa-L _v ,4	FRVLRALKTVAIIVPGLKTI VGAVIESVKNLRDVI IILTMFSLSVFALMGLQIYMGVLTQKC	300
CxNa-L _v ,5	FRVLRALKTVAIIVPGLKTI VGAVIESVKNLRDVI IILTMFSLSVFALMGLQIYMGVLTQKC	289
CxNa-L _v ,6	FRVLRALKTVAIIVPGLKTI VGAVIESVKNLRDVI IILTMFSLSVFALMGLQIYMGVLTQKC	289
CxNa-S _v ,2	FRVLRALKTVAIIVPGLKTI VGAVIESVKNLRDVI IILTMFSLSVFALMGLQIYMGVLTQKC	289
CxNa-S _v ,3	-----	
	exon7	exon8
CxNa-L _v ,4	IKEFPFDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEE GYVCLQGFGD	360
CxNa-L _v ,5	IKEFPFDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEE GYVCLQGFGD	349
CxNa-L _v ,6	IKEFPFDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEE GYVCLQGFGD	349
CxNa-S _v ,2	IKEFPFDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEE GYVCLQGFGD	349
CxNa-S _v ,3	-----	
	exon9	IP
	IS6	
CxNa-L _v ,4	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLVLR SAGPWHMLFFIVII FLGSFYLVN	420
CxNa-L _v ,5	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLVLR SAGPWHMLFFIVII FLGSFYLVN	409
CxNa-L _v ,6	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLVLR SAGPWHMLFFIVII FLGSFYLVN	409
CxNa-S _v ,2	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLVLR SAGPWHMLFFIVII FLGSFYLVN	409
CxNa-S _v ,3	-----	
	exon10	exon11
CxNa-L _v ,4	LILAI VAMS YDELQKRAEEEEAAEE EALREAE EAAAAAKQAKLEAHAAAAAAAAANPEIAKS	480
CxNa-L _v ,5	LILAI VAMS YDELQKRAEEEEAAEE GALREAE EAAAAAKQAKLEAHAAAAAAAAANPEIAKS	469
CxNa-L _v ,6	LILAI VAMS YDELQKRAEEEEAAEE EALREAE EAAAAAKQAKLEAHAAAAAAAAANPEIAKS	469
CxNa-S _v ,2	LILAI VAMS YDELQKRAEEEEAAEE EALREAE EAAAAAKQAKLEAHAAAAAAAAANPEIAKS	469
CxNa-S _v ,3	-----	
CxNa-L _v ,4	PSDFSCHSYELFVGQEKGNDDNNSEKMSIRSEGLESA SLSLPGSPNLRGRGRGSHQFTI	540
CxNa-L _v ,5	PSDFSCHSYELFVGQEKGNDDNNKEKMSIRSEGLESA SLSLPGSPNLRGRGRGSHQFTI	554
CxNa-L _v ,6	PSDFSCHSYELFVGQEKGNDDNNKEKMSIRSEGLESA SLSLPGSPNLRGRGRGSHQFTI	554
CxNa-S _v ,2	PSDFSCHSYELFVGQEKGNDDNNKEKMSIRSEGLESA SEITRTTAPTATAAGTAKARKVS	529
CxNa-S _v ,3	-----	
	exon12	
CxNa-L _v ,4	RNGRGRFVGVPGSDRKPVLVLS TYLDAQEHLPHYADDSNAVTPMSEENGAI IVPVYYANLGS	600
CxNa-L _v ,5	RNGRGRFVGVPGSDRKPVLVLS TYLDAQEHLPHYADDSNAVTPMSEENGAI IVPVYYANLGS	614
CxNa-L _v ,6	RNGRGRFVGVPGSDRKPVLVLS TYLDAQEHLPHYADDSNAVTPMSEENGAI IVPVYYANLGS	614
CxNa-S _v ,2	A-----	530
CxNa-S _v ,3	-----	
	exon13	

CxNa-L ₄	RHSSYTSHQSRISYTSHGDDLGGMTKESRLRSRTQRNTNHSIVPPANMAASAASVTGAGS	660
CxNa-L ₅	RHSSYTSHQSRISYTSHGDDLGGMTKESRLRSRTQRNTNHSIVPPANMAASAASVTGAGS	674
CxNa-L ₆	RHSSYTSHQSRISYASHGDDLGGMTKESRLRSRTQRNTNHSIVPPANVAASAASVTGAGS	674
CxNa-S ₂	-----	
CxNa-S ₃	-----	
	exon14	
CxNa-L ₄	GAPNMSYVDTNHKGQQRDFDQSQDYTDAGKI KHNDNPFIEPSQTQTVVDMKDVMLNDI	720
CxNa-L ₅	GAPNMSYVDTNHKGQQRDFDQSQDYTDAGKI KHNDNPFIEPSQTQTVVDMKDVMLNDI	734
CxNa-L ₆	GAPNMSYVDTNHKGQQRDFDQSQDYTDAGKI KHNDNPFIEPSQTQTVVDMKDVMLNDI	734
CxNa-S ₂	-----	
CxNa-S ₃	-----	
	exon15 exon16	
CxNa-L ₄	TEQAAGRHS RASDHGVS VY YFP TEDDDE DGP TFKDKAVEFGMRMI DI FCVWDC CWVWLKF	780
CxNa-L ₅	TEQAAGRHS RASDHGVS VY YFP TEDDDE DGP TFKDKAVEFGMRMI GI FCVWDC CWVWLKF	794
CxNa-L ₆	TEPAAGRHS RASDHGVS VY YFP TEDDDE DGP TFKDKAVEFGMRMI DI FCVWDC CWVWLKF	794
CxNa-S ₂	-----	
CxNa-S ₃	-----RTTTRTVRRSRTRSSSGCG*STSSACGTAAGCGSKS	86
	IIS1 IIS2	
CxNa-L ₄	QEWGSFIVFDPFVELFITLTCIVVNTLFMALDHHDMNPDMERALKSGNYFFTATFAIEATM	840
CxNa-L ₅	QEWVSFIVFDPFVELFITLTCIVVNTLFMALDHHDMNPDMERALKSGNYFFTATFAIEATM	854
CxNa-L ₆	QEWVSFIVFDPFVELFITLTCIVVNTLLMALDHHDMNPDMERALKSGNYFFTATFAIEATM	854
CxNa-S ₂	-----	
CxNa-S ₃	SSRSGCPLSCSTRSSSCSSRSASWSTRCSWRSTTTT*TRTWSGRSRAVTTSSRRRSRGQR	146
	exon17 IIS3 IIS4	
CxNa-L ₄	KLIAMSPKWFQEGWNI FDFI IVALS LLEL GLEGVQGLSVLRSFRLLRVFKLAKSWPTLN	900
CxNa-L ₅	KLIAMSPKWFQEGWNI FDFI IVALS LLEL GLEGVQGLSVLRSFRLLRVFKLAKSWPTLN	914
CxNa-L ₆	KLIAMSPKWFQEGWNI FDFI IVALS LLEL GLEGVQGLSVLRSFRLLRVFKLAKSWPTLN	914
CxNa-S ₂	-----	
CxNa-S ₃	R*S*SR*APSGTSRKVGTFSI SSSWPFRCSSSVXRAFRCQYVHVSVCFCSS*QSRSPR	206
	exon18 IIS5	
CxNa-L ₄	LLISIMGRTVGALGNLTFVLCIIIFI FAVMGMLFGKNYTDNVDRFPDKDLPRWNFTDFM	960
CxNa-L ₅	LPISIMGRTVGALGNLTSVLCIIIFI FAVMGMLFGKNYTDNVDRFPDKDLPRWNFTDFM	974
CxNa-L ₆	LLISIMGRTMGALGNLTFVLCIIIFI FAVMGMLFGGNYTDNVDRFPDKDLPRWNFADFM	974
CxNa-S ₂	-----	
CxNa-S ₃	*TYSFPSWAERWAR*VI*RLCSALSSSSLP*WGCSARSRTTSTTWTASRTRTCHGGTLVT	266
	IIP Exon1 IIS6	
CxNa-L ₄	HSEMFIVFRVLCGEWIESMWDCLVGDVSCIPFFLATVVI GNFVVLNLFLALLLSNFGSSS	1020
CxNa-L ₅	HSEMFIVFRVLCGEWIESMWDCLVGDVSCIPFFLATVVI GNFVVLNLFLALPLSIFGSSS	1034
CxNa-L ₆	HSEMFIVFRVLCGEWIESMWDCLVGDVSCIPFFLATVVI GNFVVLNLFLALLLSNFGSSS	1034
CxNa-S ₂	-----	
CxNa-S ₃	SCTHS*SCSGCCAASGSNPGTACWWATCPAFRSSWPP***EI*SFLTFS*PCFCPTPRV	326
	exon20	
CxNa-L ₄	LSAPTADNETNKIAEAFNRISRFSNWIKANIAAALKFVKNKLT SQIASVQPAEHGENERE	1080
CxNa-L ₅	LSAPTADNETNKIAEAFNRISRFSNWIKANIAAALKFVKNKLT SQIASVQPAD-----	1087
CxNa-L ₆	LSAPTADNETNKIAEAFNRDIALQLDQG-EHRGRAQVREKQVKNKPCVRAARR*-----	1088
CxNa-S ₂	-----	
CxNa-S ₃	CRRPQPTTKRTRSPRRSTGYRASPTGSRRTSRPRSSS*KTS*QARLRPCSE-----	377
	exon21ii exon22	
CxNa-L ₄	LTPDDILADGLLKKGVKEHNQLEVAIGDGMFTIHGDLKNGKKNKQLMNNNSKVI GNSIS	1140
CxNa-L ₅	----DILADGLLKKGVKEHNQLEVAIGDGMFTIHGDLKNGKKNKQLMNNNSKVI GNSIS	1143
CxNa-L ₆	AAQPSQLDMERRQRGMSMYICRAW*K*AGINSR*HPGRREKGRQGAQPAGGDRRRDGVY	1150
CxNa-S ₂	-----	
CxNa-S ₃	--PDDILADGLLKKGVKEHNQLEVAIGDGMFTIHGDPKNKNGKKNKQLMNNNSK-----	428
	exon23	
CxNa-L ₄	NHQDNKLEHELNHRGMSLQDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASKE	1200
CxNa-L ₅	NHQDNKLEHELNHRGMSLQDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASKE	1203
CxNa-L ₆	DTRPQEQGQEEQAADQFQGR*YHAYKVLWQSQESPLQGRKPGQCRNAGGRRKARRQQG	1212
CxNa-S ₂	-----	
CxNa-S ₃	-----DDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASKE	469
	exon24	

CxNa-L _v 4	DLGI DEELDDECEGEEGPLDGE MI IHAEEDEVI EDAPADC FPDNCYKRFPALAGDDDAF	1260
CxNa-L _v 5	DLGI DEELDDECEGEEGPLDGE MI IHAEEDEVI EDAPADC FPDNCYKRFPALAGDDDAF	1263
CxNa-L _v 6	GPRN*RRTRRRVRG*GGSAGRGN DHPGRGRSDRGRTRGRLLPGQLLQAVFGAGRRRRRAV	1273
CxNa-S _v 2	-----	
CxNa-S _v 3	DLGI DEELDDECEGEEGPLDGE MI IHAEEDEVI EDAPADC FPDNCYKRFPALAGDDDAF	529
	IIIS1 exon25 IIIS2	
CxNa-L _v 4	WQGWGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLPHRPILQDVLYYMDRI FT	1320
CxNa-L _v 5	WQGWGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLPHRPILQDVLYYMDRI FT	1323
CxNa-L _v 6	L AGLGQPAAQDVPADREQVLRDGRHDDPAEGPGRGCAPATPTNPAGRFVLHGQD- IHG	1333
CxNa-S _v 2	-----	
CxNa-S _v 3	WQGWGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLPHRPILQDVLYYMDRI FT	589
	IIIS3 exon26 IIIS4	
CxNa-L _v 4	VIFFLEMLIKWLALGFRVYFTDAWCWLDFTIIVM ^{Δ5} SLINFVASLCGAGGIQAFKTMRTLRA	1380
CxNa-L _v 5	VIFFLEMLIKWLALGFRVYFTNAWCWLDFTIIVM ^{Δ5} SLINFVASLCGAGGIQAFKTMRTLRA	1376
CxNa-L _v 6	DLFFRDVDQVVGAR-LPGVLYERLVLARFHHCDGVLNQLRGFTLWSGWYSSIQNYANS*G	1392
CxNa-S _v 2	-----	
CxNa-S _v 3	VIFFLEMLIKWLALGFRVYFTNAWCWLDFTIIVM ^{Δ5} SLINFVAIWGAAD-IPAFRSMRTLRA	649
	exon27 IIIS5	
CxNa-L _v 4	LRPLRAMSRMQGMRVVVNALVQAIPSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTN	1440
CxNa-L _v 5	LRPLRAMSRMQGMRVVVNALVQAIPSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTN	1436
CxNa-L _v 6	TASATCHVPYAGYEGCRQCIGTGYTVHLQRVIGVFDLLVDFRHHGRPAVCRKVLQVRRHE	1451
CxNa-S _v 2	-----VVVNALVQAIPSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTN	576
CxNa-S _v 3	LRPLRACL ^{Δ5} SLGGHESCRQCIGTGYTVHLQRVIGVFDLLVDFRHHGRPAVCRKVLQVRRHE	709
	exon28 IIP	
CxNa-L _v 4	KATLSHEIIPDVNACIAENYTWENSPMNF ^{Δ5} DHV GKAYLCLFQVATFKGWIQIMNDAIDSRD	1500
CxNa-L _v 5	KTLSHEIIPDVNACIAENYTWENSPMNF ^{Δ5} DHV GKAYLCLFQVATFKGWIQIMNDAIDSRD	1496
CxNa-L _v 6	QDDTVARDHPGRERVHRGELHLGELPDEL*PRGEGLPV FVPG----GHVQGM ^{Δ5} DPDRERR	1511
CxNa-S _v 2	KTLSHEIIPDVNACIAENYTWENSPMNF ^{Δ5} DHV GKAYLCLFQVATFKGWIQIMNDAIDSRD	636
CxNa-S _v 3	QDDTVARDHPGRERVHRGELHLGELPDEL*PRGEGLPV FVPGGHVQGM ^{Δ5} DPDHERRDLAG	769
	IIIS6 Exon29	
CxNa-L _v 4	IGKQPIRETNIYMYLYFVFFII FGSFFTLNLFIGVI IDNFNEQKKRAGGSLEMFMTEDQK	1560
CxNa-L _v 5	IGKQPIRETNIYMYLYFVFFII FGSFFTLSLFIGVI IDNFNEQKKKAGGSLEMFMT ^{Δ5} EGQK	1556
CxNa-L _v 6	RLARHWKAAHPRNQHLHLVLCV ^{Δ5} LHHLRIVLHAEPLHRCHY*QL*---RTEEEGWGIARD	1567
CxNa-S _v 2	IGKQPIRETNIYMYLYFVFFII FGSFFTLNLFIGVI IDNFNEQKKKAGGSLEMFMTEDQK	696
CxNa-S _v 3	HRKAAHPRNQHLHLVLCV ^{Δ5} LHHLRIVLHAEPLHRCHY*QL* ^{Δ5} RTEEEGWGIARDVYDGGLK	829
	exon30 IVS1	
CxNa-L _v 4	KYYNAMKMGSKKPLKAI PRPKWRPQAI VFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQ	1620
CxNa-L _v 5	KYYNAMKMGSKKPLKAI PRPKRRPQAI VFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQ	1616
CxNa-L _v 6	VYDGGPKKVLQRNEEDGLEEATEGHSAAQVATTSNSVRNLHKQKVRHDHVVHRLQHVD	1624
CxNa-S _v 2	KYYNAMKMGSKKPLKAI PRPKWRPQAI VFEICTNKSST*SSCCSSASTC* ^{Δ5} R* ^{Δ5} RWITTSR	756
CxNa-S _v 3	KVLQRNEEDGLEEATEGHSAAQVATTSNSVRNLHKQKVRHDHVVHRLQHVD ^{Δ5} DAGSLQA	889
	IVS2 IVS3	
CxNa-L _v 4	TETFSAVLDYLNMI FICIFSSSECLMKI FALRYHYFIEPWNLDFV ^{Δ5} VVILSILGLVLSDLI	1680
CxNa-L _v 5	TGTFSAVLDYLNMI FICIFSSSECLMKI FALRYHYFIEPWNLDFV ^{Δ5} VVILSILGLVLRDLI	1676
CxNa-L _v 6	G---AGSLQAVGHVQRGAGLPEHDLHLYLQ*---RVSD ^{Δ5} EDLRAALPLLYRTVEPVRFR	1684
CxNa-S _v 2	RKRSARCWTT*T*SSSVSSVASV**RSSRCATTTLSNRGTCSISSSSCFWAWC*AT* ^{Δ5} S	816
CxNa-S _v 3	DGNVQRGAGLPEHDLHLYLQ*RVSD ^{Δ5} EDLRAALPLLYRTVEPVRFRRRHPVHFGPGAERP	949
	exon31 IVS4 IVS5	
CxNa-L _v 4	EKYFVSP ^{Δ5} TLLRVVRVAKVGRVLRVLKGA ^{Δ5} KGIRTLFALAMSLPALFNICLLLFLVMFIFA	1740
CxNa-L _v 5	EKYFVSP ^{Δ5} TLLRVVRVAKVGRVLRVLKGA ^{Δ5} KGIRTLFALAMSLPALFNICLLLFLVMFIFA	1735
CxNa-L _v 6	HPVHFGPGAERPDR-----EVLRLADAAPCGARGQGRSGAASRQGRQGHPDVAVCAGHVAA	1738
CxNa-S _v 2	KSTSSRRRCSVWCAWPRSVGCCVSSRAPRASGRCLRWPCRCRCRSTSVCCCSW*CP ^{Δ5} SSE	876
CxNa-S _v 3	RKVLRLADAAPCGARGQGRSGAASRQGRQGHPDVAVCAGHVAAAGAVQHLSAAVPGDVHLR	1009
	IVP exon32	
CxNa-L _v 4	IFGMSFFMHVKDKSGLDDVYNFKTFGQSMILLFQ ^{Δ5} MSTSAGWDGVL ^{Δ5} DGIINEEDCLPPDND	1800
CxNa-L _v 5	IFGMSFFMHMKDKSGLDGVYNFKTFGQSMILLFQ ^{Δ5} MSTSAGWDGVL ^{Δ5} DGIINEEDCLPPDND	1795
CxNa-L _v 6	GAVQHLSAAVPGDVHLRHLWDVVLHAR-----EGQERAGRRVQLQDVREHDPVSDVN	1794
CxNa-S _v 2	SSGCRSSCT* ^{Δ5} RTRAGWTTCTTSRRSARA* ^{Δ5} SCCFRCQRLRGGTVCWMVSS ^{Δ5} TRTACRRIT	936

CxNa-S _v 3	HLRNVVLHAREGQERAGRRLVQLQDVRPEHDPVSDVNVCGVGRGAGWYHQRGGLPAAGYR	1069
	IVS6	exon33
CxNa-L _v 4	KGYPGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLMDDYDMYY	1860
CxNa-L _v 5	KGYPGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDYDMYY	1855
CxNa-L _v 6	VCWVGRGAGWYHQRGGLLAAG*-----RQGLPRELVRGDDRHHPA	1848
CxNa-S _v 2	RVTRGTAGRRRSASRTCWRIWSSVS*SLSTCTSLSFSRITRRPRRTCRRV*RTTTTTCTT	996
CxNa-S _v 3	QGLPRELVRGDDRHHPAGISGHQFPDRYQHVHRCHSRELLAGHGGRAGGSDGRRLRHVL	1129
CxNa-L _v 4	EIWQQFDPDGTQYIRYDQLSDFLDVLEPPLQIHKPNKYKIIISMDIPICRGDMMFCVDILD	1920
CxNa-L _v 5	EIWQQFDPDGTQYIRYDQLSDFLDVLEPPLQIHKPNKYKIIISMDIPICRGDMMFCVDILD	1915
CxNa-L _v 6	GISGHQFPDRYQHVHRCHPRELLAGHGGRAGGSDGRRLRHVLRDLAAVRSGRYAVHPVRF	1889
CxNa-S _v 2	RSGSSSIRTVRSTSGTTSCRTFWTCRNRRCRFTNRTSTRSSRWTFRSVAAT*CSAWTFWT	1056
CxNa-S _v 3	RDAAVRSGRYAVHPVPAVGLFGRAGTAAADSQTEQVQDHLDGHSDLRHRHDVLRGHSG	1189
CxNa-L _v 4	ALTKDFFARKGNPIEDSAEMGEVQQRPEDEVGYEPVSSTLWRQREEYCARLIQHAYRNFKE	1980
CxNa-L _v 5	ALTKDFFARKGNPIEDSAEMGEVQQRPEDEVGYEPVSSTLWRQREEYCARLIQHAYRNFKE	1975
CxNa-L _v 6	AVG--LFGFRAGTAAADS-QTEQVQDHLD-----GHSDSLRS	1921
CxNa-S _v 2	R*RRSSRGRSTRSRTVPRWVRSSSGRTRSVTSRFRRCGANGRSTARG*YSTRGTGLRN	1116
CxNa-S _v 3	RADEGLLRAEGQPDRCRDG*GPAAAGRRLRAGFVDVAVPTGGVLRVAVDTARVPEL*G	1249
CxNa-L _v 4	RGGVGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGSIAGGGSQANLG	2040
CxNa-L _v 5	RGGVGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGDSSIAGGGSQANLG	2035
CxNa-L _v 6	RHDVLRGHSGRADEGLLRAEGQ---PDRGQCRDG*-----GPAAAGRRLRAGFVDVAVP	1973
CxNa-S _v 2	EAVLVAAAAVEVVEEVVAKVPEMPTPMPVITSPGSGVPARSAVAAAAPAEAPRLT*AA	1176
CxNa-S _v 3	TRRCWRRRRRWRWRRRRWRRRCRR*HRRRCL**RARDRESRRGQRRWRQHRRRRLPG*PR	1309
CxNa-L _v 4	PPSPKESPDGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2092
CxNa-L _v 5	PPSPKESPDGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2095
CxNa-L _v 6	TGGVLRVAVDTTRVPEL*----GTRRCWRRRRRWRWRRRRRCRR*HRRRCL**	2021
CxNa-S _v 2	RLTQRIVRWQ**SSRSSNGRPSRK*WICN*	1205
CxNa-S _v 3	AAVTQRIARWQ**SSRSSNGRPSRK*WICN*	1339

Figure 3. Alignment of deduced amino acid transcript sequences of the *para*-type sodium channel retranscripts (Cx-Na) in HAmCq⁶⁰ *Culex* mosquitoes. Transmembrane segments are indicated on the line over the sequence. Exons are indicated above the sequence with solid triangle symbols to indicate the boundaries between exons. The differences in the aa sequences are indicated by shading. A stop codon is marked by an asterisk (*). - indicates deletions. Δ indicates insertions with the sequences of Δ1: VSEITRTTAPTATAAGTAKARKVSA; Δ2: AA; Δ3: R; Δ4: *F; Δ5: L; Δ6: G.

	exon1	exon2	
CxNa-L _v 7	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETGFGRK KKKKE	60	
CxNa-L _v 8	MTDDLDSISEEERSLFRPFTRESLLAIEERIANEQAKQRELEKKRAEGETGFGRK KKKKE	60	
CxNa-S _v 4	MTDDLDSISEEERSLFRPFARESLLVIEERIANEQAKQRELEKKRAEGETGFGRK KKKKE	60	
CxNa-S _v 5	MTEDLDSISEEERSLFRPFTRESLLVIEERIANEQAKQRELEKKRAEGETGFGRK KKKKE	60	
	exon3		
CxNa-L _v 7	IRYDDEDEDEGQPDPSTLEQGVPPIVVRMQGSFPPELASTPLEDIDAFYSNIKT FVVVSKG	120	
CxNa-L _v 8	IRYDDEDEDEGQPDPSTLEQGVPPIVVRMQGSFPPELASTPLEDIDAFYSNIKT FVVVSKG	120	
CxNa-S _v 4	IRYDDEDEDEGQPDPSTLEQGVPPIVVRMQGSFPPELASTPHEDIDAFYSNIKT FVVVSKG	120	
CxNa-S _v 5	IRYDDEDEDEGQPDPSTLEQGVPPIVVRMQGSFPPELASTPLEDIDAFYSNIKT FVVVSKG	120	
	exon4	IS1	
CxNa-L _v 7	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIIITTLGNCILMIMPSTPTVEST	180	
CxNa-L _v 8	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIIITTLGNCILMIMPSTPTVEST	180	
CxNa-S _v 4	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIIITTLGNCILMIMPSTPTVEST	180	
CxNa-S _v 5	KDIFRFSATNALYVLDPFNPIRRVAIYILVHPLFSFFIIITTLGNCILMIMPSTPTVEST	180	
	IS2	exon5	IS3
CxNa-L _v 7	EVIFTGIYTFESAVKVMARGFILQPFTYL RD AWN W DFVVI AL AYVTMGID LG NLAALRT	240	
CxNa-L _v 8	EVIFTGIYTFESAVKVMARGFILQPFTYL RD AWN W DFVVI AL AYVTMGID LG NLAALRT	240	
CxNa-S _v 4	E-----	181	
CxNa-S _v 5	E-----	181	
	exon6	IS4	IS5
CxNa-L _v 7	FRVLRALKTV AV IVPGLKTVGAVTESVKNLRDVIILTMFSLSVFALMGLQIYMGVLTQKC	300	
CxNa-L _v 8	FRVLRALKTV AV IVPGLKTVGAVTESVKNLRDVIILTMFSLSVFALMGLQIYMGVLTQKC	300	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
	exon7	exon8	
CxNa-L _v 7	IKEFPTDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEEGYVCLQGFGD	360	
CxNa-L _v 8	IKEFPTDGSWGNLTHENWERHHSNDSNWYFSETGDTPLCGNSSGAGQCEEGYVCLQGFGD	360	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
	exon9	IP	IS6
CxNa-L _v 7	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLV LR SAGPWHMLFFIVIIIFSGSFYLV D	420	
CxNa-L _v 8	NPNYGYTSFDTFGWAFLSAFRLMTQDYWENLYQLV LR SAGPWHMLV F IVIIIFLGSFYLV N	420	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
	exon10	exon11	
CxNa-L _v 7	LILAI V AMSYDELQKRAEEEEAAEEALRE A EEEEAAAKQARLEAHAAAAAANPEIAKS	480	
CxNa-L _v 8	LILAI V AMSYDELQKRAEEEEAAEEALRE A EEEEAAAKQAELEAHAAAAAANPEIAKN	480	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
CxNa-L _v 7	PSDFSCHSYELFVGQEKGNDDNNKEKMSIRSEGLSVSEITR T TAPTATAAGTAKARKVS	540	
CxNa-L _v 8	PSDFSCHSYELFVGQEKGNDDNNKEKMSIRSEGLSVSEITR T TAPTATAAGTAKARKVS	540	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
	exon12		
CxNa-L _v 7	AASLSLPGSPFNLRGRGRGSHQFTIRNGRGRFVGVPGSDRKPLVLSTYLDAQEHL P YADD	600	
CxNa-L _v 8	AASLSLPGSPFNLRGRGRGSHQFTIRNGRGRFVGVPGSDRKPLVLSTYLDAQEHL P YADD	600	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
CxNa-L _v 7	SNAVTPMSEENGSRHSSY T SHQSRISY T SHGDLGGMTKESRLRSRTQRNTNHSIVPPAN	660	
CxNa-L _v 8	SNAVTPMSEENGSRHSSY T SHQSRISY T SHGDLGGMTKESRLRSRTQRNTNHSIVPPAN	672	
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
	exon13	exon14	
CxNa-L _v 7	MAASAASVTGAGSGAPNMSYVD T NHKGQQRDFDQSQDY T DDAGKIKHNDNPFIEPSQTQT	720	
CxNa-L _v 8	MAASAASVTGAGSGAPNMSYVD T NHKGQQRDFDQSQDY T DDAGKIKHNDNPFIEPSQTQT	732	
CxNa-S _v 4	-----		

CxNa-S _v 5	-----		
		exon15	exon16
CxNa-L _v 7	VVDMKDVMLNDIIIEQAAGRHSRASDHGVSYYFPTEDDDEDGPTLKDKAVEFGMRMIDI		780
CxNa-L _v 8	VVDMKDVMLNDIIIEQAAGRHSRASDHGVSYYFPTEDDDEDGPTLKDKAVEFGMRMIDI		792
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
		IIS1	
CxNa-L _v 7	FCVWDCCWVWLKQEWVSFIVFDPFVELFITLTCIVVNTLFMALDHHDMNPDMERALKSGN		840
CxNa-L _v 8	FCVWDCCWVWLKQEWVSFIVFDPFVELFITLTCIVVNTLFMALDHHDMNPDMERALKSGN		852
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
		IIS2	exon17
		IIS3	IIS4
CxNa-L _v 7	YFFTATFAIEATMKLIAMSPKWFQEGWNI FDFIIVALSLLELGLGVQGLSVLRSFRLL		900
CxNa-L _v 8	YFFTATFAIEATMKLIAMSPKWFQEGWNI FDFIIVALSLLELGLGVQGLSVLRSFRLL		912
CxNa-S _v 4	-----		
CxNa-S _v 5	-----		
		exon18	IIS5
CxNa-L _v 7	RVFKLAKSWPTLNLLISIMGRIMGALGNLTFVLCIIIFI FAVMGMQLFGKNYIDNVDRFP		960
CxNa-L _v 8	RVFKLAKSWPTLNLLISIMGRIMGALGNLTFVLCIIIFI FAVMGMQLFGKNYIDNVDRFP		972
CxNa-S _v 4	-----		188
CxNa-S _v 5	-----		188
		exon19	IIP
		IIS6	
CxNa-L _v 7	DKDLPRWNFTDFMHSFMIVFRVLCGEWIESMWDCLVGDVSCIPFFLATVVIIGNFVVLNL		1020
CxNa-L _v 8	DKDLPRWNFTDFMHSFMIVFRVLCGEWIESMWDCLVGDVSCIPFFLATVVIIGNFVVLNL		1032
CxNa-S _v 4	QGPA TVELHRLHALIHDRVPGAVRRVDRIHVGLHAGGRRVLHSVLLGHRSDRKFCRSYTL		248
CxNa-S _v 5	QGPA TVVNPRLHALIHDRVPGAVRRV-IESMWDCLVGDVSCIPFFLATVVIIGNFVVLNL		247
		exon20	
CxNa-L _v 7	FLALLLSNFGSSLSAPTADNETNKIAEAFNRISRFSNWI KANIAAALKFVKNKLT SQIA		1080
CxNa-L _v 8	FLALLLSNFGSSLSAPTADNETNKIAEAFNRISRFSNWI KANIAAALKFVKNKLT SQIA		1092
CxNa-S _v 4	FLALLLSNFGSSLSAPTAGNETNKIAEAFNRISRFSNWI KANIAAALKFVKNKLT SQIA		308
CxNa-S _v 5	FLALLLSNFGSSLSAPTADNETNKIAEAFNRISRFSNWI KANIAAALKFVKNKLT SQIA		307
		exon21i	exon21ii
CxNa-L _v 7	SVQPAGKGVCPICISAEHGENELELTPDDILADGLLKKGVKEHNQLEVAIGDGMEFTIHGD		1140
CxNa-L _v 8	SVQPA-----EHGENELELTPDDILADGLLKKGVKEHNQLEVAIGDGMEFTIHGD		1142
CxNa-S _v 4	SVQPAGKGVCPICISAEHGENELELTPDDILADGLLKKGVKEHNQLEVAIGDGMEFTIHGD		381
CxNa-S _v 5	SVQPAGKGVCPICISAEHGENELELTPDDILADGLLKKGVKEHNQLEVAIGDGMEFTIHGD		380
		exon22	exon23
CxNa-L _v 7	LKNKGKKNKQLMNNSKDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASREDLG		1200
CxNa-L _v 8	LKNKGKKNKQLMNNSKDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASKEDLG		1202
CxNa-S _v 4	LKNKGKKNKQLMNNSQDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRGASKEDLG		467
CxNa-S _v 5	LKNKGKKNKQLMNNSKDDDTASIKSYGSHKNRPFKDESHKGS AETLEGE EKRDASKEDLG		440
		exon24	
CxNa-L _v 7	IDEELDDECEGEEGPLDGEMI IHAEEDEVI EDAPADCFPDNCYKRFPALAGDDDAPFWQG		1260
CxNa-L _v 8	IDEELDDECEGEEGPLDGEMI IHAEEDEVI EDAPADCFPDNCYKRFPALAGDDDAPFWQG		1262
CxNa-S _v 4	IDEELDDECEGEEGPLDGEMI IHAEEDEVI EDAPADCFPDNCYKRFPALAGDDDAPFWQG		527
CxNa-S _v 5	IDEELDDECEGEEGPLDGEMI IHAEEDEVI EDAPADCFPDNCYKRFPALAGDDDAPFWQG		500
		IIS1	exon25
		IIS2	
CxNa-L _v 7	WGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLP HRPILQDVLYYMDRIFTVIF		1320
CxNa-L _v 8	WGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLP HRPILQDVLYYMDRIFTVIF		1322
CxNa-S _v 4	WGNLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLP HRPILQDVLYYMDRIFTVIF		587
CxNa-S _v 5	WGSLRLKTFQLIENKYFETAVITMILLSSLALALEDVHLP HRPILQDVLYYMDRIFTVIF		560
		IIS3	exon26
		IIS4	
CxNa-L _v 7	FLEMLIKWLALGFRVYFTNAWCWLDIFIIMVSLIN FVASL C GAGGIQAFKTMRTL RALRP		1380
CxNa-L _v 8	FLEMLIKWLALGFRVYFTNAWCWLDIFIIMVSLIN FVASL C GAGGIQAFKTMRTL RALRP		1382
CxNa-S _v 4	FLEMLIKWLALGFRVYFTNAWCWLDIFIIMVSLIN FVASL C GAGGIQAFKTMRTL RALRP		647
CxNa-S _v 5	FLEMLIKWLALGFRVYFTNAWCWLDIFIIMVSLIN FVASL C GAGGIQAFKTMRTL RALRP		620
		exon27	IIS5
CxNa-L _v 7	LRAMSRMQGMRVVVNALVQAIPSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTNKTT		1440
CxNa-L _v 8	LRAMSRMQGMRVVVNALVQAIPSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTNKTT		1442

CxNa-S ₄	LRAMSRMQGMRVVVNALVQAI PSI FNVLLVCLIFWLI FAIMGVQLFAGKYFKCVDTNKTT	707
CxNa-S ₅	LRAVSRMQGMRVVVNALVQAI PSI FNVLLVCLISWLI FAIMGVQLFAGKYFKCVDTNKTT	680
	exon28 IIP	
CxNa-L ₇	LSHEIIPDVNACIAENYTWENSPMNFHDHVGKAYLCLFQVATFKGWIQIMNDAIDSRDIGK	1500
CxNa-L ₈	LSHEIIPDVNACIAENYTWENSPMNFHDHVGKAYLCLFQVATFKGWIQIMNDAIDSRDIGK	1502
CxNa-S ₄	LSHEIIPDVNACIAENYTWENSPMNFHDHVGKAYLCLFQVATFKGWIQIMNDAIDSRDIGK	767
CxNa-S ₅	LSHEIIPDVNACIAENYTWENSPMNFHDHVGKAYLCLFQVATFKGWIQIMNDAIDSRDIGK	740
	IIIS6 Exon29	
CxNa-L ₇	QPIRETNIYMYLYFVFFIIFGSFFTLNLFIVGIIDNFNEQKKKAGGSLEMFMTEDQKKYY	1560
CxNa-L ₈	KPIRETNIYMYLYFVFFIIFGSFFTLNLFIVGIIDNFNEQKKKAGGSLEMFMTEDQKKYY	1562
CxNa-S ₄	QPIRETNIYMYLYFVFFIIFGSFFTLNLFIVGIIDNFNEQKKKAGGSLEMFMTEDQKKYY	827
CxNa-S ₅	QPIRETNIYMYLYFVFFIIFGSFFTLNLFIVGIIDNFNEQKKKAGGSLEMFMTEDQKKYY	800
	exon30 IVS1	
CxNa-L ₇	NAMKKMGSKKPLKAI PRPKRRPQAIVFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQTET	1620
CxNa-L ₈	NAMKKMGSKKPLKAI PRPKRRPQAIVFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQTET	1622
CxNa-S ₄	NAMKKMGSKKPLKAI PRPKRRPQAIVFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQTET	887
CxNa-S ₅	NAMKKMGSKKPLKAI PRPKRRPQAIVFEICTNKKFDMI IMLFIGFNMLTMTLDHYKQTET	860
	IVS2 IVS3	
CxNa-L ₇	FSAVL DYLNMI FICIF SSECLMKIFALRYHYFIEPWNLFDFV VVILSILGLVLSDLIEKY	1680
CxNa-L ₈	FSAVL GYLNMI FICIF SSECLMKIFALRYHYFIEPWNLFDFV VVILSILGLVLSDLIEKY	1682
CxNa-S ₄	FSAVL DYLNMI FICIF SSECLMKIFALRYHYFIEPWNLFDFV VVILSILGLVLSDLIEKY	947
CxNa-S ₅	FSAVL DYLNMI FICIF SSECLMKIFALRYHYFIEPWNLFDFV VVILSILGLVLSDLIEKY	920
	exon31 IVS4 IVS5	
CxNa-L ₇	FVSPTLLRVVRVAKVGRVLR LRVKGAKGIR TLLFALAMSLPALFNICLLLFLVMFIFAIFG	1740
CxNa-L ₈	FVSPTLLRVVRVAKVGRVLR LRVKGAKGIR TLLFALAMSLPALFNICLLLFLVMFIFAIFG	1742
CxNa-S ₄	FVSPTLLRVVRVAKVGRVLR LRVKGAKGIR TLLFALAMSLPALFNICLLLFLVMFIFAIFG	1007
CxNa-S ₅	FVSPTLLRVVRVAKVGRVLR LRVKGAKGIR TLLFALAMSLPALFNICLLLFLVMFIFAIFG	980
	IVP exon32	
CxNa-L ₇	MSFFMHVKDKSGLDDVYNFKTFGQSMILLFQMST SAGWDGVL DGI INEEDCLPPDNDKGY	1800
CxNa-L ₈	MSFFMHVKDKSGLDDVYNFKTFGQSMILLFQMST SAGWDGVL DGI INEEDCLPPDNDKGY	1802
CxNa-S ₄	MSFFMHVKDKSGLDDVYNFKTFGQSMILLFQMST SAGWDGVL DGI INEEDCLPPDNDKGY	1067
CxNa-S ₅	MSFFMHVKDKSGLDDVYNFKTFGQSMILLFQMST SAGWDGVL DGI INEEDCLPPDNDKGY	1040
	IVS6 exon33	
CxNa-L ₇	PGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYYEIW	1860
CxNa-L ₈	PGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYYEIW	1862
CxNa-S ₄	PGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYYEIW	1127
CxNa-S ₅	PGNCGSATIGITYLLAYLVISFLIVINMYIAVILENYSQATEDVQEGLTDDDDYDMYYEIW	1100
CxNa-L ₇	QQFDPDGTQYIRYDQLSDFLDVLEPPLQIHKPNKYKIIISMDIPICRGDMMFCVDILDALT	1920
CxNa-L ₈	QQFDPDGTQYIRYDQLSDFLDVLEPPLQIHKPNKYKIIISMDIPICRGDMMFCVDILDALT	1922
CxNa-S ₄	QQFDPDGTQYIRYDQLSDFLDVLEPPLQIHKPNKYKIIISMDIPICRGDMMFCVDILDALT	1187
CxNa-S ₅	QQFDPDGTQYIRYDQLSGFLDVLEPPLQIHKPNSNKIISMDIPICRGDMMFCVDILDALT	1160
CxNa-L ₇	KDFFARKGNPIEDSAEMGGVQQRPEVGYEPVSSTLWRQREYCARLIQHAYRNFKERGG	1980
CxNa-L ₈	KDFFARKGNPIEDSAEMGEVQQRPEVGYEPVSSTLWRQREYCARLIQHAYRNFKERGG	1982
CxNa-S ₄	KDFFARKGNPIEDSAEMGGVQQRPEVGYEPVSSTLWRQREYCARLIQHAYRNFKERGG	1247
CxNa-S ₅	KDFFARKGNPIEDSAEMGEVQQRPEVGYEPVSSTLWRQREYCARLIQHAYRNFKERGG	1220
CxNa-L ₇	VGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGSIAGGGSQANLGPPS	2040
CxNa-L ₈	VGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGSIAGGGSQANLGPPS	2042
CxNa-S ₄	VGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGSIAGGGSQANLGPPS	1307
CxNa-S ₅	VGGGGGGGGGGGGGGEGAGDDTDADACDNEPGIGSPGAVSGGGGSIAGGGSQANLGPPS	1280
CxNa-L ₇	PKESP DGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2089
CxNa-L ₈	PKESP DGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	2091
CxNa-S ₄	PKESP DGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	1356
CxNa-S ₅	PKESP DGNNDPQGRQTAVLVESDGFVTKNGHRVVIHSRSPSITSRADV*	1329

Figure 4. Alignment of deduced amino acid transcript sequences of the *para*-type sodium channel transcripts (Cx-Na) in HAmCq⁶⁸ *Culex* mosquitoes. Transmembrane segments are indicated on the line over the sequence. Exons are indicated above the sequence with solid triangle symbols to indicate the boundaries between exons. The differences in the aa sequences are indicated by shading. A stop codon is marked by an asterisk (*). – indicates deletions. Δ indicates insertions with the sequences of Δ1: GAIIVPVYYANL Δ2: GEQHSLSLWIIWSE; Δ3: GEQHNHLSWIIWSE; Δ4: VIGNSISNHQDNKLEHNLNHRGMSLQ.

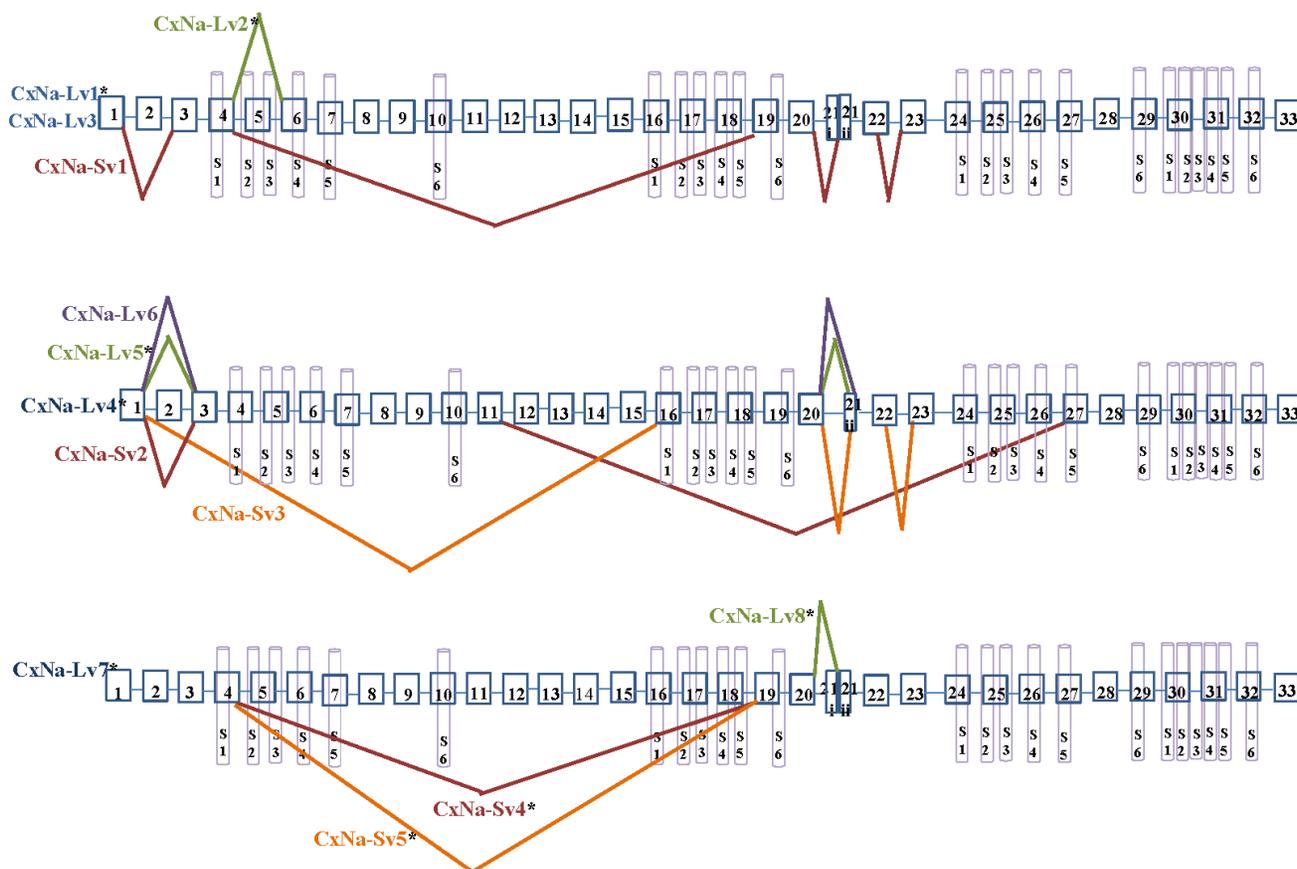


Figure 5. Alternative splicing of Cx-Nav from mosquitoes *Culex quinquefasciatus*. Boxes represent exons. The junctions of exons are indicated with straight lines or bridge lines. The schematic of the predicted 6 segments (S1 to S6) in each of the 4 domains (I, II, III, and IV) in the structure of Cx-Nav protein are shown. *The transcript had an entire ORF.

Discussion

Voltage-gated sodium channels are essential for the action potential generation of the neuron membrane and play a critical role in membrane excitability [6-7]. Over the last few years, a great deal of evidence has accumulated that supports the expression of diverse distinct sodium channel variants in insects through extensive alternative splicing of a single gene [16-23, 34]. The growing interest in alternative splicing of the sodium channels is propelled by its prominent contribution as a key mechanism generating the structural and functional diversity of sodium channels [15, 19]. Following the first reported cloning, sequencing and characterization of multiple variant transcripts from *Drosophila melanogaster* [32], the al-

ternative splicing of sodium channels has now been characterized in many medically or agriculturally important insect and arachnid pest species, including *Drosophila melanogaster* [17, 20], the house fly *Musca domestica* [16], German cockroach *Blattella germanica* [19], the mosquito *Anopheles gambiae* [34], diamond-back moth *Plutella xylostella* [22], silkworm *Bombyx mori* [35], and varroa mite *Varroa destructor* [36]. The current study represents the first investigation of the transcripts of sodium channels in *Cx. quinquefasciatus* and has revealed multiple variants of sodium channels generated from extensive alternative splicing and small deletions/ insertions, which is consistent with the results of the previous studies of the sodium channels of other insect species.

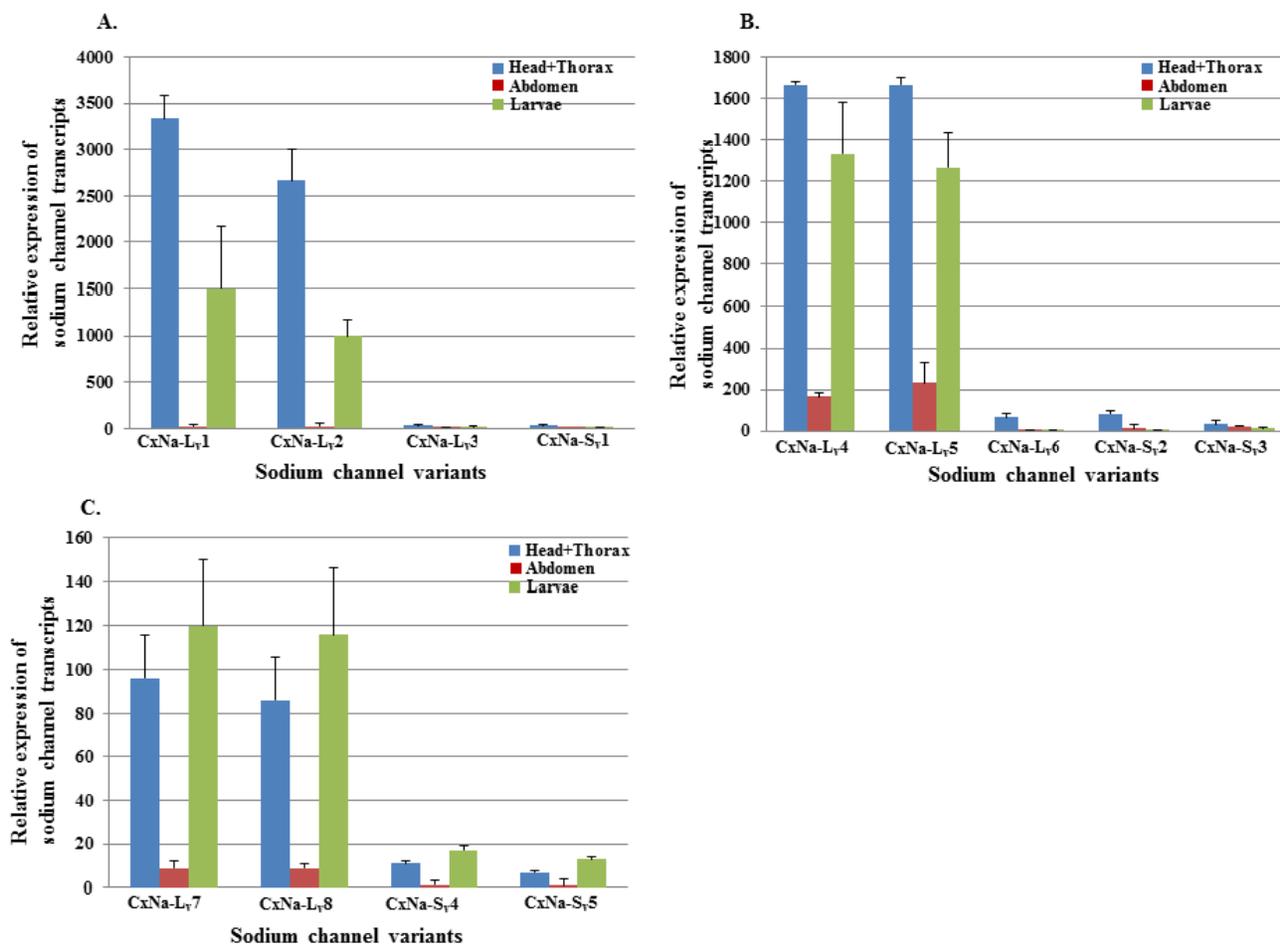


Figure 6. Expression of *CxNav* in larvae and head+ thorax and abdomen tissues of 2-3 day-old female adult *Culex* mosquitoes. The relative level of gene expression shown along the Y axis represents the ratio of the gene expression in each tissue from the adults or larvae compared to that measured in the abdomen tissue of the same strain (ratio=1 indicates equal amounts). The experiments were performed three times. The results are shown as the mean \pm S.E. No significant difference ($P \leq 0.05$) in the levels of sodium channel transcript expression was found in samples labeled with the same alphabetic letter (i.e., a, b, or c).

These multiple variants of *para*-type sodium channel transcripts presented in the mosquito *Cx. quinquefasciatus* can be classified in terms of two categories, CxNa-L and CxNa-S, based on their distinguishing sizes of ~ 6.5 kb and ~ 4.0 kb, which were present in all three mosquito strains tested - the susceptible S-Lab strain, the low resistant HAMCq^{G0} strain, and the highly resistant HAMCq^{G8} strain. The main difference in the sequences obtained for these two subcategories is the presence of multiple internal exons obtained through alternative splicing. In all, nine alternatively splice variants were identified in *Culex* mosquitoes. In the CxNa-L sodium channel category, four splice variants were identified, of which three were full length variants with three optional exons (2, 5, and 21i) and one incorporated in-frame-stop codons. Exon 2 is located in the N-terminus, which is an optional exon corresponding

to optional exon 2 of the sodium channel in the silkworm and optional exon j of the *para* in *Drosophila* and which is also conserved in other insect sodium channel genes [35]. Exon 5 is located between IS2 and IS3. Interestingly, skipping of exon 5 also occurs in the silkworm [35], German cockroaches [54] and the mosquito *Anopheles gambiae* [34], suggesting that exon 2 and exon 5 may be a conserved optional exon in insects. Exon 21 is located in the intracellular linker connecting domains II and III of the *Culex* mosquito sodium channels. The 5' portion of exon 21, named 21i, is optional in *Culex* mosquitoes. Exon 21i corresponds to optional exon f in the *para* gene of *Drosophila* and exon 22i in the silkworm [35]. These variants with optional exons 2, 5, and/or 21i are all entire ORFs of sodium channels, which may suggest the functional importance of these transcripts in mosquitoes. It has been reported that, when expressed in

Xenopus oocytes, the alternative splicing variants could exhibit different gating properties and generate sodium channel proteins with differing sensitivities to pyrethroids [18-19]. Whether these variants identified in the *Culex* mosquitoes also have different protein properties and different responses to pyrethroids remains to be seen.

Investigation of the putative amino acid sequences of alternative splicing variants in the CxNa-S sodium channel category, i.e. the ~4.5 kb transcripts, revealed that in contrast to the findings of CxNa-L, the alternative splicing identified in the sodium channel of *Culex* mosquitoes has resulted in large size or multi-exon-splicing. All the CxNa-S splicing variants in both the susceptible S-Lab and low resistance parental HAmCq^{G0} strains had in-frame stop codons, suggesting that these splicing variants and any resulting proteins would be truncated from those regions onward. As it has been reported that a truncated channel does not produce any sodium current when it expressed in *Xenopus* oocytes [19], the transcripts identified in our study that contain in-frame stop codons may not be functional transcripts. Furthermore, the ~1000 to ~3000-fold lower expression of the splice variants with stop codons compared to the CxNa-L splicing variances may further support the conclusion that these variances in mosquitoes are relatively unimportant. Nevertheless, two alternative splicing variants of CxNa-S splicing in HAmCq^{G8} had no in-frame stop codons but still had ORFs encoding sodium channel transcripts lacking exons 5 to 18. In addition, these two variants in HAmCq^{G8} had relatively high expression levels, with only ~10-fold lower expression levels compared with the CxNa-L variants. Nevertheless, these variants both lacked IS4 and IIS4 as a result of the alternative splicing. Since the S4 segments act as voltage sensors that initiate voltage-dependent activation [34-35], the issue of whether these two alternative splicing variants identified in the highly resistant HAmCq^{G8} strain perform some function in the sodium channels of mosquitoes requires further investigation.

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Competing Interests

The authors have declared that no competing

interest exists.

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