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REVIEW ARTICLE

Identification and inhibition of carbonic anhydrases from nematodes

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Abstract

Carbonic anhydrases (CAs) are metalloenzymes, and classified into the evolutionarily distinct α , β , γ , δ , ζ , and η classes. α -CAs are present in many living organisms. β - and γ -CAs are expressed in most prokaryotes and eukaryotes, except for vertebrates. δ - and ζ -CAs are present in phytoplanktons, and η -CAs have been found in *Plasmodium* spp. Since the identification of α - and β -CAs in *Caenorhabditis elegans*, the nematode CAs have been considered as an emerging target in research focused on antiparasitic CA inhibitors. Despite the presence of α -CAs in both helminths and vertebrates, structural studies have revealed different kinetic and inhibition results. Moreover, lack of β -CAs in vertebrates makes this enzyme as an attractive target for inhibitory studies against helminthic infection. Some CA inhibitors, such as sulfonamides, have been evaluated against nematode CAs. This review article aims to present comprehensive information about the nematode CAs and their inhibitors as potential anthelmintic drugs.

Introduction

Carbonic anhydrases (CAs, EC 4.2.1.1) are classified into six evolutionarily distinct classes: α , β , γ , δ , ζ , and η ^{1,2}. The active sites of these enzymes contain most commonly a zinc ion (Zn^{2+}), which plays a crucial role in the catalytic activity of the metalloenzymes³. ζ and γ -CAs contain cadmium (ζ), iron (γ), or cobalt (γ) as cofactors^{3,4} instead of Zn^{2+} . CAs catalyze the reversible hydration of carbon dioxide (CO_2) to bicarbonate ions (HCO_3^-) and protons (H^+). α -CAs are present in many prokaryotic and eukaryotic organisms, such as vertebrates, invertebrates, and plants. In total, 13 enzymatically active α -CAs have been discovered in mammals, including: CA I, CA II, CA III, CA IV, CA VA, CA VB, CA VI, CA VII, CA IX, CA XII, CA XIII, CA XIV, and CA XV⁵. β -CAs are expressed in many archaea, prokaryotes, and eukaryotes (fungi, algae, plants, protozoans, arthropods, and nematodes)^{5–10}. γ -CAs are found in archaea, plants, and some bacteria. δ - and ζ -CAs are present in many species of marine phytoplankton⁵. The newly discovered η -CAs are the only genus specific CAs, present in *Plasmodium* spp. (the causative protozoan of malaria), and contain Zn^{2+} in their catalytic active site². CAs catalyze several important metabolic and biochemical functions, such as pH homeostasis¹¹, electrolyte transfer¹², calcification¹³, gluconeogenesis¹⁴, lipogenesis¹⁵, and ureagenesis¹⁶. β -CA is a critical metalloenzyme that catalyzes many biological pathways in both prokaryotes and eukaryotes

Keywords

Acetazolamide, carbonic anhydrase, carbonic anhydrase inhibitors, nematode, sulfonamide

History

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including protozoans, insects, and nematodes. β -CA produces bicarbonate for carboxylases in *Corynebacterium glutamicum*¹⁷, urease in *H. pylori*¹⁸, and cyanase to detoxify cyanate in *Escherichia coli*¹⁹ and *Ascaris lumbricoides*²⁰. Crystal structures of β -CAs demonstrated that two cysteines and one histidine are conserved and are ligated to a zinc ion in the catalytic active site of the enzyme²¹. A study from 2010 introduced two metazoan β -CAs that were encoded by two different β -CA genes (*y116a8c(0).28* and *bca-1*) in *Caenorhabditis elegans*^{6,22}. In another study of 2010, a β -CA gene (*DmBCA*) was detected from *Drosophila melanogaster*⁶.

α -CAs are generally present in all metazoan species (vertebrates and invertebrates), whereas β -CAs are found only in invertebrate metazoans⁶ (arthropods and nematodes). Nematodes are categorized into several phyla: Annelida (segmented worms), Chaetognatha (arrow worms), Gnathostomulid (jaw worms), Hemichordata (acorn/tongue worms), Nematoda (roundworms), Nematomorpha (horsehair worms), Nemertea (ribbon worms), Onychophora (velvet worms), Phoronida (horseshoe worms), Platyhelminthes (flatworms), Priapulida (phallus worms), and Sipuncula (peanut worms). Most of α - and β -CA-containing nematodes (both pathogenic and nonpathogenic) have been classified into Nematoda and Platyhelminthes phyla, respectively²³. The details of α - and β -CA expressing nematodes, platyhelminthes, annelids, and hemichordates are shown in Table 1. Among different phyla, some groups, such as Nematoda and Platyhelminthes, are very important as zoonotic helminths in both human and veterinary medicine. Some phyla, such as Hemichordata and Annelida, are generally considered as nonpathogenic nematodes. However, CAs have also been

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Table 1. α - and β -CA expressing nematoda, platyhelminthes, annelida, and hemichordate.

Name	Phyla	α -CA IDs from UniProt	Subcellular location*	β -CA IDs from UniProt	Subcellular location*
<i>Ancylostoma caninum</i>	Nematoda	–	S	ANCCAN_03834**	–
<i>Ancylostoma ceylanicum</i>	Nematoda	A0A016S6V2	S	–	–
<i>Ancylostoma duodenale</i>	Nematoda	A0A0C2HC60	–	–	–
<i>Angiostrongylus cantonensis</i>	Nematoda	A0A0K0DQ44	S	–	–
<i>Anisakis simplex</i>	Nematoda	A0A0M3KDS4	–	–	–
<i>Ascaris lumbricoides (A. suum)</i>	Nematoda	F1L837	S	F1LE18	–
<i>Brugia malayi</i>	Nematoda	A0A0K0JIY2	S	–	–
<i>Brugia pahangi</i>	Nematoda	A0A0N4TVP9	–	–	–
<i>Caenorhabditis brenneri</i>	Nematoda	B3GEK5	M	G0MSW4 G0MRG1	M M
<i>Caenorhabditis briggsae</i>	Nematoda	A8XNL8	–	G0MSW4 A8WN21	– M
<i>Caenorhabditis elegans</i>	Nematoda	Q27504	–	Q22460 Q2YS41 D3NQA9	– – –
<i>Caenorhabditis japonica</i>	Nematoda	H2W178	S	–	–
<i>Caenorhabditis remanei</i>	Nematoda	E3LD70	S	E3LDN3 E3MK96	– M
<i>Clonorchis sinensis</i>	Platyhelminthes	H2KQV0	S	–	–
<i>Dictyocaulus viviparus</i>	Nematoda	A0A0D8XQR7	–	A0A0D8XFQ1	–
<i>Dracunculus medinensis</i>	Nematoda	A0A0N4US17	–	A0A0N4UN75	–
<i>Echinococcus granulosus</i>	Platyhelminthes	W6UBF1	–	–	–
<i>Enterobius vermicularis</i>	Nematoda	A0A0N4V7Z0	–	A0A0N4V5S3	M
<i>Haemonchus contortus</i>	Nematoda	U6PI84	S	U6PDI1	M
<i>Haemonchus placei</i>	Nematoda	A0A0N4X8K2	S	–	–
<i>Helobdella robusta</i>	Annelida	T1FNV0	S	–	–
<i>Hymenolepis microstoma</i>	Platyhelminthes	A0A068X7B2	S	–	–
<i>Loa loa</i>	Nematoda	E1FQZ7	S	–	–
<i>Necator americanus</i>	Nematoda	W2TSS6	–	W2SJ13	–
<i>Nippostrongylus brasiliensis</i>	Nematoda	A0A0N4YJY2	S	A0A0N4XIZ5	M
<i>Oesophagostomum dentatum</i>	Nematoda	A0A0B1SZR2	–	–	–
<i>Onchocerca volvulus</i>	Nematoda	A0A044SJH1	S	–	–
<i>Opisthorchis viverrini</i>	Platyhelminthes	A0A074ZVU6	–	–	–
<i>Parastrongyloides trichosuri</i>	Nematoda	A0A0N4ZSS2	–	A0A0N4ZFD7 A0A0N5A3V6	– –
<i>Pristionchus pacificus</i>	Nematoda	H3FHA2	S	–	–
<i>Saccoglossus kowalevskii</i>	Hemichordata	–	–	NP_001171747.1***	M
<i>Schistosoma haematobium</i>	Platyhelminthes	A0A095AIF7	–	–	–
<i>Schistosoma japonicum</i>	Platyhelminthes	Q5DFH8	–	Sjp_0056790**	–
<i>Schistosoma mansoni</i>	Platyhelminthes	G4VP62	–	G4V6B2	–
<i>Strongyloides papillosus</i>	Nematoda	A0A0N5C6N3	–	A0A0N5B1Z3	–
<i>Strongyloides ratti</i>	Nematoda	A0A090KUC2	S	A0A090LV46	–
<i>Strongyloides stercoralis</i>	Nematoda	A0A0K0DY00	S	A0A0K0E635	–
<i>Strongyloides venezuelensis</i>	Nematoda	A0A0K0FAM6	S	A0A0K0EVN4	–
<i>Syphacia muris</i>	Nematoda	A0A0N5A923	–	A0A0N5AQS5	M
<i>Thelazia callipaeda</i>	Nematoda	A0A0N5D8E0	–	–	–
<i>Toxocara canis</i>	Nematoda	A0A0B2V882	S	A0A0B2UWQ8	–
<i>Trichinella spiralis</i>	Nematoda	E5SX27	S	E5SH53	M
<i>Trichuris muris</i>	Nematoda	A0A0N5DXC0	–	A0A0N5DWJ5	M
<i>Trichuris suis</i>	Nematoda	A0A085M2M2	–	A0A085MP73	–
<i>Trichuris trichiura</i>	Nematoda	A0A077YWY0	–	A0A077YZT0	M
<i>Wuchereria bancrofti</i>	Nematoda	J9EPL8	–	–	–

*Abbreviations: S (CAs containing signal peptide for the secretory pathway) and M (CAs containing mitochondrial targeting sequence).

**IDs from WormBase Parasite database (<http://parasite.wormbase.org/>)⁴⁶.

***IDs from NCBI database (<http://www.ncbi.nlm.nih.gov/>)⁴⁷.

discovered in a few annelids, namely in *Hirudo medicinalis*²⁴, *Riftia pachyptila*²⁵, and *Osedax* bone worms²⁶.

In this review article, we present recent discoveries regarding nematode α - and β -CAs. Moreover, the inhibition studies of these enzyme families are described as they represent plausible targets for designing novel anti-infective drugs.

α -CA expressing nematodes

A wide range of different α -CA proteins are expressed in nematodes. Despite only one representative α -CA protein ID shown for each species in Table 1, α -CA protein sequences can

differ both within and between nematodes. Previous studies have identified α -CAs from some nematodes, including *C. elegans* and *Ostertagia ostertagi*^{27–29}. The genome of *C. elegans* encodes for six α -CAs, namely CAH-1, CAH-2, CAH-3, CAH-4, CAH-5, and CAH-6²⁹, with CAH-4 present as two isoforms CAH-4a and CAH-4b. In 2011, Fasseas et al. concluded that only CAH-3, CAH-4, and CAH-5 possess the three conserved zinc-binding histidine residues which are also present in active human CAs. CAH-3 was shown to be an active enzyme, and CAH-4 was found to be active *in vitro*, while the other four CAs (CAH-1, CAH-2, CAH-5, and

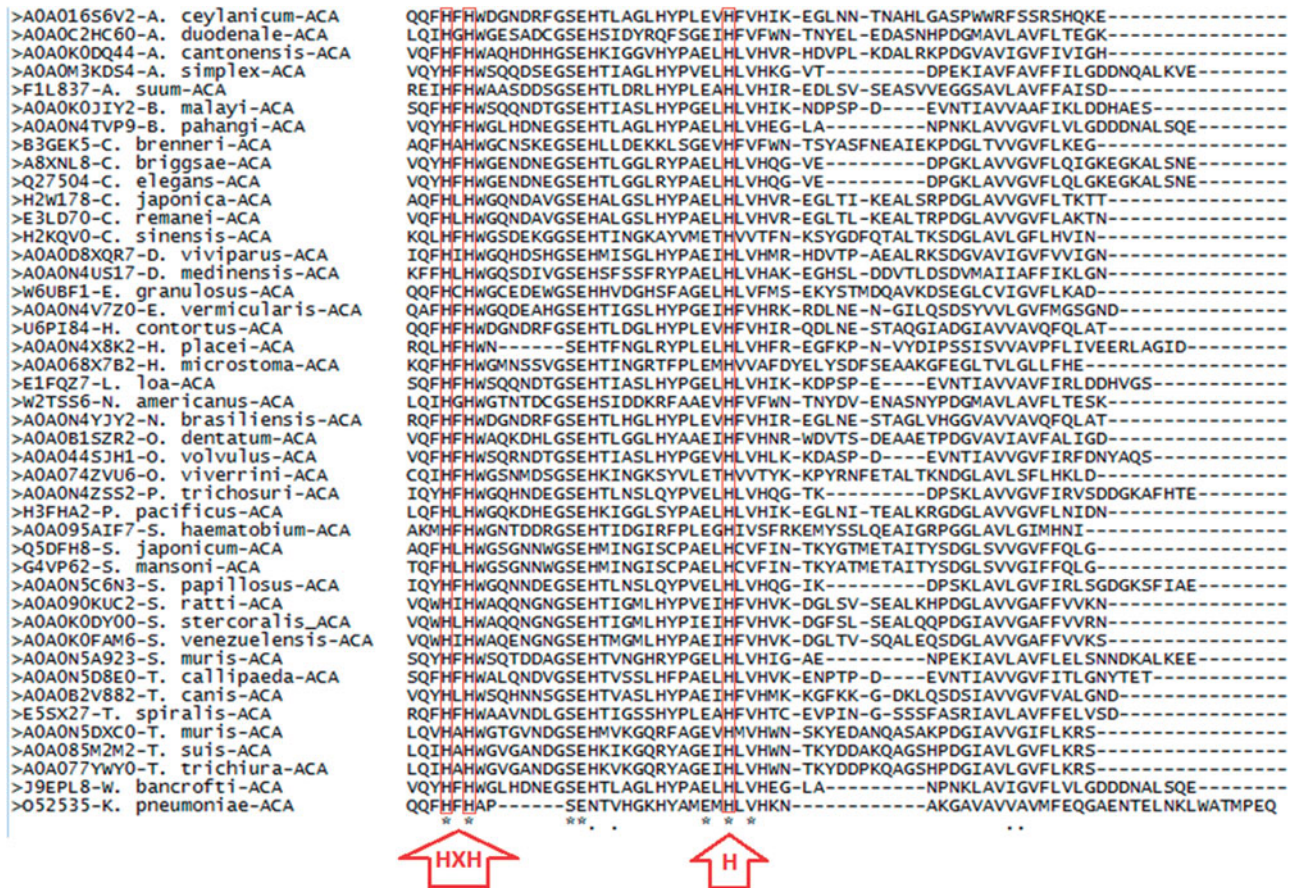


Figure 1. Multiple sequence alignment (MSA) of α -CA protein sequences from nematodes. MSA of 43 and one α -CA protein sequences from nematodes and *Klebsiella pneumoniae* (outgroup), respectively, aligned using Clustal Omega algorithm from EMBL-EBI database (<http://www.ebi.ac.uk/Tools/msa/clustal/>)⁴⁵. MSA was conducted on 60 amino acids of α -CA protein sequences starting three amino acids prior to the first highly conserved histidine. The three highly conserved histidines locate in the catalytic active site of α -CAs and participate in binding with the Zn^{2+} ion (shown by red arrows).

CAH-6) were presented as CA-related proteins (CARPs) without any CA activity (Figure 1). They also discovered that the silencing of *cah-3* and *cah-4* genes seemed to affect the lifespan of *C. elegans*.

O. ostertagi (Brown Stomach Worm) is a parasitic nematode (helminth) and the causative agent of ostertagiosis in cattle. The CA gene from *O. ostertagi* has been named as *OoCA*²⁷. The nucleotide sequence of *OoCA* gene is 78% and 55% identical with the *cah-6* and *CA3* genes of *C. elegans* and human, respectively. Studies have suggested that *O. ostertagi* CA may play a critical role in the immediate early developmental events following exsheathment initiation. Exsheathment is the first step at the beginning of *O. ostertagi* infection, and involves the casting of the second larval stage cuticle, which is retained by the infective third-stage larvae. Inhibition of this *O. ostertagi* development process may hinder the formation of the infective forms of *O. ostertagi*. In addition, it has been previously shown that ethoxzolamide affected the development of *H. contortus* via some changes in the excretory cells and esophagus during exsheathment³⁰. The potential of parasitic α -CAs as drug targets is limited by possible or even probable effects on host α -CAs, which predispose to various adverse effects.

β -CA expressing nematodes

β -CAs from nematodes are particularly interesting, because these enzymes are not found in vertebrates (including humans). Inhibition of nematode β -CAs presents possibilities to treat or restrict many helminthic infections with minimal side effects on

the hosts. Noteworthy is the fact that even though the β -CAs and other CA groups catalyze the same reaction, their protein structure is different. First, the Zn^{2+} ion in the active site of β -CAs is coordinated by two cysteines and one histidine instead of three histidines (Figure 2)³¹. Second, β -CAs can be found in many oligomeric states, whereas α -CAs mainly occur as monomers and γ -CAs as trimers. Thus far, a variety of multimeric crystal structures, including dimeric, tetrameric, hexameric, and octameric β -CAs have been reported^{32–34}. The monomeric components of a dimeric β -CA bind to each other usually by noncovalent interactions, and in some cases via a short polypeptide linker. The latter case is called a ‘‘pseudo-dimer’’³⁵. Tetrameric and octameric β -CAs are formed whenever dimers form dimer-of-dimers and dimer-of-dimer-of-dimers, respectively. The most frequently available quaternary structure of β -CAs is the tetrameric state. However, a dimeric β -CA seems to be the fundamental structural unit in β -CA protein structures.

Phylogenetic analysis of nematode α - and β -CAs

Nematode α -CAs and β -CAs were identified by BLASTP searches of the NCBI and UniProt databases using previously annotated members of both groups as query sequences, and all parameters as default. For each group, retrieved sequences were aligned using Clustal Omega and visually inspected for regions of incompleteness or poor quality. For those species containing a suspect sequence, the whole genome was downloaded and utilizing the exonerate program the remaining proposed high-quality sequences used as templates to predict gene and

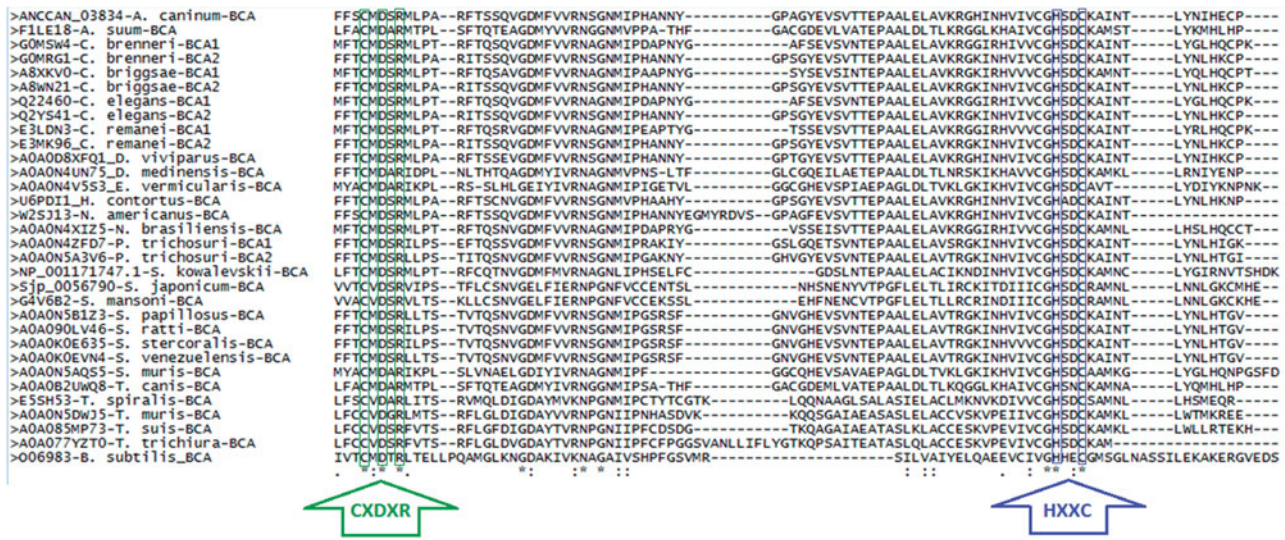


Figure 2. Multiple sequence alignment (MSA) of β -CA protein sequences from nematodes. MSA of 31 and one β -CA protein sequences from nematodes and *Bacillus subtilis* (outgroup), respectively, aligned using Clustal Omega algorithm from EMBL-EBI database (<http://www.ebi.ac.uk/Tools/msa/clustalo/>)⁴⁵. MSA was conducted on 115 amino acids of β -CA protein sequences starting three amino acids prior to the first highly conserved sequence (CXDXR; C: Cysteine, D: Aspartic acid, R: Arginine, D: any residue). The first (CXDXR) and second (HXXC; H: Histidine, C: Cysteine, X: any residue) highly conserved sequences locate in the catalytic active site of β -CAs and are coordinated with the Zn^{2+} ion (shown by green and blue arrows, respectively).

protein sequences. Subsequently, 14 genomes were analyzed for suspect sequences in the α -CA group and eight predictions kept, and ten genomes for the β -CA group with five predictions kept. In total, 54 α -CAs and 41 β -CAs protein sequences were aligned independently and used to perform phylogenetic analyses. The PhyML program was used to perform the phylogenetic analyses, utilizing the LG model and 1000 bootstraps; the results were visualized using FigTree and are presented as trees in Figures 3 and 4. Super-computing resources from the Center for Science and Computing of the Ministry of Finland were used to perform these analyses. Even at the amino acid level, the sequences for the nematode CAs were significantly different, which is evidenced in low bootstrap values within some subclades. Conversely, most branch points delineating subgroups of like organisms are well supported. This could imply that these species have possessed their CA sequences for a long time, and due to the fact that nontruncated versions of the sequences were used, ancillary domains accompanying the CA domain are providing a variation in function or localization of protein by species.

Subcellular location of nematode α - and β -CAs

The plant β -CAs have been localized to the cytoplasm of cells and thylakoid space of chloroplastic stroma³⁶. In cyanobacteria, β -CA is localized in the carboxysome organelle, and is therefore involved in the CO_2 -concentration process^{36,37}. Subcellular localization studies have indicated that DmBCA is probably a mitochondrial enzyme^{6,7,38}. The prediction of subcellular localization of α - and β -CAs from nematodes was performed using TargetP 1.1 Server (<http://www.cbs.dtu.dk/services/TargetP/>)³⁹. The results are shown in Table 1. The prediction results revealed that many nematode α -CAs contain signal peptides which target them to the secretory pathway. The prediction results further revealed that some nematode β -CAs including those in *C. brenneri* (G0MSW4 and G0MRG1), *C. briggsae* (A8WN21), *C. remanei* (E3MK96), *E. vermicularis* (A0A0N4V5S3), *H. contortus* (U6PDI1), *Nippostrongylus brasiliensis* (A0A0N4XIZ5), *S. kowalevskii* (NP_001171747.1), *S. muris* (A0A0N5AQ55), *T. spiralis* (E5SH53), *T. muris* (A0A0N5DWJ5), and *T. trichiura* (A0A077YZT0) contain a

mitochondrial targeting sequence. In fact, both α - and β -CAs from *C. brenneri* seem to contain a mitochondrial targeting sequence.

Inhibitory studies on nematode α -CAs

To evaluate the effect of a CA inhibitor, acetazolamide, on a nematode species, it was first tested against live *C. elegans*. The test revealed that this inhibitor could not penetrate the nematode cuticle²⁸. Additionally, thiabendazole-5-sulfonamide (a sulfonamide derivative of thiabendazole) was tested, and it inhibited efficiently (K_i 9.5 nM) the CAH-4b of *C. elegans*⁴⁰. Thiabendazole is widely used as an antiparasitic agent against both human and animal parasitic infections. The mechanism of action for thiabendazole is poorly understood, but it has been suggested that it interferes with the formation of cytoplasmic microtubules and cytoskeletons. Moreover, 2-(hydrazinocarbonyl)-3-substituted-phenyl-1H-indole-5-sulfonamides have been tested against *C. elegans* CAH-4b. Some of the tested compounds, including acetazolamide, ethoxzolamide, and a series of sulfonamide derivatives possessing various 2-, 3-, or 4-substituted phenyl groups with methyl-, halogeno-, and methoxy-functionalities, as well as the perfluorophenyl moiety, showed very significant inhibitory effects on CAH-4b with K_i s between 6.0 and 13.4 nM⁴¹.

Inhibitory studies on nematode β -CAs

Inhibition data available for nematode β -CAs are still very limited. The first studies on nematode enzymes were performed on *C. elegans* and *A. lumbricoides*^{20,22}. In 2009, Fasseas et al. characterized *C. elegans* β -CA for the first time²². They discovered two β -CAs in *C. elegans*, BCA-1, and Y116A8C.28, of which the latter was found to possess catalytic activity with k_{cat} and k_{cat}/K_m of $2.77 \times 10^4 s^{-1}$ and $6383 \times 10^5 M^{-1}s^{-1}$, respectively. However, the sequence for BCA-1 was obviously incorrect, suggesting that both β -CAs from *C. elegans* might be active enzymes⁶. The RNAi studies of *C. elegans* β -CA did not reveal any visible phenotype, while silencing the β -CA gene in fruit fly *Drosophila melanogaster* caused complete infertility in females³⁸. Hence, this result suggested crucial biochemical and physiological roles for β -CAs in insects, and possibly all invertebrates.

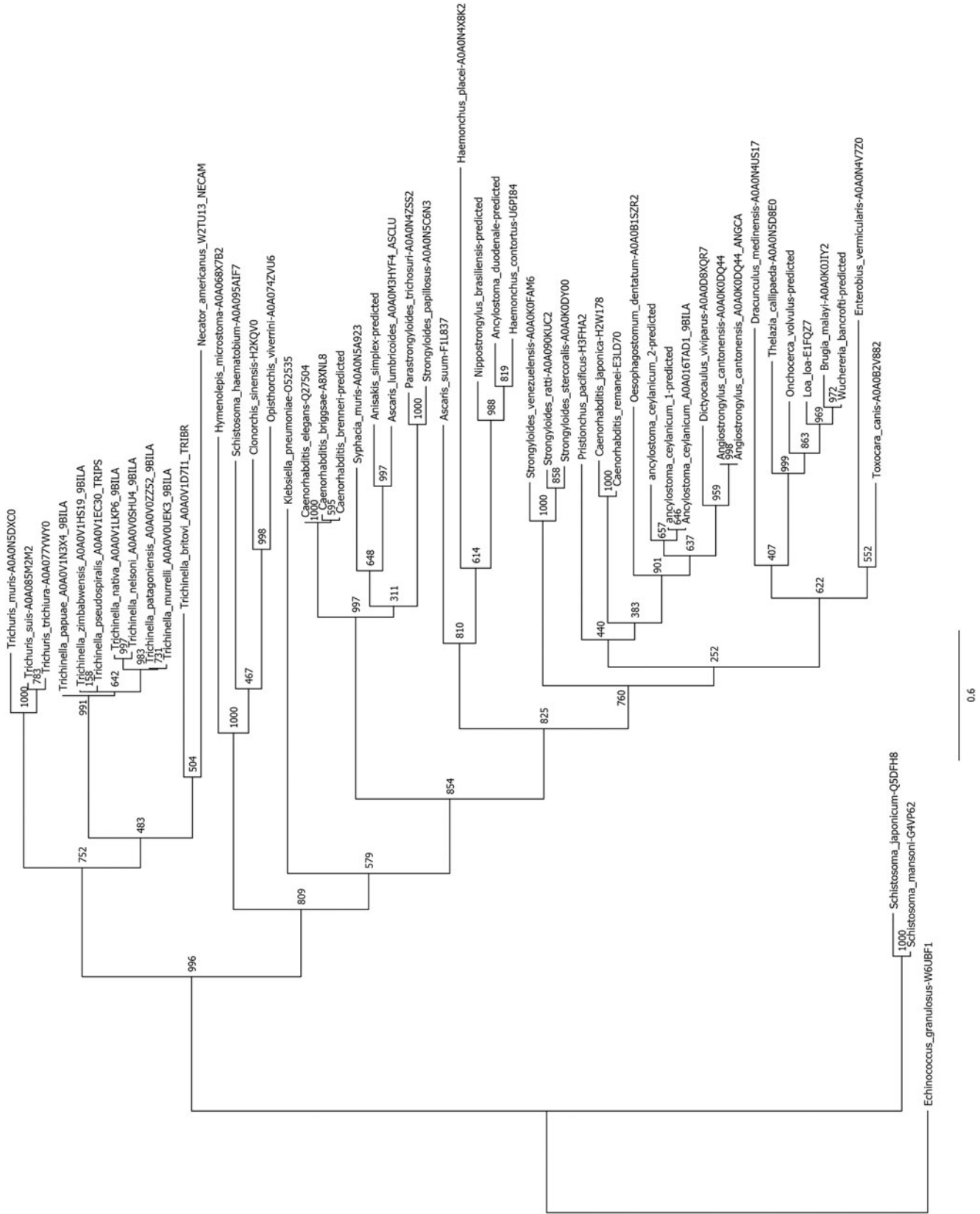


Figure 3. Phylogenetic analysis of nematode α -CAs. A total of 54 nematode α -CAs were aligned using Clustal Omega and used to perform a phylogenetic analysis using the LG model in the PhyML program, with 1000 bootstraps. Node values indicate bootstrap values. Any sequences which were predicted from the full genomic sequence are labeled as “predicted”.

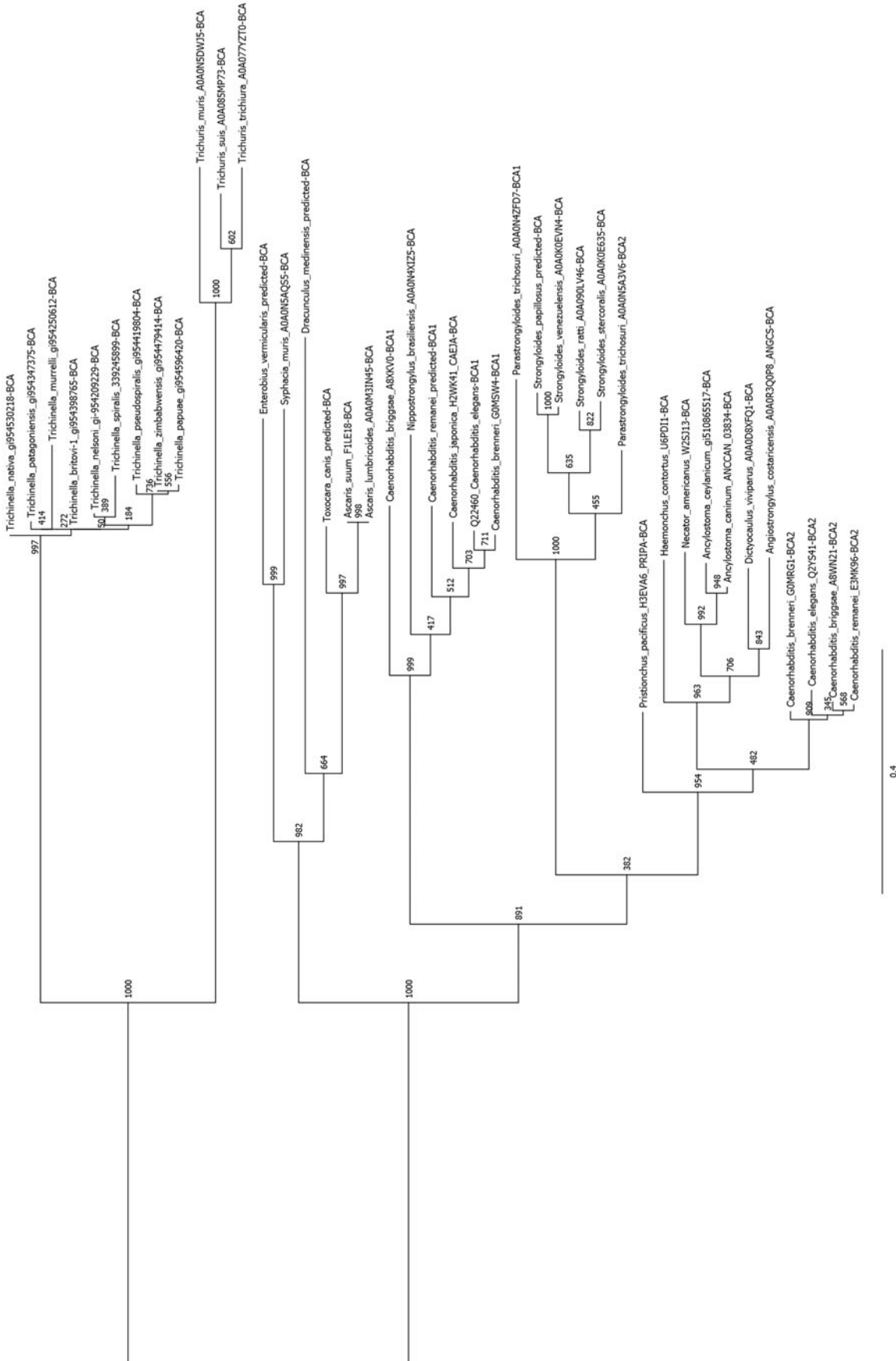


Figure 4. Phylogenetic analysis of nematode β -CAs. A total of 41 nematode β -CAs were aligned using Clustal Omega and used to perform a phylogenetic analysis using the LG model in the PhyML program, with 1000 bootstraps. Node values indicate bootstrap values. Any sequences which were predicted from the full genomic sequence are labeled as “predicted”.

Table 2. Enzyme activity and inhibition data of β -CAs from protozoa, nematode, and insects.

Enzyme	CA class	k_{cat} (s^{-1})	k_{cat}/K_m ($M^{-1} \times s^{-1}$)	K_i (acetazolamide) (nM)*
LdcCA	B	9.35×10^5	5.9×10^7	91.7 ± 5.7
DmBCA	β	9.5×10^5	1.1×10^8	516 ± 24
AgaCA	β	7.2×10^5	5.6×10^7	27.3 ± 2.0
AIBCA	β	$(6.0 \pm 0.1) \times 10^5$	$(4.3 \pm 0.2) \times 10^7$	84.1 ± 2.9

The results include enzyme activity values and inhibition results with acetazolamide on the β -CAs from *Leishmania donovani chagasi* (LdcCA), *Drosophila melanogaster* (DmBCA), *Anopheles gambiae* (AgaCA), and *Ascaris lumbricoides* (AIBCA).

Table 3. Predicted antigenic sites of 31 β -CAs from nematodes.

Name	β -CA IDs from UniProt	The most antigenic epitopes
<i>Ancylostoma caninum</i>	ANCCAN_03834*	110 INHVIVCGHSDCKAINTLYNIHECPHTFDP 139
<i>Ascaris lumbricoides</i> (A. suum)	FILE18	102 KHAIVCGHSDCKAMST 117
<i>Caenorhabditis bremeri</i>	G0MSW4	98 RHIVVCGHSDCKAINTLYGLHQCPKNF 124
	G0MRG1	101 INHVIVCGHSDCKAINTLYNLHKCPKS 127
<i>Caenorhabditis briggsae</i>	A8XKV0	97 IRHVVVCGHSDC 108
	A8WN21	101 INHVIVCGHSDCKAINTLYNLHKCPKS 127
<i>Caenorhabditis elegans</i>	Q22460	98 RHIVVCGHSDCKAINTLYGLHQCPKNF 124
	Q2YS41	101 INHVIVCGHSDCKAINTLYNLHKCPKS 127
<i>Caenorhabditis remanei</i>	E3LDN3	97 IRHVVVCGHSDCKAINTLYRLHQCPKE 123
	E3MK96	101 INHVIVCGHSDCKAINTLYNLHKCPKS 127
<i>Dictyocaulus viviparus</i>	A0A0D8XFQ1	101 INHVIVCGHSDCKAINTLYNIHKCPKSF 128
<i>Dracunculus medinensis</i>	A0A0N4UN75	82 IKHAVVCGHSDCKAMK 97
<i>Enterobius vermicularis</i>	A0A0N4V5S3	72 GETVLGGCGHEVSPAEPAGLDLTVKLGKIKHV IVCGHSDCAVTLTDIY 120
<i>Haemonchus contortus</i>	U6PDI1	102 INHVIVCGHADCKAINTLYNLH 123
<i>Necator americanus</i>	W2SJ13	109 INHVIVCGHSDCKAINTLYNIHTCPQN 135
<i>Nippostrongylus brasiliensis</i>	A0A0N4XIZ5	98 RHIVVCGHSD 108
<i>Parastrongyloides trichosuri</i>	A0A0N4ZFD7	101 INHVIVCGHSDCKAINTLYNLH 122
	A0A0N5A3V6	101 INHVIVCGHSDCKAINTLYNLH 122
<i>Saccoglossus kowalevskii</i>	NP_001171747.1**	98 NHVIVCGHSDC 108
<i>Schistosoma japonicum</i>	Sjp_0056790*	68 VTPGFLELTLIRCKITDIICGHSDC 93
<i>Schistosoma mansoni</i>	G4V6B2	78 ENCVPGFLELTLRRCRINDIICGHSDC 106
<i>Strongyloides papillosus</i>	A0A0N5B1Z3	101 INHVIVCGHSDCKAINTLYNLHTGV 125
<i>Strongyloides ratti</i>	A0A090LV46	101 INHVIVCGHSDCKAINTLYNLHTGV 125
<i>Strongyloides stercoralis</i>	A0A0K0E635	101 INHVIVCGHSDCKAINTLYNLHTGV 125
<i>Strongyloides venezuelensis</i>	A0A0K0EVN4	101 INHVIVCGHSDCKAINTLYNLHTGV 125
<i>Syphacia muris</i>	A0A0N5AQS5	73 FGGCQHEVSAVAEPAGLDLTVKLGKIKHVIVCGHSDCAAMK 113
<i>Toxocara canis</i>	A0A0B2UWQ8	102 LKHAIVCGHSNC 113
<i>Trichinella spiralis</i>	E5SH53	100 KDIVVCGHSDC 110
<i>Trichuris muris</i>	A0A0N5DWJ5	77 SGAIAEASASLELACCVSKVPEIIVCGHSDCKAMKL 112
<i>Trichuris suis</i>	A0A085MP73	119 EATASLKLACCESKVEVIVCGHSDCKAMKLLWLL 153
<i>Trichuris trichiura</i>	A0A077YZT0	94 TASLQLACCESKVEVIVCGHSDCKAMKLLWS 125

*IDs from WormBase Parasite database (<http://parasite.wormbase.org/>)⁴⁶.

**IDs from NCBI database (<http://www.ncbi.nlm.nih.gov/>)⁴⁷.

β -CA has been characterized recently from *A. lumbricoides*, the causative agent of zoonotic ascariasis. The enzyme was identified using bioinformatic and computational biology methods. *A. lumbricoides* recombinant β -CA protein (AIBCA) was produced in Sf9 insect cells, and the kinetic parameters were investigated. Based on the results²⁰, AIBCA possesses high catalytic activity with K_m $6.0 \times 10^5 s^{-1}$ and k_{cat}/K_m $4.3 \times 10^7 M^{-1} s^{-1}$. In addition, the K_i for inhibition of AIBCA by acetazolamide was 84.1 nM. Meanwhile, the kinetic and inhibition studies were also performed on the produced recombinant β -CAs from *D. melanogaster* (DmBCA)⁴², *Anopheles gambiae* (AgaCA)⁴³, and *Leishmania donovani*⁹. These results are shown for comparison in Table 2.

In vivo studies have not been conducted so far, but functional predictions of *A. lumbricoides* β -CA suggested that this enzyme may play important roles in bicarbonate dependent biosynthetic/metabolic pathways, such as gluconeogenesis and detoxification of metabolically produced cyanate by bicarbonate-dependent cyanase.

β -CAs from nematodes as vaccine candidates

The β -CA enzyme is highly distributed among infectious agents, including helminths. Therefore, it is a potential molecular target for controlling parasites and pests in all fields of human and veterinary medicine and agriculture¹⁰. Absence of β -CA in vertebrates also makes this enzyme a potential target protein for vaccines. The detection of antigenic sites of antigens and proteins is an important step in designing an effective vaccine candidate. For this purpose, 31 β -CA protein sequences from nematodes were analyzed with the European Molecular Biology Open Software Suite (EMBOSS) program Antigenic (<http://emboss.bioinformatics.nl/cgi-bin/emboss/antigenic>), which is based on the Kolaskar and Tongaonkar method⁴⁴. The antigenic site prediction results revealed that the second highly conserved sequence (HXXC) represents an epitope with the highest score for a probable antigenic site among the nematode β -CAs (Table 3). On the other hand, a previous homology modeling study on β -CA from

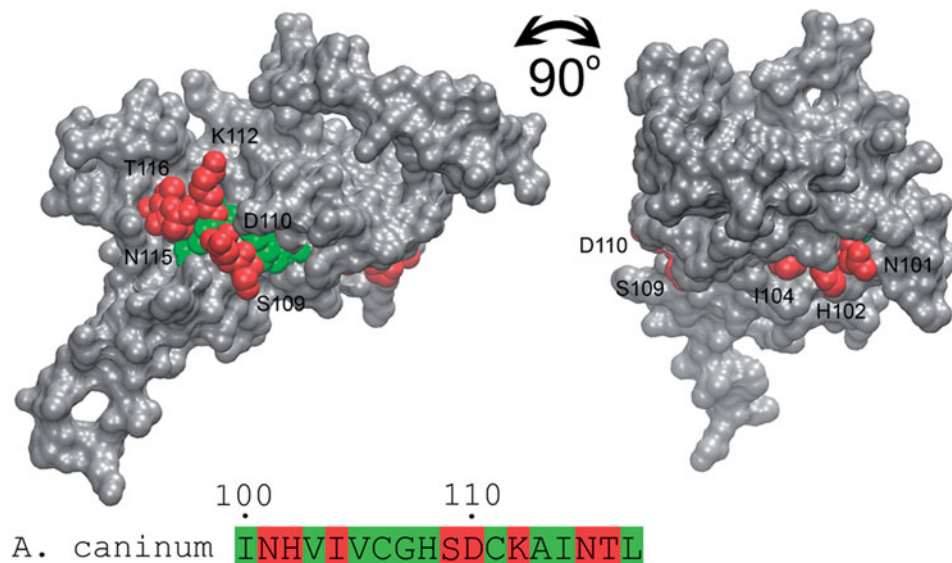


Figure 5. Accessibility identification of the predicted antigenic epitope of β -CA from *A. caninum*. The molecular surface of the homology model of *A. caninum* β -CA is shown as solid gray, and the second highly conserved sequence (HXXC) as the target epitope is buried from the surface of the protein. The exposed and buried residues of epitope are shown with red and green spheres and numbered. Figure adopted with author's permission from open access .

A. caninum defined that this epitope is located in the active site of enzyme and is mainly buried (Figure 5). In addition, most β -CAs are intracellular proteins, which make them inaccessible for immunological responses of the host. Therefore, β -CA inhibitors should be considered as a better option for developing new treatment strategies against parasitic or helminthic infections.

Conclusion

As the overall conclusion, inhibitory studies have demonstrated that acetazolamide is able to efficiently inhibit β -CA from a nematode, *A. lumbricoides*. Other studies have also shown that both acetazolamide and ethoxzolamide significantly inhibit α -CA from *C. elegans* (CAH-4b). Even though the literature on nematode β -CAs is still rather limited, β -CAs can be considered more attractive than α -CAs as potential targets for anti-helminthic drugs. This is based on the fact that β -CAs are absent from the proteomes of vertebrates. Therefore, β -CAs could represent a helminthic-specific drug targets with minimal side effects on the infected vertebrate host.

Declaration of interest

The authors declare that they have no competing interests.

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