

2017

Potential new drug targets and therapeutic approaches for parasitic nematode infections

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**Potential new drug targets and therapeutic approaches for parasitic nematode
infections**

by

Melanie Abongwa

A dissertation submitted to the graduate faculty
in partial fulfillment of the requirements for the degree of

DOCTOR OF PHILOSOPHY

Major: Toxicology

Program of Study Committee:
Richard J. Martin, Co-major Professor
Alan P. Robertson, Co-major Professor
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Douglas E. Jones

The student author and the program of study committee are solely responsible for the content of this dissertation. The Graduate College will ensure this dissertation is globally accessible and will not permit alterations after a degree is conferred.

Iowa State University

Ames, Iowa

2017

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DEDICATION

This
dissertation research
is dedicated to
my loving and caring parents
James T. and Comfort A. Abongwa,
and my siblings
Delphine N. Terence A., and Willibrod A. Abongwa.

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ACKNOWLEDGEMENTS

I lack words to express my gratitude to my supervisors: Distinguished Professor Richard J. Martin and Dr Alan P. Robertson, for accepting me into their lab and for educating me throughout my PhD program. Their self-less guidance, immeasurable support and encouragement made me the productive young scientist I am today. I will forever remain grateful to Dr Robertson for spending long hours on the bench with me just to make sure I fully understood the techniques used in my research; not forgetting to mention the times he allocated during weekends to work on my manuscripts and Schlumberger project. I am grateful to my program of study committee (POSC) members: Dr Michael J. Kimber, Dr Vellareddy Anantharam and Dr Douglas E. Jones, for agreeing to be on my POSC and for the academic guidance they provided me during my doctoral studies.

I would like to thank my lab colleagues, both past and present, especially Dr Samuel Buxton, Dr Sreekanth Puttachary, Dr Saurabh Verma, Dr Sudhanva Kashyap, Mark McHugh, Shivani Choudhary, Fudan Zheng and Dr Yoko Nagamori for the wonderful experience I had working with them. Special thanks to Dr Buxton for training me during my early days in the lab.

I would like to acknowledge our collaborators Professor Fidelis Cho-Ngwa and Dr Godfred A. Ayimele at the University of Buea, Cameroon for granting us access to their facilities and for providing insightful suggestions for the plant natural products project. I would like to thank all the members of Professor Cho-Ngwa's lab and the Organic Chemistry lab at the University of Buea, especially Dr Moses Samje, Smith Babiaka, Emmanuel Menang and Stanley Gamua for helping out with my research in Cameroon. I would also like to acknowledge the traditional healers and indigenes of Bambui, NW Cameroon for their

direction on the selection of the medicinal plants used in my research and for providing useful information on the traditional uses of these plants.

A special “Thank You” to Dr Jesse Goff, Dr Nicholas Koszewski, Cathy Martens and Carmen Reynolds for the help they gave me during my time in their lab. I would like to particularly thank Dr Koszewski for his recommendations and training on fractionating the plant extracts used in my research. I would like to thank Dr Bryan Bellaire for granting me access to his lab and for allowing me use the Worminator system in his lab. I would also like to thank Dr Vellareddy Anantharam and Adhithiya Charli for their help and training on cytotoxicity studies.

I would like to thank the Interdepartmental Toxicology program coordinator Linda Wild and the Department of Biomedical Sciences staff especially Kim Adams, Linda Erickson (retired), Amy Brucker, Rochelle Loonan and Emma Hashman for making my stay at Iowa State University a successful one at the departmental/administrative level.

I would like to thank the National Institutes for Health (NIH) and the Schlumberger Foundation for providing funding for my research. I would like to thank the Burroughs Wellcome Fund for providing me with a Collaborative Research Travel Award to visit Dr Judy Sakanari’s lab at the University of California San Francisco (UCSF) and also Christina Bulman and Chelsea Bidlow for assisting with the Worminator experiments at UCSF.

I would like to thank the University of Missouri-Columbia (UMC, Columbia, MO) and the NIAID/NIH Filariasis Research Reagent Resource Center (FR3) (Athens, GA) for their generous supply of adult *Brugia pahangi* used in my research. I would like to thank the members of the JBS Pork Plant at Marshalltown, Iowa, especially Rodney Howze for help collecting adult *Ascaris suum* for my research.

I would like to express my heartfelt gratitude to my American grandpa Mr Charles P. Andrews and grandma Mrs Elizabeth B. Eure for the love and support they gave me throughout my stay in Ames, Iowa. I would forever cherish my moments with grandpa and grandma and would never forget the lessons they taught me. I would like to thank my Heartland Baptist Church (HBC) family in Ames, Iowa for their prayers and love.

My deepest gratitude to my family and ALL my friends, relatives and well-wishers who during the course of my career provided any form of support to me. I am forever indebted to my parents, Mr James Tangwing Abongwa and Mrs Comfort Apongse Abongwa, for the enormous sacrifices they made in life to see that I succeed in my career pursuits as well as for their love, care, prayers, encouragement, and blessings. My special regards to my siblings: Delphine, Terence and Willibrod, who have always believed in me and have stood by me at ALL times whether good or bad.

ABSTRACT

Parasitic nematode infections remain a serious global public health threat to humans and animals. These infections cause debilitating conditions in humans and significant economic losses through infection of livestock and crop damage. Control of parasitic nematode diseases has continued to rely on use of anthelmintic drugs as there is presently no effective vaccine for the majority of these infections. Over the years, anthelmintic drug discovery has been very slow, and the majority of anthelmintic drugs used in human medicine today were initially developed for animal use as those affected live in the world's poorest nations that lack the financial means to afford conventional drugs. However, resistance to all the major anthelmintic drug classes has been reported in numerous veterinary parasite species and there are increasing concerns of resistance development in human parasite species. The emergence of widespread resistance therefore underscores the urgent need for the search of new targets, leads and strategies for anthelmintic drug discovery and development.

We have identified the nicotinic acetylcholine receptor (nAChR) subunit ACR-16 from *Ascaris suum* and showed that ACR-16 forms a functional homopentameric nAChR when expressed in *Xenopus* oocytes. *A. suum* is a gastrointestinal (GI) tract parasitic nematode of pigs that is very closely related to the human equivalent *A. lumbricoides*. ACR-16 is not activated by cholinergic anthelmintics and, although ACR-16 is most closely related to vertebrate $\alpha 7$ receptors based on amino acid sequence alignment, it has some marked pharmacological differences from vertebrate $\alpha 7$ receptors. As opposed to vertebrate $\alpha 7$ receptors, ACR-16 was insensitive to α -bungarotoxin and the effects of ivermectin, genistein and PNU120596 on ACR-16 were inhibitory rather than potentiating. The relative calcium

permeability ratio for ACR-16 was about 50x lower than that for vertebrate $\alpha 7$ receptors. We have showed using reverse transcription polymerase chain reaction (RT-PCR) that mRNA for ACR-16 is widely distributed throughout *Ascaris* tissues; suggesting ACR-16 may have functions other than neurotransmission. Our results showed, for the first time, the characterization of the pharmacology of ACR-16 from a parasitic nematode. Based on the pharmacology and expression pattern of ACR-16 in different tissues of the parasite, we suggest ACR-16 is an attractive new anthelmintic drug target with ‘resistance-busting’ properties that should be further exploited for therapeutic drug development.

Secondly, we have showed that the plants *Daniellia oliveri* and *Psorospermum febrifugum* have potential as sources of lead compounds for the development of the much-needed filaricidal drugs to treat onchocerciasis (river blindness) and lymphatic filariasis (elephantiasis). We prepared extracts of different polarities from *D. oliveri* and *P. febrifugum* and showed these extracts to be active against *Onchocerca ochengi* microfilariae and adults, and against adult *Brugia pahangi* based on visual motility scoring, MTT/formazan assay and the Worminator motility measurement system. Importantly, some extracts with *O. ochengi* microfilariae activity were also active on the adult worm. These extracts also showed activity against adult *B. pahangi*. We further fractionated the active extracts using Sep-Pak cartridges and High Performance Liquid Chromatography (HPLC) and showed some of these fractions retained activity against adult *B. pahangi*. We recommend that the active HPLC fractions be further purified to allow for the isolation of the bioactive compounds. This could significantly contribute to chemotherapeutic control of filarial infections currently hampered by the lack of macrofilaricides (adulticides).

Lastly, we have demonstrated that use of combination therapy over single drug therapy is a potentially useful tool for increasing efficacy, spectrum of action and reducing the likelihood of resistance development. We showed the combination of derquantel and abamectin to produce a greater inhibition of acetylcholine and pyrantel responses of expressed pyrantel/tribendimidine nAChRs from *Oesophagostomum dentatum* than derquantel or abamectin used alone. These nAChRs comprise of UNC-29, UNC-63 and UNC-38 subunits. Our results also showed abamectin acts on nAChRs, in addition to its known effects on glutamate-gated chloride channels (GluCl_s), implying abamectin has multiple targets. We further showed the action of abamectin on the expressed *O. dentatum* pyrantel/tribendimidine nAChRs to be bi-phasic, suggesting two allosteric sites of action: a high affinity negative allosteric modulation (NAM) site causing antagonism at lower concentrations ($\leq 0.1 \mu\text{M}$) and a lower affinity positive allosteric modulation (PAM) site causing a reduction in the antagonism at higher concentrations ($\geq 0.3 \mu\text{M}$).

CHAPTER 1. GENERAL INTRODUCTION

1.1 Introduction

Parasitic nematodes are a significant threat to both animals and humans, particularly in tropical and subtropical regions of the world. Parasitic nematodes also cause economic losses through infection of livestock and crop damage. In humans and animals, control of infections caused by parasitic nematodes relies mainly on the use of anthelmintic drugs, of which there are a limited number, and the majority of these act on ion channels. Anthelmintic drugs are grouped into different classes based on chemical structure and mode of action. The three major classes are the benzimidazoles (BZs), imidazothiazoles/tetrahydropyrimidines and macrocyclic lactones (MLs). The benzimidazoles (e.g thiabendazole, mebendazole, albendazole, flubendazole) target β -tubulin, an important protein in maintaining parasite cell structure. Imidazothiazoles/tetrahydropyrimidines (e.g levamisole, pyrantel, oxantel, morantel) act on nicotinic acetylcholine receptors (nAChRs), which are prototypical ligand-gated ion channels (LGICs) that mediate fast signal transmission at parasite neuromuscular and nerve-nerve junctions. Macrocyclic lactones (e.g ivermectin, abamectin, moxidectin) act on glutamate-gated chloride channels (GluCl_s). More recent anthelmintic drug classes include the amino-acetonitrile derivatives (AADs) (e.g monepantel), spiroindoles (e.g derquantel) and cyclooctadepsipeptides (e.g emodepside). Monepantel acts on the DEG-3-type nAChRs: ACR-20, ACR-23 and MPTL-1. Derquantel acts as an antagonist of several nAChR types. Emodepside acts on both SLO-1 potassium channels and latrophilin receptors. The recently introduced anthelmintic drug, tribendimidine, targets nAChRs just as imidazothiazoles/tetrahydropyrimidines, and is approved for human use in China.

Anthelmintic drugs exhibit their effects by interfering with locomotion, feeding, egg laying

or growth. Regrettably, resistance has been reported for all three major anthelmintic drug classes, as well as the AAD monepantel, thus, underscoring the pressing need for strategies to slow down or overcome resistance. Therefore, these PhD studies seek to address three main strategies by which anthelmintic resistance can be overcome. The first aim was to characterize the pharmacology of a new nAChR drug target, ACR-16, from the pig parasite, *Ascaris suum*, a good laboratory model for the human parasite, *A. lumbricoides*. The second aim was to demonstrate that plant natural products may serve as potential sources for new anthelmintics by investigating the efficacy and cytotoxicity of extracts from traditional medicinal plants against *Onchocerca ochengi*, the best-known laboratory model for the human equivalent, *O. volvulus*, and against *Brugia pahangi*, a good model for *B. malayi*. The third aim was to investigate interactions between derquantel, abamectin and expressed nAChRs from *Oesophagostomum dentatum* to gain mechanistic insight into this recently developed combination therapy.

1.2 Thesis Organization

In this thesis, a general introduction is provided about parasitic nematodes and the target sites of anthelmintic drugs used to treat nematode infections. Ion channels are highlighted as targets for the majority of available anthelmintic drugs and an emphasis is placed on anthelmintic drug resistance and the need to overcome drug resistance. Three strategies are proposed as ways of overcoming drug resistance and these are: the characterization of new drug targets, the development of new drugs from plant natural products and the use of combination therapy. In chapter 2, I have reviewed the literature relating to parasitic nematodes particularly *Ascaris suum*, *Onchocerca volvulus* and *Brugia malayi*, nicotinic acetylcholine receptors (nAChRs) of parasitic nematodes, and the medicinal

plants, *Daniellia oliveri* and *Psorospermum febrifugum*. In chapters 3, 4 and 5, I present research work done by myself and collaborators that has been published (chapters 3 and 5) or in preparation for publication (chapter 4). Chapter 3 describes the cloning and pharmacological characterization of a new homomeric nicotinic acetylcholine receptor ACR-16 from *Ascaris suum* (*Asu*-ACR-16). ACR-16 may serve as a potential target for the development of new ‘resistance-busting’ anthelmintic drugs. I did all the work outlined in this paper, except *Asu-acr-16* cloning which was done by our collaborators at Institut National de la Recherche Agronomique (INRA-Nouzilly) in France and isolation of cytoplasm for single-cell PCR which was done in our lab. Chapter 4 shows the efficacy of extracts of *Daniellia oliveri* and *Psorospermum febrifugum* against *Onchocerca ochengi* and *Brugia pahangi*, bioassay-guided fractionation and cytotoxicity of active extracts of *D. oliveri* and *P. febrifugum*. All the work in this chapter was done by me, with significant input from our collaborators at the University of Buea, Cameroon, University of California San Francisco and Iowa State University. Chapter 5 describes the effects of the recently developed derquantel and abamectin combination on expressed pyrantel/tribendimidine nAChRs from *Oesophagostomum dentatum*. I did all the work presented in this paper, except the cloning of the receptor subunits which was done by a former graduate student in our lab. Chapter 6 is a general discussion and conclusions of my PhD research and suggestions for future work. Appendix A is a research paper on acetylcholine receptor diversity in *Oesophagostomum dentatum*. Appendix B is an invited review on advances in anthelmintic drug development. Appendix C is a research paper on modeling the *Ascaris suum* ACR-16 receptor. Appendix D is a research paper on the mode of action of the cholinomimetic

morantel on the *Ascaris suum* ACR-16 receptor. Lastly, Appendix E is a list of all conference abstracts, awards and funding obtained.

CHAPTER 2. LITERATURE REVIEW

2.1 Parasitic Nematodes

Parasites are organisms that live on or in another organism known as the host, and benefit at the expense of the host. Parasites are harmful to the host and may even cause death. Most generally, the host-parasite relationship is such that the host does not benefit from the relationship and stressors associated with harboring parasites can be deleterious. Parasites are classified as ectoparasites if the parasites live outside the body, and as endoparasites if they live inside the body. In animals, ectoparasites live on the skin and can cause itching and rashes, while endoparasites may live in the blood, muscles, liver, brain or digestive tract (Hopla *et al.*, 1994).

Nematodes (or roundworms) belong to the phylum Nematoda. There are over 25,000 known nematode species, of which more than 50% are parasitic (Zhang, 2013). These include the soil-transmitted helminths (STHs) and filarial worms. Parasitic nematode infections are a global public health problem. These infections include four of the seventeen diseases that are classified as “Neglected Tropical Diseases” (NTDs) by the World Health Organization (WHO). The seventeen NTDs are Buruli ulcer, Chagas disease, Dengue and Chikungunya, Dracunculiasis (guinea-worm disease), Echinococcosis, Foodborne trematodiasis, Human African trypanosomiasis (sleeping sickness), Leishmaniasis, Leprosy (Hansen’s disease), Lymphatic filariasis, Onchocerciasis (river blindness), Rabies, Schistosomiasis, Soil-transmitted helminthiasis, Taeniasis/Cysticercosis, Trachoma and Yaws (Endemic treponematoses) (Johnston *et al.*, 2014). Of these seventeen NTDs, thirteen have been identified as core (Table 2.0), (Feasey *et al.*, 2010). Among the core NTDs are the

Table 2.0 The thirteen core NTDs. (Modified from Feasey *et al.*, 2010, pp. 182-183)

Disease	Name of causative agent	Class of causative agent	Usual mechanism of acquisition	Site of infection with mature agent	Clinical features	Estimated number infected (millions)	Estimated DALYs lost (millions), 2002	Control strategy	Aim of control strategy
Ascariasis*	<i>A. lumbricoides</i>	Helminth	Ingestion of eggs	Small intestine	Abdominal distension, pain malabsorption, intestinal obstruction, impaired growth, reduced school performance	807–1221	1.8	Periodic mass deworming of children using benzimidazole antihelminthics	Prevention of morbidity in children living in endemic areas
Dracunculiasis	<i>D. medinensis</i>	Helminth	Ingestion of water containing copepods infected with larval stage	Subcutaneous tissues	Painful skin bulla that progresses to an ulcer, from which a worm protrudes	0.002	Not known	Provision of protected water sources, education, filtration of drinking water, case detection and containment, cyclopicides	Eradication
Hookworm infection*	<i>A. duodenale</i> , <i>N. americanus</i>	Helminth	Skin penetration by soil-dwelling infective (third-stage) larvae	Upper part of small intestine	Intestinal blood loss, iron deficiency, protein malnutrition, impaired growth, reduced school performance	576–740	0.06	Periodic mass deworming of children using benzimidazole antihelminthics	Prevention of morbidity in children living in endemic areas
Lymphatic filariasis*	<i>W. bancrofti</i> , <i>B. malayi</i> , <i>B. timori</i>	Helminth	Skin penetration by infective (third-stage) larvae at the site of the bite from the mosquito vector (<i>Anopheles</i> , <i>Aedes</i> , <i>Culex</i> , <i>Mansonia</i> , or <i>Ochlerotatus</i>), after escaping from the mosquito's proboscis	Lymphatic vessels	Hydrocoele, lymphoedema and elephantiasis	120	5.8	Annual mass drug administration of albendazole plus either diethylcarbamazine or (where co-endemic with onchocerciasis) ivermectin	Elimination as a public health problem by 2020
Onchocerciasis*	<i>O. volvulus</i>	Helminth	Injection of infective (third-stage) larvae in the saliva of a biting, parasitized female blackfly (<i>Simulium sp.</i>)	Subcutaneous tissues	Subcutaneous nodules, pruritus, skin atrophy, skin pigmentation, blindness	37	0.5	Annual mass drug administration of ivermectin	Elimination as a cause of blindness by 2020

9

Table 2.0 (Continued)

Disease	Name of causative agent	Class of causative agent	Usual mechanism of acquisition	Site of infection with mature agent	Clinical features	Estimated number infected (millions)	Estimated DALYs lost (millions), 2002	Control strategy	Aim of control strategy
Schistosomiasis*	<i>S. mansoni</i> , <i>S. haematobium</i> , <i>S. japonicum</i> , <i>S. intercalatum</i> , <i>S. mekongi</i>	Helminth	Penetration of skin by cercariae that have emerged from water-dwelling snail intermediate hosts	Perivesical venous plexus or mesenteric veins	Haematuria, bladder obstruction, renal failure, bladder cancer (<i>S. haematobium</i>); periportal fibrosis, portal hypertension, ascites and varices (mesenteric schistosomes). Colitis, chronic dysentery, rectal prolapsed, impaired growth, reduced school performance	200	1.7	Annual mass drug administration of praziquantel, improved access to safe water and sanitation, and health education	Prevention of morbidity in children living in endemic areas
Trichuriasis*	<i>Trichuris trichiuria</i>	Helminth	Ingestion of eggs	Large intestine, especially caecum	Cardiomyopathy, cardiac dysrhythmia, mega-oesophagus, mega-colon	604–795	1.0	Periodic mass deworming of children using benzimidazole antihelminthics	Prevention of morbidity in children living in endemic areas
Chagas disease	<i>T. cruzi</i>	Protozoan	Inoculation by host's fingers into conjunctival sac or site of bite following excretion of mature parasite in faeces of biting triatomine bug	Intracellularly in tissues throughout the body	Cardiomyopathy, cardiac dysrhythmia, mega-oesophagus, mega-colon	15	0.7	Vector control, insecticide-treated bed nets, dog collars, adequate housing	Varies by region
Human African trypanosomiasis	<i>T. brucei</i>	Protozoan	Injection by parasitized tsetse fly	Blood, lymph, cerebrospinal fluid	Fever, headache lymphadenopathy, neurological decline, daytime somnolence, coma, death	<0.1	1.5	Vector control, rapid diagnosis and prompt treatment	Not yet defined
Leishmaniasis	More than 20 species of <i>Leishmania</i>	Protozoan	Injection by parasitized sandfly	CL skin MCL: skin plus oropharynx VL: disseminated disease	CL: skin ulcer MCL: skin ulcer plus oropharyngeal destruction VL: fevers, night sweats, weight loss, anaemia, immuno-suppression	12	2.1	Vector control, rapid diagnosis and prompt treatment	VL: elimination as a public health problem in Bangladesh, India and Nepal by 2015

Table 2.0 (Continued)

Disease	Name of causative agent	Class of causative agent	Usual mechanism of acquisition	Site of infection with mature agent	Clinical features	Estimated number infected (millions)	Estimated DALYs lost (millions), 2002	Control strategy	Aim of control strategy
Buruli ulcer	<i>M. ulcerans</i>	Bacterium	Unknown	Skin	Skin ulcer with an undermined edge	Unknown	Unknown	Rapid diagnosis and prompt treatment	Reduction in morbidity and socio-economic burden
Leprosy	<i>M. leprae</i>	Bacterium	Unknown	Skin and nerves	Skin changes, anaesthesia	0.4	0.2	Rapid diagnosis and prompt treatment with life-long follow-up	Microbiological cure, prevention of disability
Trachoma*	<i>C. trachomatis</i>	Bacterium	Mechanical transfer of elementary bodies by flies, fomites or fingers	Conjunctiva	Conjunctivitis, trachomatous scarring, trichiasis, corneal opacity, blindness	84	2.3	SAFE strategy: surgery for trichiasis, antibiotics (by MDA) to treat infection, face washing and environmental improvement to reduce transmission	Elimination as a public health problem by 2020

*Diseases have both high prevalence and excellent prospects for control.

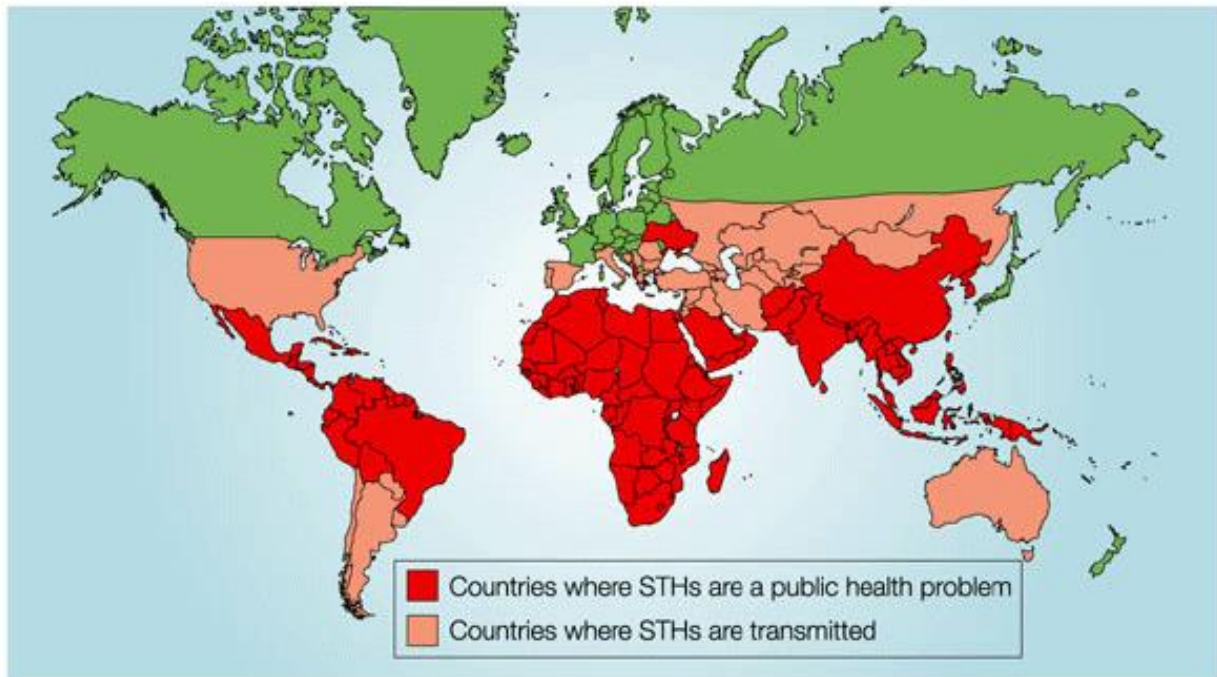
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nematode infections: soil-transmitted helminthiases caused by intestinal parasitic worms and filariases (lymphatic filariasis and onchocerciasis) caused by filarial worms. Over 3 billion people, primarily in developing countries with poor sanitation and lack of health education programs are infected with parasitic nematodes (Chan, 1997). Parasitic nematode infections do not only cause debilitating conditions in humans but also cause serious problems in livestock production worldwide. They cause significant economic losses and are a threat to food security (Fitzpatrick, 2013; Hotez *et al.*, 2009; Hotez & Kamath, 2009). As a result, affected communities are constantly trapped in a cycle of poverty and disease.

2.1.1 Soil-transmitted helminthiases

2.1.1.1 Ascariasis. Soil-transmitted helminthiases (STHs) are a group of NTDs caused by roundworms (*Ascaris lumbricoides*), hookworms (*Ancylostoma duodenale* and *Necator americanus*) and whipworms (*Trichuris trichuria*) (Bethony *et al.*, 2006). STHs are a public health concern in Africa, Latin America, Middle East and Asia (Figure 2.0) (Savioli & Albonico, 2004). Ascariasis is commonly seen in tropical and subtropical areas around the world where the infection has been strongly associated with poor hygiene, poor sanitation and use of human feces as fertilizers. Over 1 billion people worldwide are infected with *A. lumbricoides* (Crompton, 1988; de Silva *et al.*, 2003). The infection is most prevalent among school-aged children in rural areas (Fernandez *et al.*, 2002; Luong, 2003; Rayan *et al.*, 2010).

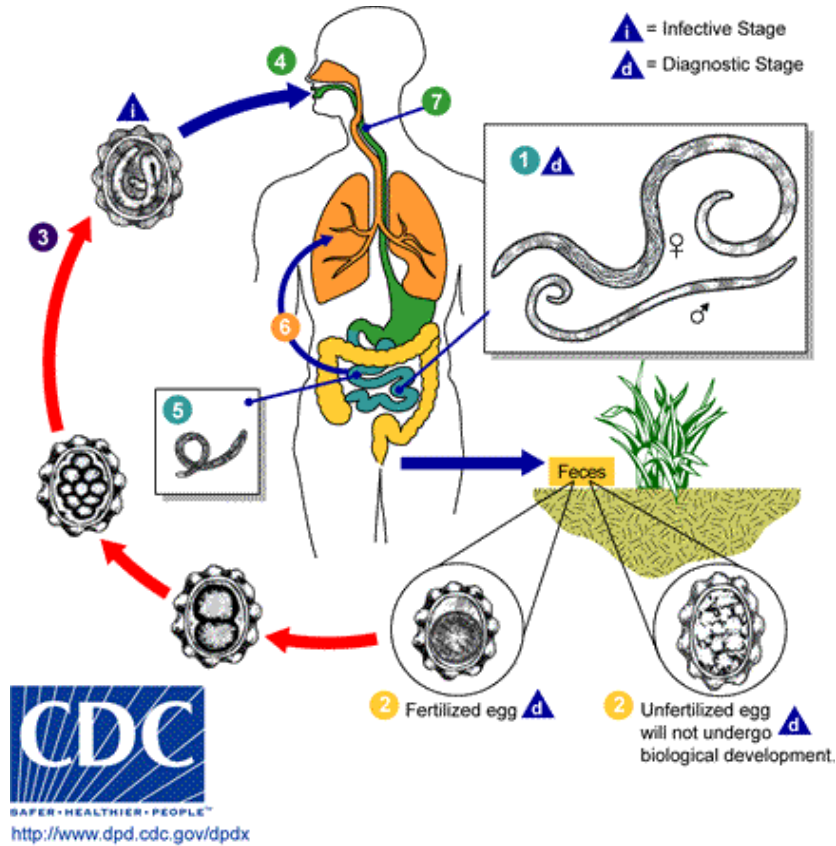
The life cycle of *Ascaris lumbricoides* requires only humans as the definitive host; there is no intermediate host (Figure 2.1). Adult female worms are larger (20 – 35 cm) than males (15 – 30 cm). The worms live in the lumen of the small intestine of infected persons. Eggs are passed in the feces and the infection is passed from one person to another by ingestion of soil that is contaminated with feces from infected persons. This can occur by



Source: Savioli & Albonico, 2004, p. 618.

Figure 2.0 Global distribution of soil-transmitted helminthiases (STHs). STHs are a major public health problem in Africa, Latin America, Middle East and Asia. Transmission of STHs also occurs in Australia and a few European countries, although not a major public health concern in these areas.

putting hands that have come in contact with contaminated soil in the mouth or by consuming improperly washed or peeled vegetables or fruits. An adult female produces up to 200,000 eggs per day which may be fertilized or unfertilized. Only fertilized eggs become infective while unfertilized eggs do not. Depending on environmental conditions, the fertilized eggs become infective after 18 days to several weeks after they embryonate. Moist, warm, shaded soil provides optimum conditions for this to occur. Once swallowed, the larvae hatch, invade the intestinal mucosa and are transported via the portal and systemic circulation to the lungs. While in the lungs, the larvae further mature in about 10 to 14 days and then



Source: Accessed on 03-19-17 at 11:45PM CST, from https://www.cdc.gov/parasites/images/ascariasis/ascariasis_lifecycle.gif

Figure 2.1 Life cycle of *Ascaris lumbricoides*.

penetrate the alveolar walls and ascend the bronchial tree to the throat and are swallowed. Once they reach the small intestine, they develop into adults which typically live for up to 1 – 2 years.

Infected persons are often asymptomatic. When symptoms occur, they range from light, such as abdominal discomfort to heavy, such as anemia, malnutrition, intestinal blockage and impaired physical and mental growth in children (Bethony *et al.*, 2006; Gyorkos *et al.*, 2011; Hughes *et al.*, 2004). Cough may occur as a result of migration of the worms through the (Hoenigl *et al.*, 2010). Irrespective of age, the prevalence of ascariasis is

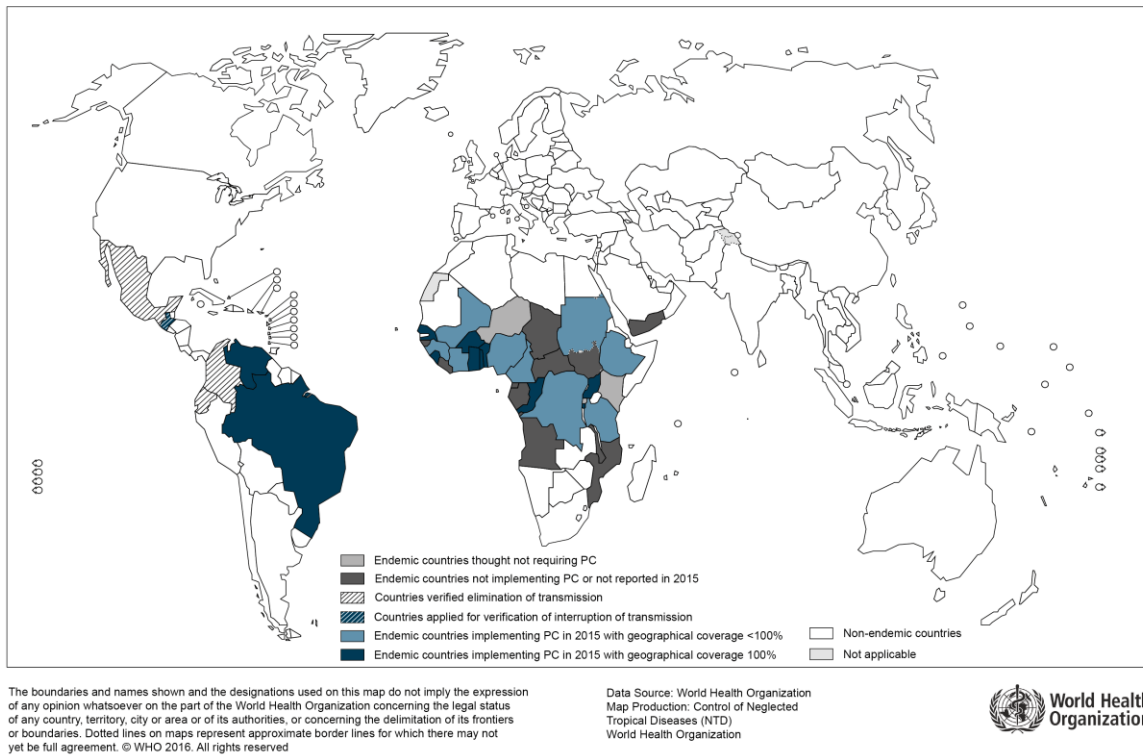
higher among females than males (Elkins *et al.*, 1986; Elkins *et al.*, 1988; Haswell-Elkins *et al.*, 1989). *Ascaris* infection is diagnosed by microscopic examination of stool for the presence of eggs. A single dose of albendazole (400 mg) or mebendazole (500 mg) is effective in treating *Ascaris* infections (Albonico *et al.*, 1994; Norhayati *et al.*, 1997).

2.1.2 Filariases

2.1.2.1 Onchocerciasis (River blindness). *Onchocerca* is a genus of filarial nematodes of the order Spirurida, family Onchocercidae. Of the various *Onchocerca* species, only one, *O. volvulus* infects humans (Krueger *et al.*, 2007; Morales-Hojas *et al.*, 2006). *O. volvulus* is the causative agent of human onchocerciasis or river blindness, and is transmitted by the blackfly, *Simulium damnosum* (Nelson, 1970; Sharp, 1927). The disease is called river blindness because the blackfly vector breeds along fast flowing rivers (Winthrop *et al.*, 2011). Consequently, the disease is most prevalent around these rivers. These areas usually constitute fertile farmlands which are often abandoned for less fertile areas as an escape strategy from the bite of the blackfly and hence, transmission of onchocerciasis. Most of the endemic areas are often inhabited by peasant farmers, therefore, migration from fertile to infertile lands causes agricultural and economic losses (Bradley, 1976; Stingl, 1987). The scientific literature on onchocerciasis dates as far back as 1875 when O'Neill first detected *O. volvulus* microfilariae in the skin of patients with "craw-craw" in Ghana. In 1893, *O. volvulus* adult worms were described by Leuckart from subcutaneous nodules collected from patients in Ghana, and in the 1920s, Blacklock in Sierra Leone identified the blackfly *S. damnosum* as the disease vector. Hissette and Robles in the Congo and Guatemala respectively, associated blindness with onchocerciasis (Burnham, 1998; Cupp *et al.*, 2011; Nelson, 1991). Globally, onchocerciasis is endemic in 36 countries of sub-Saharan Africa,

the Yemen and Latin America, 30 of which are in Africa (Figure 2.2). An estimated 37 million people suffer from onchocerciasis, with 99% of infected persons living in Africa. Another 120 million people worldwide are at risk of contracting the disease, of which 90 million live in Africa (Basanez *et al.*, 2006; Gustavsen *et al.*, 2011). Onchocerciasis is the world's second leading infectious cause of blindness after trachoma (Thylefors *et al.*, 1995). About 1 million of infected persons have ocular onchocerciasis, with an estimated 500,000 having impaired vision and 270,000 blinded as a result of the infection (Boatin & Richards, 2006). In hyperendemic areas, infection rates can be as high as 100%, with about 50% of the population blinded as a result of onchocerciasis (Etya'ale, 2002; Taylor, 1990). Eye and skin lesions and severe itching produced by the microfilariae are the greatest burdens of onchocerciasis (Kale, 1998). Blindness and skin disease due to onchocerciasis have been associated with reduced life expectancy, poverty, decreased productivity, poor academic performance, higher rates of school dropout of children (predominantly females) of infected parents and social stigmatization, particularly among women (Benton, 1998; Brieger *et al.*, 1998; Malatt & Taylor, 1992; Vlassoff *et al.*, 2000).

Onchocerciasis is a chronic infection. Clinical manifestations develop years after infection. The most common early symptom of infection with onchocerciasis is pruritis which is as a result of localized host inflammatory responses to dead and dying microfilariae in the skin (Somorin, 1983; Udall, 2007). Other symptoms include disfiguring dermatitis or leopard skin, onchocercomata (subcutaneous nodules), lymphadenopathies and ocular lesions (Browne, 1960; Connor & Palmieri, 1985; Enk *et al.*, 2003; Okulicz *et al.*, 2004). Ocular lesions constitute the most serious of these clinical manifestations as they can progress to



Source: Accessed on 02-22-17 at 12:00AM CST, from:
http://www.who.int/entity/mediacentre/factsheets/Onchocerciasis_2015_310_px.png

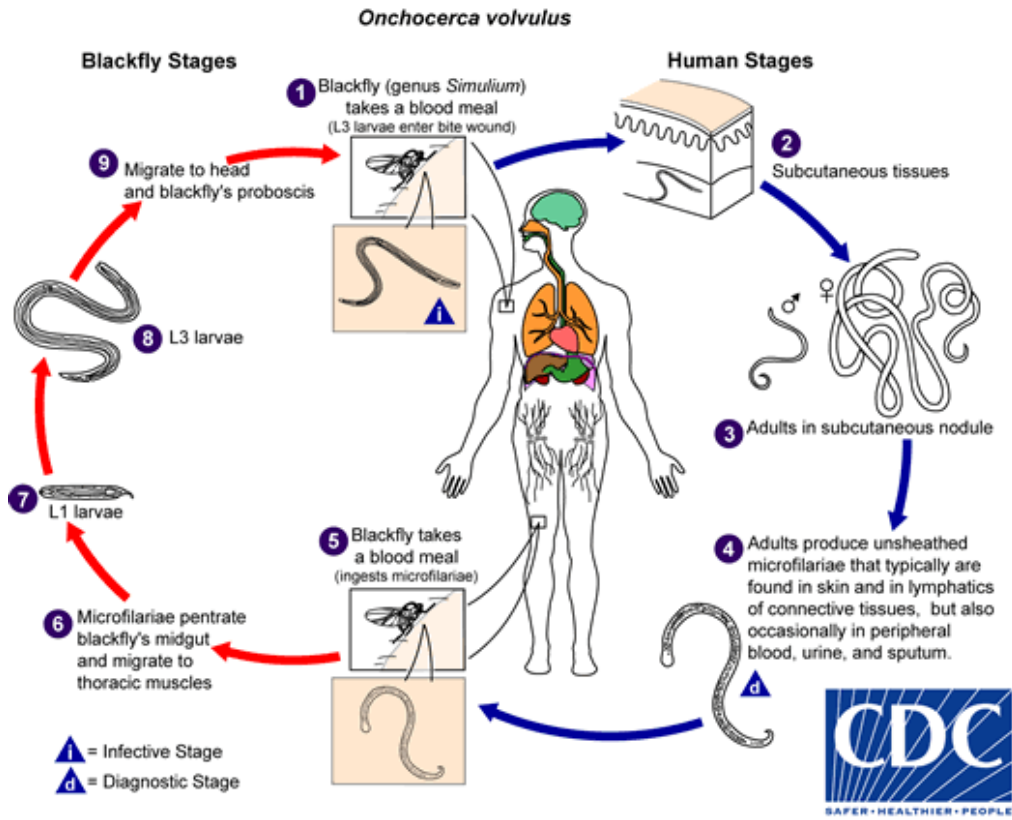
Figure 2.2 Global distribution of onchocerciasis

blindness. It is thought that antigens of *Wolbachia* endobacteria which live in a symbiotic relationship with *O. volvulus* greatly contribute to the pathological reactions associated with onchocerciasis (Brattig, 2004; Saint Andre *et al.*, 2002). Presumptive diagnosis of onchocerciasis in endemic areas is therefore based on physical examination of these clinical manifestations. Nonetheless, it is important to differentiate clinical manifestations associated with onchocerciasis from those due to other skin infections such as scabies and contact dermatitis. For this reason, definitive methods ranging from use of microscopy to detect microfilariae through detection of *O. volvulus* specific antigens and antibodies to DNA

probes have been developed for diagnosis of onchocerciasis (Boatin *et al.*, 1998; Bradley & Unnasch, 1996; Harnett, 2002; Zimmerman *et al.*, 1994).

The life cycle of *O. volvulus* involves the blackfly and human stages (Figure 2.3). Adult female worms, during a blood meal, inject infective third stage (L3) larvae into the human host via the bite wound. Next, the L3 larvae develop into adults in subcutaneous nodules. Nodules typically contain on average 2 – 3 female worms and 1 – 2 adult male worms. Females are usually confined to nodules while males can migrate from nodule to nodule, perhaps in search of females (Schulz-Key & Karam, 1986). Adult female worms are generally larger, and measure 270 – 400 μm in diameter and 33 – 50 cm in length, compared to the adult male worms which measure 130 – 210 μm in diameter and 1.9 – 4.2 cm in length. Adult worms have a life span of up to 15 years. After mating, females produce hundreds of unsheathed microfilariae daily which are typically found in the skin and lymphatics of connective tissues, but sometimes in peripheral blood, urine, sputum and the eyes (Anderson *et al.*, 1975a; Anderson *et al.*, 1975b; Schulz-Key, 1990). Female worms are capable of producing microfilariae for up to 9 years. The microfilariae measure 5 – 9 μm in diameter and 220 – 360 μm in length and have a life span of up to 2 years. The blackfly during another blood meal from an infected person ingests microfilariae which migrate from the blackfly's gut to thoracic muscles where they moult into the first larval stage (L1). L1 larvae subsequently develop into L3 larvae which eventually migrate to the blackfly's head region and proboscis, ready to be injected into a human host during the next blood meal.

Control against onchocerciasis includes measures directed against the blackfly vector and the parasites by use of insecticides and chemotherapeutic agents respectively. Vector



Source: Accessed on 02-21-17 at 08:38PM CST, from https://www.cdc.gov/dpdx/onchocerciasis/modules/o_volvulus_lifecycle.gif

Figure 2.3 Life cycle of *Onchocerca volvulus*.

control though successful to an extent, has some limitations; it is costly and also the thick canopies of the tropical forests prevent insecticides from reaching the breeding sites. Vector control is further limited by increasing resistance of the blackfly to insecticides (Davies, 1994). Therefore, chemotherapy remains the most efficient method of controlling onchocerciasis. Ivermectin, administered at a dose of 150 µg/kg, is the sole drug of choice for the control of onchocerciasis. Although ivermectin effectively kills microfilariae produced by adult worms (macrofilariae), it has little or no effects on the adults which may live for up to 15 years in human hosts (Duke, 1972). Hence, parasite control is hindered by

the lack of an effective adulticide (macrofilaricide) (Hopkins, 2005). There are also concerns about the development of resistance to ivermectin owing to its large scale repeated use (Osei-Atweneboana *et al.*, 2011; Richards *et al.*, 2001). Additionally, ivermectin can provoke severe life-threatening adverse reactions including encephalopathy, coma and death in patients heavily infected with the filarial parasite, *Loa loa* (eye worm) (Boussinesq *et al.*, 2003; Gardon *et al.*, 1997; Mackenzie *et al.*, 2007). These adverse reactions produced by the death of *L. loa* microfilariae greatly hinder use of ivermectin for treatment of onchocerciasis in areas of co-endemicity with loiasis. Studies have shown that targeting the endosymbiotic bacteria *Wolbachia* with the antibiotic, doxycycline for 4 to 6 weeks causes adult female worm sterility and a reduction in worm viability, development, embryogenesis and survival (Hoerauf *et al.*, 2002; Hoerauf *et al.*, 2008; Hoerauf *et al.*, 2009; Taylor *et al.*, 2000; Turner *et al.*, 2010). Treatment of onchocerciasis with doxycycline is also advantageous in patients co-infected with *L. loa* because of its lack of activity against *L. loa* microfilariae or adult worms (Wanji *et al.*, 2009). Although antibiotics have demonstrated activity against adult worms, the long treatment regimes required with antibiotic treatment present logistical problems for mass drug administration. Another limitation is contraindication of antibiotics in pregnant women and children under the age of 8 (Tamarozzi *et al.*, 2011). Ultimately, new drugs are needed for the effective control and elimination of onchocerciasis (Hotez, 2007).

Due to ethical constraints obtaining *O. volvulus* and difficulty maintaining *O. volvulus* under experimental conditions, other appropriate animal equivalents have been explored for studies on chemotherapy, host-parasite relationships and immunology of onchocerciasis. In this regard, the bovine *O. ochengi* has been identified as the closest relative to human *O. volvulus* (Makepeace & Tanya, 2016; Trees *et al.*, 1998). Both *O.*

ochengi and *O. volvulus* share the same *Simulium* vectors (Wahl *et al.*, 1998a). For this reason, a reduction in the vector biting rate for humans and hence a reduction in the transmission of human onchocerciasis has been observed in regions where there is a high bovine population and for which bovine and human onchocerciasis are endemic (Eisenbarth *et al.*, 2016; Wahl *et al.*, 1998b). *O. ochengi* and *O. volvulus* also demonstrate comparable drug sensitivities (Trees *et al.*, 2000). These similarities, along with the relative availability and low cost of obtaining *O. ochengi* make *O. ochengi* the best laboratory model for anti-*Onchocerca* drug screens and the study of host-parasite interplay in human onchocerciasis.

2.1.2.2 Lymphatic filariasis (Elephantiasis). Lymphatic filariasis (LF), commonly known as elephantiasis is a neglected tropical disease that is caused by filarial nematodes of the family Filariodidea. These include *Wuchereria bancrofti*, *Brugia malayi* and *Brugia timori*. *W. bancrofti* accounts for 90% of LF cases, while *B. malayi* and *B. timori* account for the remaining 10% (Palumbo, 2008). Bancroftian filariasis occurs in both urban and rural areas, while Brugian filariasis occurs mainly in rural areas. The parasites that cause LF are transmitted to humans by mosquitoes of the genera *Culex*, *Anopheles*, *Mansonia* and *Aedes*. *Culex* mosquitoes are found across urban and semi-urban areas, *Anopheles* are found mainly in rural areas, and *Aedes* are found mainly in endemic islands in the Pacific. Urban *W. bancrofti* is primarily transmitted by *Culex quinquefasciatus*, whereas *Anopheles* and *Aedes spp* mosquitoes are typical vectors of rural *W. bancrofti*. Brugian filariasis is mainly transmitted by *Mansonia*, *Anopheles* and *Aedes spp* mosquitoes (Mak, 1987). LF can lead to an altered lymphatic system and abnormal swelling of body parts, causing pain and severe disability, ranking as the second leading cause of permanent disability worldwide after mental illness (Noordin, 2007; Wynd *et al.*, 2007). Globally, over 120 million people are

infected with LF, with another 1.2 billion at risk and about 40 million disfigured and incapacitated as a result of the disease (Fenwick, 2012; Nutman, 2013). The majority of LF cases are seen in Africa (Figure 2.4).

The majority of infected persons are asymptomatic, but can show acute symptoms such as inflammation of the skin, lymph nodes and lymphatic vessels which often progress to chronic conditions like lymphedema (tissue swelling) or elephantiasis (tissue/skin thickening) of limbs and hydrocele (scrotal swelling) (Babu & Nutman, 2012; Shenoy, 2008).

Of these symptoms, elephantiasis is the most chronic and obvious, occurring in about 10% of LF cases. Chronic LF has serious mental, social and economic effects which include stigma and poor economic output, hence, poverty. The role of gender in social stigmatization due to chronic LF has been reported, with the burden falling more on women (Bandyopadhyay, 1996; Coreil *et al.*, 1998; Gyapong *et al.*, 1996). The conventional method



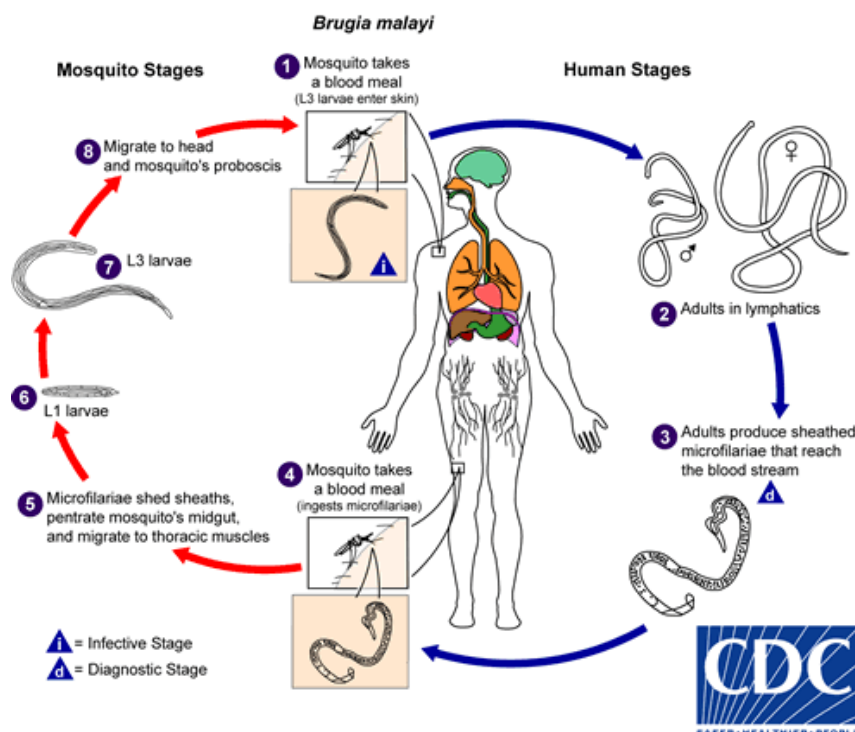
Source: Accessed on 03-20-17 at 04:15PM CST, from https://www.cdc.gov/parasites/images/lymphaticfilariasis/lf_geo_distrib.jpg

Figure 2.4 Global distribution of lymphatic filariasis indicated in red.

of diagnosing LF is microscopic detection of microfilariae in blood smears. Blood samples for microfilariae detection are usually collected at night because during the day, microfilariae hide in blood capillaries of internal organs. However, this conventional method has low sensitivity, leading to the development of more sensitive PCR-based methods, immunological and serological techniques (Melrose *et al.*, 2004; Weil & Ramzy, 2007). These methods also allow for blood samples to be collected from patients at anytime of the day.

The life cycle of parasites that cause LF is similar to that of *O. volvulus*, involving mosquito and human stages (Figure 2.5). Infected mosquitoes during a blood meal introduce L3 larvae into the body of a human host which migrate to the lymphatic vessels and develop into adult worms. Adult *B. malayi* females are larger (measuring 43 – 55 mm in length by 130 – 170 μm in width) than adult males (measuring 13 – 23 mm in length by 70 – 80 μm in width). Adult *W. bancrofti* are similar to adult *B. malayi* except both sexes are larger. Adult worms produce sheathed microfilariae (measuring 177 – 230 μm in length by 5 – 7 μm in width) which typically enter the bloodstream and are ready to be ingested by the mosquito during another blood meal. As with *O. volvulus*, once ingested by the arthropod vector, microfilariae shed their sheaths and migrate to mosquito's thoracic muscles via midgut where they moult into L1 larvae and subsequently develop into L3. L3 larvae then migrate to the mosquito's head and proboscis, ready to infect another human, thus continuing the transmission cycle.

Chemotherapy is the most cost-effective tool to control LF. This is achieved by mass treatment with a combination of albendazole (200 mg) with either ivermectin (150 – 200



Source: Accessed on 03-05-17 at 02:08AM CST, from https://www.cdc.gov/parasites/images/lymphaticfilariasis/b_malayi_lifecycle.gif

Figure 2.5 Life cycle of *Brugia malayi*.

$\mu\text{g}/\text{kg}$) or diethylcarbamazine (DEC) (6 mg/kg) (Karam & Ottesen, 2000; Ottesen *et al.*, 1997). However, these drugs are only microfilaricidal, with limited activity against adult worms which can live for an average of 5 – 10 years and will continue to produce microfilariae. Clearly, new drugs effective against adult worms are needed. DEC is further contraindicated in onchocerciasis due to the possibility for the occurrence of severe treatment adverse reactions involving the skin and eye (Mazzotti reaction) (Awadzi & Gilles, 1992). Ideally, LF patients who are co-infected with onchocerciasis should be treated with the albendazole and ivermectin combination. Recently, the combination of DEC, albendazole and ivermectin was demonstrated to be more efficient than the DEC and albendazole

combination for the treatment of Bancroftian filariasis. Twelve patients who received a single dose of the DEC, albendazole and ivermectin combination tested negative for microfilariae at 12 and 24 months after treatment, suggesting adult worm death or sterility (Thomsen *et al.*, 2016). However, more studies are needed to ascertain the safety of this triple drug therapy, particularly in individuals who are co-infected with onchocerciasis and loiasis. Studies have also shown that targeting the *Wolbachia* endosymbiont with doxycycline (200 mg for 4 – 6 weeks) can result in adult worm sterility (Hoerauf *et al.*, 2003).

Due to the constraints in obtaining large numbers of *B. malayi* for drug screens, *B. pahangi* which naturally infects cats and wild animals is used. Cats respond to *B. pahangi* in a similar manner as humans respond to *B. malayi* and *W. bancrofti* (Denham & Fletcher, 1987). Likewise, *B. pahangi* is equally susceptible to drugs that act on *B. malayi*. Also, given the relatively high costs of maintaining cats, the gerbil-*B. pahangi* system is used as a suitable model for drug screens and host-parasite studies (Bulman *et al.*, 2015).

2.2 Nematode Neuromuscular System

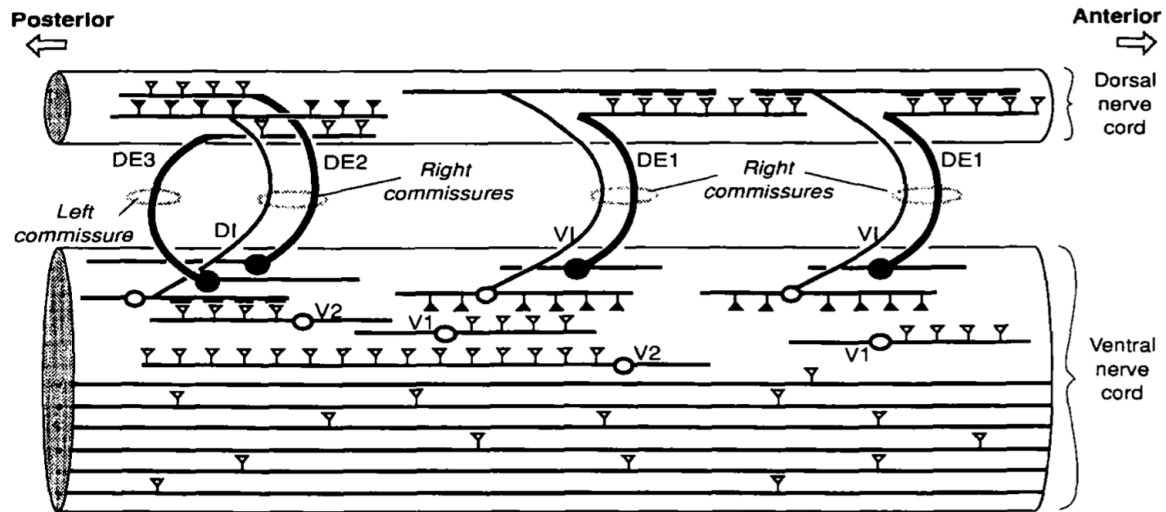
Here we focus on the neuromuscular system of *Ascaris lumbricoides* var. *suum*. The neuromuscular system of *Ascaris spp* is the earliest and well-studied nematode neuromuscular system. The nematode neuromuscular system is unique in several ways. For instance, projections are sent from muscle cells to nerves as opposed to from nerves to muscle cells in vertebrates. Like other nematodes, *Ascaris spp* has a fixed number of cells and cell divisions. Other unique features are the small and constant number of neurons (*ca* 250) in the nervous system and the large cells which make up the musculature (del Castillo *et al.*, 1989).

2.2.1 Nervous System

The nervous system of *Ascaris* is made up of three components namely: (i) nerve ring and associated ganglia in the anterior region, (ii) major dorsal and ventral nerve cords and smaller subdorsal and subventral nerve cords, and (iii) a smaller set of ganglia in the posterior region. The motor nervous system (remaining region of the nervous system in a decapitated and tailless *Ascaris* that can still control movement) of *Ascaris* is composed of five repeating units or segments. Each unit or segment contains eleven motoneurons which based on morphology were classified into seven types with all their somata positioned in the ventral nerve cord (Stretton *et al.*, 1978). Three of the seven types namely; DI, DE2 and DE3 occur only once in each segment whereas the other four types namely; DE1, VI, V1 and V2 occur twice. Of these seven types, two (V1 and V2) are confined to the ventral nerve cord while the other five have processes in both dorsal and ventral nerve cords. The processes in dorsal and nerve cords of these motoneurons are linked by lateral processes known as commissures. Additionally, there are six non-segmental interneurons, three right-hand commissures and one left-hand commissure in each segment (Figure 2.6) (Martin, 1997; Martin *et al.*, 1991; Stretton *et al.*, 1978). The six non-segmental interneurons are located in the ventral nerve cord with their somata in the head or tail segments.

2.2.2 Muscular System

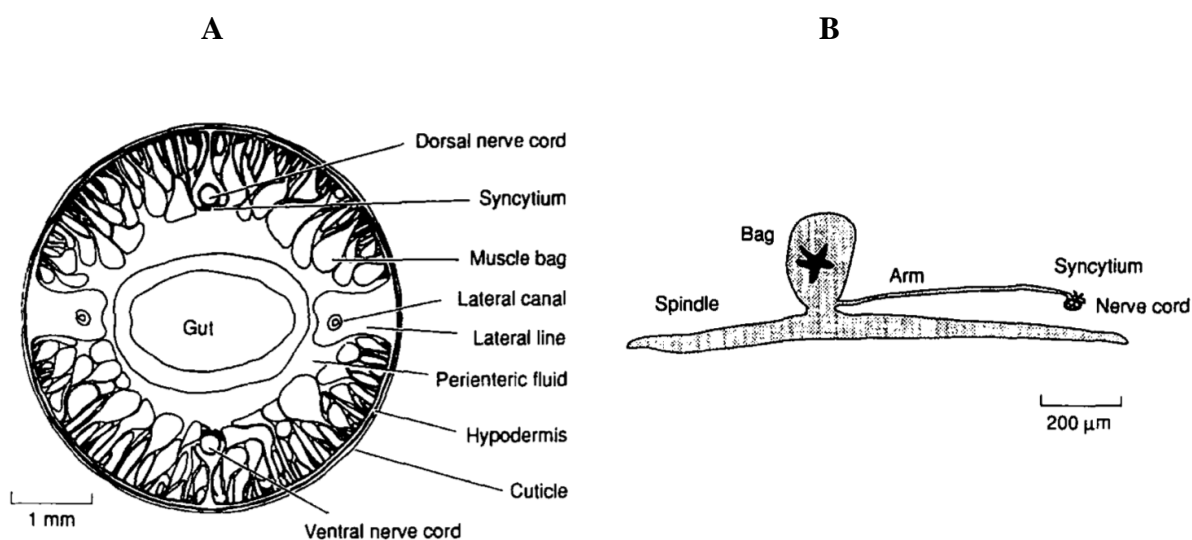
Transversely, the anterior portion of *Ascaris* body (from outside to inside, Figure 2.7A) shows the body to be composed of three concentric rings of cuticle, hypodermis and somatic muscle layer which surrounds the perienteric cavity containing the gut (Martin, 1997; Martin *et al.*, 1991). Two fields (dorsal and ventral) of mononucleated muscle cells (5×10^4 in number) which form the somatic muscle layer are separated by the two lateral lines



Source: Martin, 1997, p. 14.

Figure 2.6 Organization of *Ascaris suum* motor nervous system in one segment. Each segment contains eleven motoneurons and six non-segmental interneurons. The seven morphological types of motoneurons are indicated as DI: dorsal inhibitory, VI: ventral inhibitory, DE1: dorsal excitatory 1, DE2: dorsal excitatory 2, DE3: dorsal excitatory 3, V1 and V2: ventral excitatory.

(Stretton, 1976). Anchored to the hypodermis is the obliquely striated contractile substance known as the spindle or fibre which has an average length of *ca* 2 mm (del Castillo *et al.*, 1989; Rosenbluth, 1965a). The muscle cell forms a large, balloon-like structure called the bag or belly around mid-point of the spindle. The muscle bag (Figure 2.7B) measures *ca* 200 – 250 μ m in diameter and contains the single nucleus of the cell. Each muscle cell sends out processes called muscle arms which project from the base of the bag and transversely cross the muscle field to reach the syncytium over the nerve cord. Most muscle cells have more than one muscle arm, the mean number of arms is 2.7 (Stretton, 1976). Each arm branches from the nerve cord into thin terminal processes or fingers. The fingers of one arm form tight,



Source: Martin, 1997, p. 14.

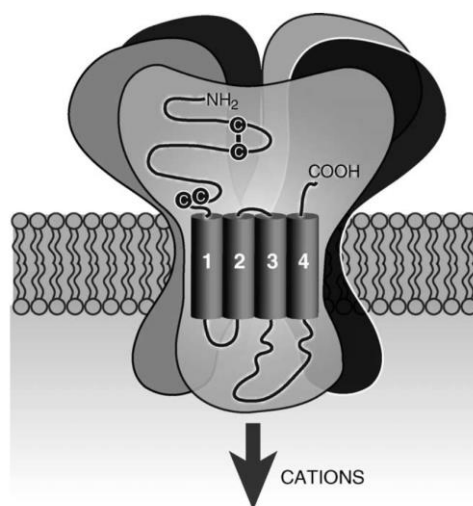
Figure 2.7 Transverse section of anterior section of *Ascaris* body showing arrangement of the three concentric rings of cuticle, hypodermis, somatic muscle layer, perienteric fluid and gut (A) and *Ascaris* muscle cell showing the muscle bag, spindle, arm, syncytium and nerve cord (B).

interwined junctions with those of adjacent arms at the syncytium. The interwound fingers extend longitudinally apposed to the nerve cord and are responsible for electrical coupling of muscle cells (Debell *et al.*, 1963; Rosenbluth, 1965b).

2.3 Nicotinic Acetylcholine Receptors (nAChRs)

Nicotinic acetylcholine receptors (nAChRs) are prototypical Cys-loop ligand-gated ion channels that mediate fast synaptic transmission in the neuromuscular and nervous system of vertebrates and invertebrates. They are an important target for many anthelmintics (Brown *et al.*, 2006). Other members of the Cys-loop superfamily of ligand-gated ion channels (LGICs) include ionotropic receptors for 5-hydroxytryptamine (5-HT), γ -aminobutyric acid (GABA) and glycine (Connolly & Wafford, 2004). The electric ray

Torpedo californica nAChR is the most carefully studied nAChR (Changeux *et al.*, 1996). The structure of the nAChR of a related species (*Torpedo marmorata*) has also been resolved at 4.6Å and 4.0Å (Unwin, 2005). nAChRs are composed of five protein subunits arranged around a central pore that is permeable to cations in most cases (Changeux, 2012; Karlin, 2002). Each nAChR subunit consists of an N-terminal, extracellular domain that contains the cys-loop (two cysteine residues separated by 13 amino acids), six loops (A – F) and four transmembrane domains (TM1 – TM4) (Figure 2.8). TM2 forms the lining of the ion pore. The subunits are differentiated as α and non- α , whereby α subunits contain two adjacent cysteine residues (linked by a disulfide bond) in loop C which are essential for acetylcholine binding, non- α subunits lack the adjacent cysteines. nAChRs are further differentiated on the basis of their subunit composition as homopentamers, in which all five subunits that make up the pentamer are identical, or as heteropentamers, where the subunits are non-identical and



Source: Brown *et al.*, 2006, p. 619.

Figure 2.8 Structure of the nicotinic acetylcholine receptor. Each nAChR consists of five subunits arranged around a cationic channel pore. The cys loop, the vicinal cysteines characteristic of an α subunit and four transmembrane regions (TM1-4) are shown for one subunit

contain at least two α subunits (Bouzat, 2012; Taly *et al.*, 2009). The ligand binding domain of nAChRs has been carefully elucidated using the acetylcholine binding protein (AChBP) from *Lymnaea stagnalis* (Brejc *et al.*, 2001). AChBP though a structural and functional homolog of the N-terminal ligand binding domain of a nAChR subunit, lacks the domains required to form a transmembrane ion channel. AChBP forms a stable homopentamer comprising of 210 residues. It is most closely related to vertebrate nAChR α subunits. Acetylcholine binding involves both an α and an adjacent subunit which could be an α or non- α depending on nAChR pentamer composition. Loops A – F contribute to the ligand binding sites, loops A, B, C from the principal face of the α subunit and loops D, E, F from the complementary face of the adjacent subunit (Arias, 1997).

2.3.1 *Caenorhabditis elegans* nAChRs

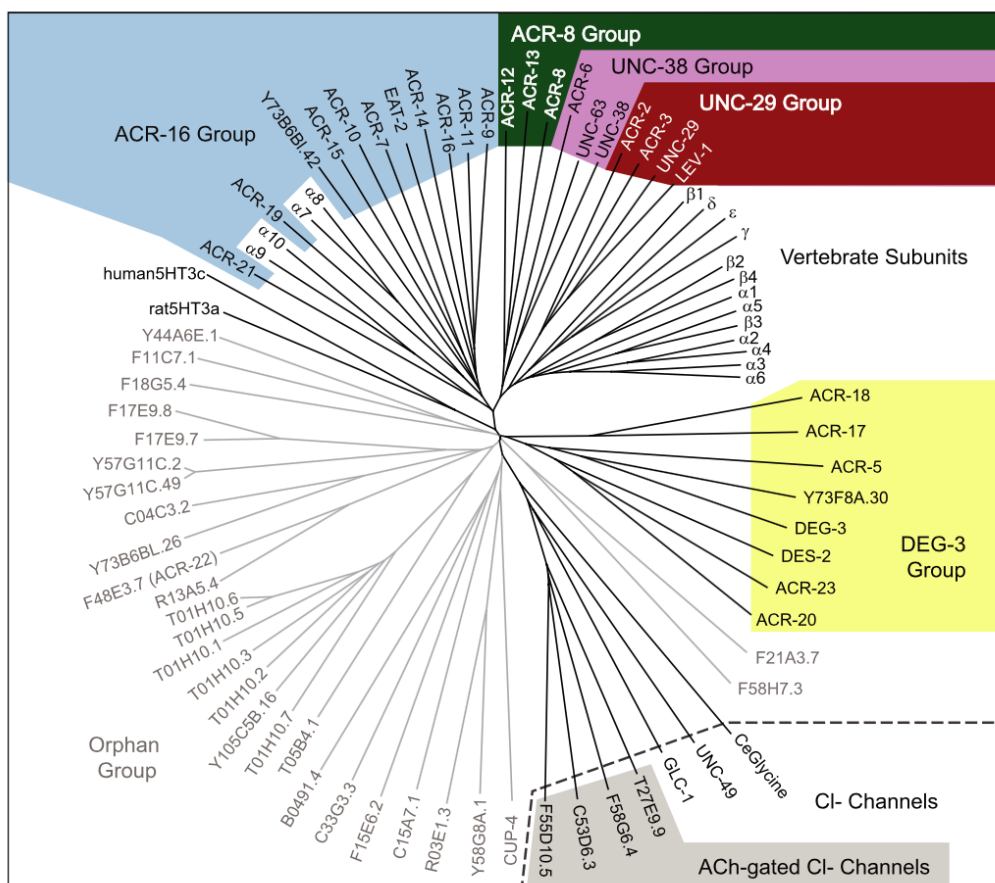
C. elegans nAChRs are the most widely studied compared to parasitic nematode or vertebrate nAChRs. Hence, the free-living nematode, *C. elegans*, is a powerful tool for providing insights into the molecular basis of the pharmacology of nAChRs. There are at least 32 nAChR subunits in the model nematode *C. elegans*, 22 of which are α subunits. These subunits are divided into five groups, on the basis of sequence homology, with each group named after the first member to be identified in that group (Holden-Dye *et al.*, 2013). The five groups are DEG-3, ACR-16, ACR-8, UNC-38 and UNC-29 (Figure 2.9). Subunits which display significant homology to nAChRs but do not fall within the five core groups are designated ‘Orphan subunits’, many of whose function is unknown (Brown *et al.*, 2006).

Almost all the members of the DEG-3, ACR-16, ACR-8 and UNC-38 groups are α subunits while those in the UNC-29 group are non- α subunits (Table 2.1). Notably, some

members of the ACR-16 group closely resemble vertebrate homomeric neuronal $\alpha 7$ receptor subunits (Mongan *et al.*, 2002). Different nAChR subunit combinations make up different nAChR types and on this basis, four major nAChR types have been described namely, levamisole-sensitive, nicotine-sensitive, DEG-3/DES-2 and EAT-2 nAChRs. These nAChR types also show different expression patterns and play vital roles in a variety of physiological functions including feeding, motility, development and reproduction. Levamisole-sensitive and nicotine-sensitive receptors are expressed in body wall muscle (Richmond & Jorgensen, 1999). DEG-3/DES-2 receptors are also expressed in neurons (Treinin *et al.*, 1998). EAT-2 receptors are expressed in the pharynx, and require a small transmembrane protein, EAT-18, for pharyngeal pumping (McKay *et al.*, 2004). Still in *C. elegans* (and also parasitic nematodes), different stoichiometry of nAChR subunits produces further different nAChR subtypes (Figure 2.10).

Levamisole (levamisole-sensitive) receptors are the most widely explored group of receptors in both *C. elegans* and parasitic nematodes. The nAChR subunit genes *lev-1*, *unc-29* and *unc-38* have been identified as important for levamisole sensitivity. However, when these subunits were injected in *Xenopus laevis* oocytes, expression levels were generally low as revealed by the small current responses to the major excitatory neurotransmitter, acetylcholine, and the anthelmintic, levamisole (Fleming *et al.*, 1997). Fleming *et al.*, 1997, also showed mecamylamine and neosurugatoxin but not α -bungarotoxin to inhibit the levamisole current responses. Richmond and Jorgensen later showed from *in vivo* recordings from *C. elegans* body wall muscle cells, evidence for the presence of two nAChR types.

These included alevamisole-sensitive receptor, requiring both *unc-29* and *unc-38* subunit genes for its activity, and a second receptor type that was activated by both nicotine



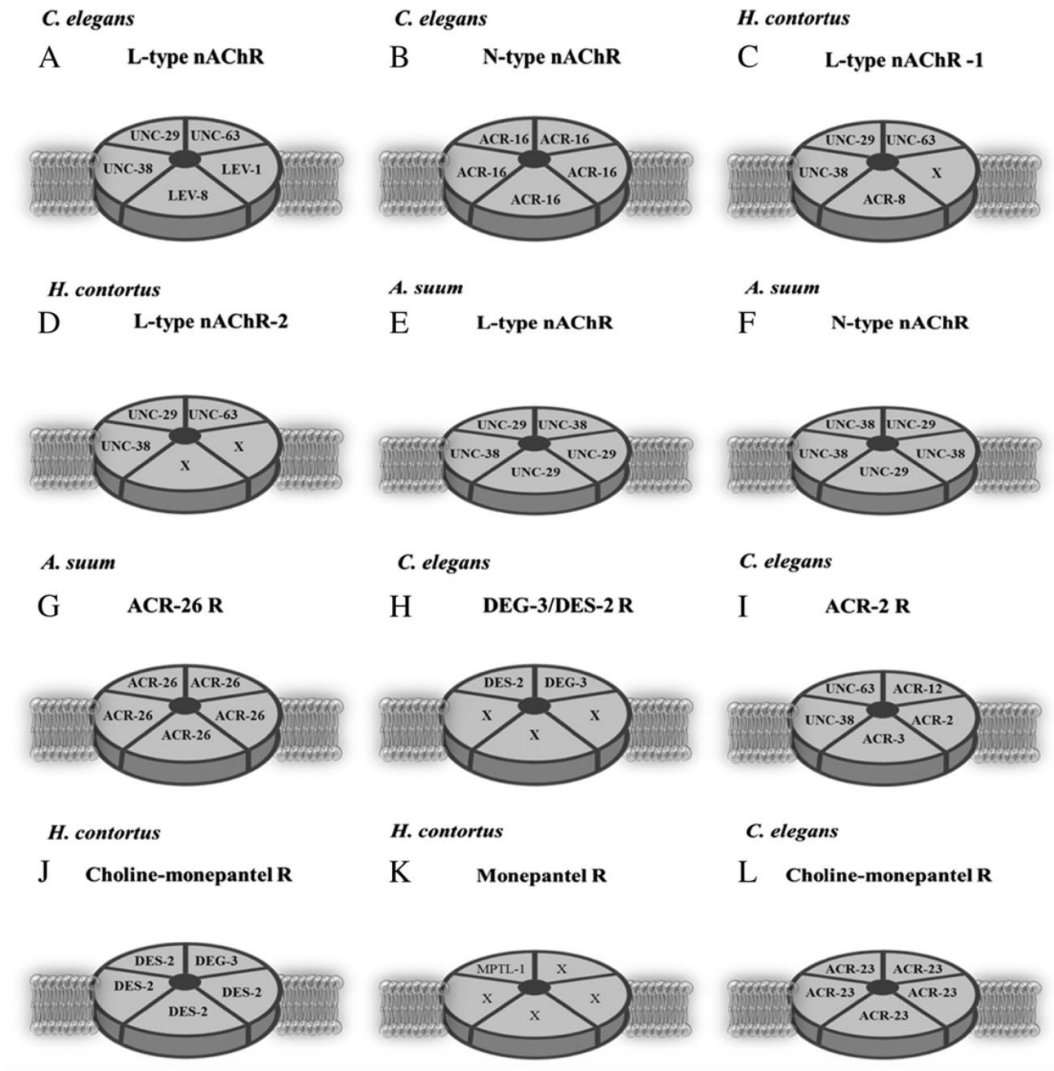
Source: Brown *et al.*, 2006, p. 620.

Figure 2.9 Tree showing the five core groups of nAChR subunits (indicated by the colored regions). Other groups such as the acetylcholine-gated chloride channels and the orphan group are also shown.

and acetylcholine. The receptor that was activated by both nicotine and acetylcholine was present in *unc-29* and *unc-38* mutants and showed rapid desensitization. Also, the levamisole response in wild-type *C. elegans* was completely blocked by d-tubocurarine whereas in *unc-29* mutants, the nicotine response was completely blocked by dihydro- β -erythroidine which caused only a slight block of the levamisole response. The acetylcholine response in wild-type *C. elegans* was only about 50% blocked by dihydro- β -erythroidine. While locomotion in

Table 2.1 Summary of the five core groups of nAChR subunits and their expression pattern in *C. elegans*. (Source: Holden-Dye *et al.*, 2013, p. 607.)

Group	Subunit	Expression
DEG-3	ACR-17 α	?
	ACR-18 α	Body wall muscle and nervous system
	ACR-20 α 7-like	Body wall muscle and nervous system
	ACR-22 non- α (lcg-11)	?
	ACR-23 α 7-like	Body wall muscle and nervous system
	DES-2 α (ACR-4)	Body wall muscle (head) and nervous systems IL2, FLP, PVD, PVC, ALA, and AVG
	DEG 3 α	PVC,, sensory endings of IL2, ALM, and PLM
	ACR-24 α	Role in fast neurotransmission?
	ACR-5 α	Nervous system – head neurons, neurons along body, tail neurons
	ACR-16	ACR-7 α 7 like
ACR-9 non- α		Neurons
ACR-10 α 7 like		Body wall muscle and nervous systems?
ACR-11 α		Muscle
ACR-14 non- α		DA, VB, AS, DB, DD, HSN, VC4&5, AIY, head and motoneurons, muscle, and intestine
ACR-15 α		Muscle (head and body wall), AVA, AVB, DVA, RID, PVQ, SMB?, SMD, 15, RIM, SAA, SIA, and SIB, all ventral nerve cord motoneurons except DD
ACR-16 α 7 like		Body wall muscle & subset of neurons, AVA, RIB, RID, SIB, SMD, DM motoneuron head and tail neurons
ACR-19 α		Neurons?
ACR-21 α		Ventral nerve cord cholinergic neurons
ACR-25 non- α ?		?
ACR-8	EAT-2 non- α	Pharyngeal muscle (pm4&5)
	ACR-8 α	All body wall muscle, head & tail neurons, anal and vulval muscles, nerve ring, nerve cord, ventral nerve cord motoneurons
	ACR-12 α	Ventral nerve cord neurons, head & tail nervous system
UNC-38	LEV-8(ACR-13) α	Body wall (strongest in head region) and vulval muscles, head neurons, mechanosensory neurons, many ventral nerve cord motoneurons, socket cells
	UNC-38 α	Body wall and vulval muscles, nervous system, colocalizes with TAX-6, ACR-8, ACR-12, and UNC-29; dorsal and ventral nerve cord
	UNC-63 α	Body wall & vulval muscle, ventral cord motoneurons, AS, DA, DB, VB, VD, DV, and VC, widespread in neurons
UNC-29	ACR-6 α	Role in fast neurotransmission
	ACR-2 non α	Forms functional channel with UNC-38, muscle & nervous system, ventral cord neurons, e.g., VA, VB, DA, DB (cholinergic motoneurons); PVQ, DVC, IL-1, RMD; tail neurons
	ACR-3 non- α	Body wall muscle and nervous systems, forms functional channels with UNC-38
	UNC-29 non- α	Body wall and head muscles, nervous system, ventral & dorsal cords, nerve ring
	LEV-1 (ACR-1) non- α	All body wall muscles, some ventral cord neurons



Source: From Holden-Dye *et al.*, 2013, p. 608.

Figure 2.10 Proposed stoichiometry of nAChRs in *C. elegans* and parasitic nematodes, showing possible subunit combinations for the various nAChR types.

unc-29 and *unc-38* mutants was impaired, the response to acetylcholine was maintained, suggesting an equal contribution of the nicotine-sensitive, N-AChR and the levamisole-sensitive, L-AChR to the acetylcholine response (Richmond & Jorgensen, 1999). In addition to *lev-1*, *unc-29* and *unc-38*, the *C. elegans* *unc-63* subunit gene has been shown to confer levamisole sensitivity (Culetto *et al.*, 2004). Subsequently, the L-AChR was described in *X*.

laevis oocyte expression studies to require five nAChR subunits, UNC-29, UNC-38, UNC-63, LEV-1 and LEV-8 (also known as ACR-13), LEV-1 and UNC-29 are non- α subunits while UNC-38, UNC-63 and LEV-8 are α subunits. All five subunits, in addition to three ancillary proteins (RIC-3, UNC-50 and UNC-74) were required for functional expression of the L-AChR (Boulin *et al.*, 2008). The ancillary proteins RIC-3, UNC-50 and UNC-74 are respectively involved in the maturation, trafficking and folding of the receptor (Eimer *et al.*, 2007; Halevi *et al.*, 2002; Haugstetter *et al.*, 2005). Boulin *et al.*, 2008, also showed d-tubocurarine, methyllycaconitine and hexamethonium to be potent antagonists of the L-AChR, while α -bungarotoxin and dihydro- β -erythroidine had modest blocking effects, in agreement with observations by Richmond & Jorgensen (1999). Another subunit, ACR-8, has been identified in *C. elegans* body wall muscle but its role is uncertain as it neither contributes to levamisole-sensitive or insensitive nAChRs (Touroutine *et al.*, 2005).

Nicotine-sensitive nAChRs or N-AChRs are sensitive to nicotine but insensitive to levamisole. Unlike levamisole receptors which are composed of heteropentamers, N-AChRs are homopentamers. Five ACR-16 subunits make up a N-AChR in *C. elegans* (formerly called Ce21) which is closely related to vertebrate $\alpha 7$ receptors (Ballivet *et al.*, 1996; Raymond *et al.*, 2000). Also, N-AChRs require only RIC-3 for their functional expression in *X. laevis* oocytes. Ballivet *et al.* (1996), further demonstrated that levamisole not only failed to activate the *C. elegans* ACR-16 receptor but also antagonized acetylcholine responses. Additionally, dihydro- β -erythroidine acted as a potent antagonist of the *C. elegans* ACR-16 receptor, as opposed to very weak antagonism on L-AChRs. *C. elegans* ACR-16 is also strongly antagonized by d-tubocurarine but weakly antagonized by methyllycaconitine and

α -bungarotoxin. Ballivet *et al.* (1996), showed the *C. elegans* ACR-16 receptor to desensitize rapidly following application of acetylcholine or nicotine. Although nicotine was a more potent agonist of the *C. elegans* ACR-16 receptor than acetylcholine (EC₅₀ 12.6 μ M for nicotine versus 55.4 μ M for acetylcholine), the maximum response for nicotine was lower than that for acetylcholine, suggesting nicotine is a partial agonist of the *C. elegans* ACR-16 receptor. Interestingly, *acr-16* mutants showed no obvious behavioral phenotype but *unc-63:acr-16* or *unc-29:acr-16* double mutants showed more severe locomotory deficits than either *unc-63* or *unc-29* mutants (Li *et al.*, 2014; Touroutine *et al.*, 2005).

Members of the DEG-3 group of nAChRs are preferentially activated by the amino-acetonitrile derivative, monepantel, causing spastic paralysis of body wall and pharyngeal muscles. DEG-3-like nAChRs have been identified only in nematodes. The major subunit member is ACR-23 which is expressed mainly in *C. elegans* body wall muscles and in unidentified head and tail neurons (Rufener *et al.*, 2013). Rufener *et al.* (2013), also reconstituted functional receptors made up of *C. elegans* ACR-23 subunits in *Xenopus* oocytes and showed that these receptors responded to monepantel, in addition to choline, nicotine, and acetylcholine, in order of current response magnitude, with choline responses strongly potentiated by monepantel. Another subunit member of the DEG-3 group is ACR-20 which forms homomeric receptors just like ACR-23 (Baur *et al.*, 2015). According to Baur *et al.* (2015), low concentrations (<1 nM) of monepantel produced positive allosteric modulatory effects on the *C. elegans* ACR-20 receptor, while high concentrations (>0.1 μ M) produced direct agonist effects on the receptor. Functional receptors comprising of *C. elegans* DEG-3 and DES-2 subunits have also been reconstituted in *X. laevis* oocytes where

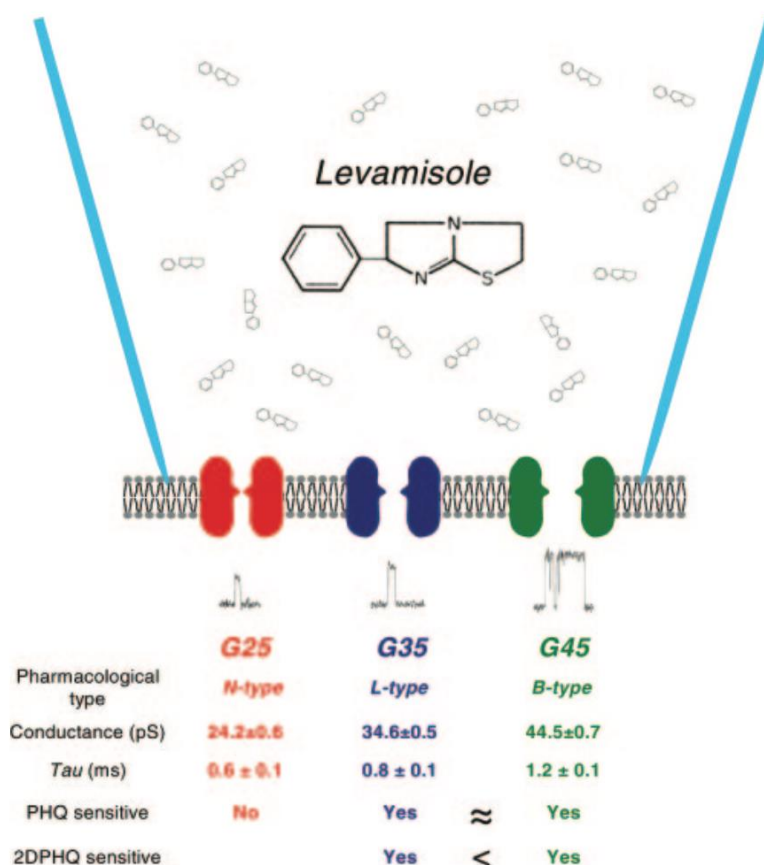
the receptors were activated by choline and acetylcholine, with choline as the more potent agonist (Treinin *et al.*, 1998; Yassin *et al.*, 2001).

EAT-2 nAChRs are not a well-exploited target for anthelmintic drug development. These receptors are localized postsynaptically on pharyngeal muscle and require interaction with the protein EAT-18 for nicotinic transmission in *C. elegans* pharynx (McKay *et al.*, 2004). Hence, EAT-2 receptors are believed to play a role in pharyngeal pumping and therefore, feeding. At present, it is not known if EAT-2 is homomeric or requires other subunits to form the receptor.

2.3.2 Parasitic nematode nAChRs

Parasitic nematode nAChRs are therapeutic targets for many anthelmintics including levamisole, pyrantel, oxantel, bphenium and morantel. The nAChR from the pig parasitic nematode *Ascaris suum* (clade III) is the most extensively studied parasitic nematode nAChR. Initial patch clamp recordings from *Ascaris* muscles revealed the presence of at least two acetylcholine-activated channel types (Pennington & Martin, 1990). Single channel recordings from *Ascaris* muscle later showed low levamisole concentrations (1 – 10 μM) to cause channel opening and high levamisole concentrations (30 and 90 μM) to cause flickering channel block. The channel conductance was in the range of 18 – 50 pS (Robertson & Martin, 1993). Pyrantel and oxantel were also shown to act as agonists and open channel blockers of these channels (Dale & Martin, 1995; Robertson *et al.*, 1994). Muscle contraction studies using different agonists and antagonists revealed the existence of more than one nAChR type on *Ascaris* body wall muscle with different sensitivities to agonists and antagonists (Robertson *et al.*, 2002). Three nAChR types on *Ascaris* muscle having different channel conductances and mean open times have been characterized at the single channel

level using the patch clamp technique (Qian *et al.*, 2006). These nAChR types have been named after their preferred agonist and include the L-type preferentially activated by levamisole, the N-type preferentially activated by nicotine and the B-type preferentially activated by buprenorphine (Figure 2.11). The single channel conductance and mean open times are respectively, 24 pS and 0.6 ms for the N-type, 35 pS and 0.8 ms for the L-type, and 45 pS and 1.3 ms for the B-type. Unlike in *C. elegans* where the actions of levamisole and nicotine

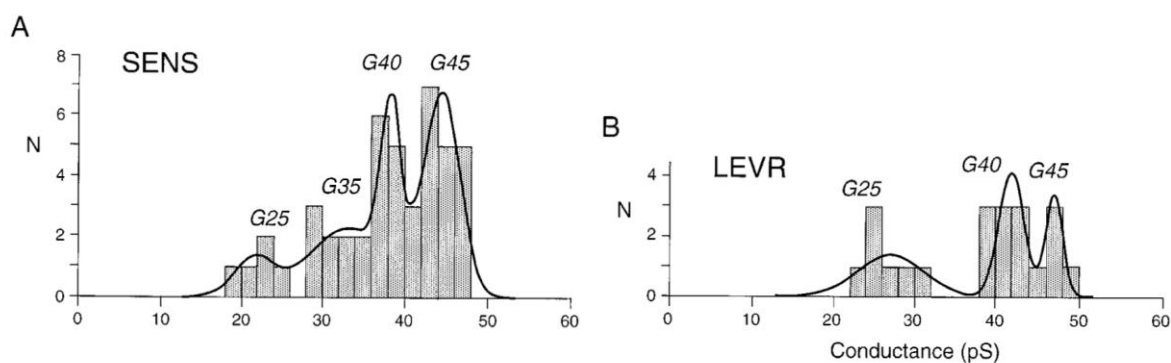


Source: Qian *et al.*, 2006, p. E2115.

Figure 2.11 Summary diagram of nAChR subtypes on *Ascaris suum* somatic muscle cell membrane. The single channel as well as agonist and antagonist pharmacological properties of each subtype are indicated. N-subtype prefers nicotine, L-subtype prefers levamisole and B-subtype prefers buprenorphine. The subtypes show different sensitivities to the competitive antagonists paraherquamide (PHQ) and 2-desoxoparaherquamide (2DPHQ).

are selective (levamisole-sensitive currents are not activated by nicotine and vice versa), the differences in agonist action are subtler in *A. suum*. For instance, although levamisole preferentially activates L-type channels, it also opens N- and B-type channels to a lesser extent. Bephenium preferentially activates B-type channels but also opens some L-type but not N-type channels. Hence, nAChR types in *A. suum* are less distinct in terms of agonist pharmacology than those in *C. elegans*. At high concentrations, levamisole activates all three nAChR types in *A. suum*.

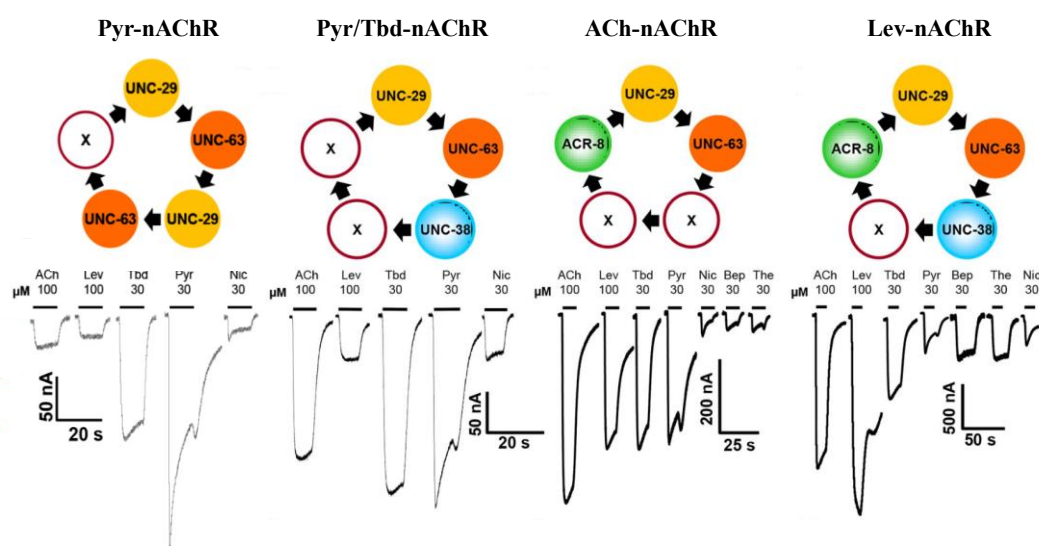
In addition to the 25 pS, 35 pS and 45 pS single channel conductances, a fourth levamisole-activated subtype with a conductance of 40 pS has been revealed in the strongylid nematode *Oesophagostomum dentatum* (clade V), suggesting the presence of four nAChR types in *O. dentatum* (Robertson *et al.*, 1999). Robertson *et al.* (1999), also showed loss of the G35 channel in levamisole-resistant (LEVR) parasites which was present in levamisole-sensitive (SENS) parasites (Figure 2.12). Therefore, just as in *A. suum*, the G35 channel is the L-type nAChR.



Source: Robertson *et al.*, 1999, p. 757.

Figure 2.12 Frequency histograms of single channel conductances for SENS (A) and LEVR (B) parasites.

In *O. dentatum*, different nAChR subunit combinations expressed in *Xenopus* oocytes have revealed the presence of four distinguishable nAChR subtypes based on agonist sensitivities (Buxton *et al.*, 2014). These include the pyrantel (Pyr)-nAChR composed of UNC-29 and UNC-63 subunits, the pyrantel/tribendimidine (Pyr/Tbd)-nAChR composed of UNC-29, UNC-63 and UNC-38 subunits, the acetylcholine (ACh)-nAChR composed of UNC-29, UNC-63 and ACR-8 subunits, and the levamisole (Lev)-nAChR composed of UNC-29, UNC-63, UNC-38 and ACR-8 subunits (Figure 2.13). Note that the LEV-8 subunit has not been detected in any nematode parasite, however, a related subunit (ACR-8) can replace LEV-8 to reconstitute L-AChRs in the parasites. In accordance with *in vivo* studies, Buxton *et al.* (2014), showed the levamisole-nAChR comprising of UNC-29, UNC-63,



Source: Modified from Buxton *et al.*, 2014, pp. 5 & 7.

Figure 2.13 Summary of the four *O. dentatum* nAChR subtypes based on different combinations of subunits reconstituted in *Xenopus laevis* oocytes. The pyrantel (Pyr)-nAChR is composed of UNC-29 and UNC-63 subunits, the pyrantel/tribendimidine (Pyr/Tbd)-nAChR is composed of UNC-29, UNC-63 and UNC-38 subunits, the acetylcholine (ACh)-nAChR is composed of UNC-29, UNC-63 and ACR-8 subunits, and the levamisole (Lev)-nAChR is composed of UNC-29, UNC-63, UNC-38 and ACR-8 subunits.

UNC-38 and ACR-8 subunits to have a single channel conductance of 35 pS. These authors also demonstrated that varying the subunit stoichiometry of the pyrantel-nAChR comprising of UNC-29 and UNC-63 subunits produced changes in its pharmacological properties. When the ratio of *unc-29:unc-63* injected cRNA was 1:5, the pyrantel and tribendimidine current responses were significantly increased, and when it was 5:1, the nicotine and levamisole current responses became significantly bigger than the acetylcholine response.

Two L-AChR subtypes have also been identified in *A. suum* by varying the stoichiometry using different ratios of UNC-38 and UNC-29 subunits (Williamson *et al.*, 2009). Oocytes injected with *unc-38* and *unc-29* cRNA at ratios of 5:1 and 1:5 produced robust current responses compared to those injected at ratios of 10:1 and 1:10 which produced very small current responses. Also, when the *unc-38:unc-29* ratio was 5:1, nicotine acted as a full agonist and levamisole acted as a partial agonist, whereas when the ratio was 1:5, levamisole was a full agonist and nicotine a partial agonist. Still with the 5:1 ratio, oocytes responded to oxantel but not pyrantel, while with the 1:5 ratio, oocytes responded to pyrantel but not oxantel.

Genes encoding UNC-38, UNC-29, UNC-63 and ACR-8 have been identified in *Hemonchus contortus*, which belongs to Clade V just as *O. dentatum* and *C. elegans*. Two types of L-AChRs namely Hco-L-AChR1 and Hco-L-AChR2 were identified in *H. contortus* by varying subunit combinations (Boulin *et al.*, 2011). The receptor Hco-L-AChR1 which is made up of all four subunits UNC-38, UNC-29, UNC-63 and ACR-8 was more sensitive to levamisole than acetylcholine and was weakly sensitive to pyrantel and nicotine. Omitting ACR-8 from the combination produced the Hco-L-AChR2 receptor which was more sensitive to pyrantel and acetylcholine than levamisole. Recently, four copies of the *unc-29*

L-AChR subunit gene (Hco-UNC-29.1, Hco-UNC-29.2, Hco-UNC-29.3 and Hco-UNC-29.4) were identified in *H. contortus*, and duplication of the *unc-29* L-AChR subunit gene was shown to be a common feature of the clade V parasitic nematodes (Duguet *et al.*, 2016). Substituting each of the four UNC-29 copies in the Hco-L-AChR1 receptor subunit composition produced three functional receptor types which differed from each other in terms of agonist and antagonist pharmacology. UNC-29.2 failed to reconstitute a functional receptor. L-AChR1.1 comprised of UNC-38, UNC-29.1, UNC-63 and ACR-8 subunits and was more responsive to levamisole than acetylcholine. Additionally, mecamylamine was a potent antagonist of L-AChR1.1. When the UNC-29.1 subunit was replaced with UNC-29.2 (L-AChR1.2), the oocytes did not produce any detectable current responses. When UNC-29.1 was replaced with UNC-29.3 (L-AChR1.3), the acetylcholine response was greater than the levamisole response and mecamylamine was a less potent antagonist. When UNC-29.1 was replaced with UNC-29.4 (L-AChR1.4), levamisole and acetylcholine responses were about equal and mecamylamine was more potent (Figure 2.14).

2.3.3 Vertebrate nAChRs

Vertebrate nAChRs contain five subunits namely α , β , γ , δ and ϵ and are important therapeutic targets for various neurodegenerative diseases including Alzheimer's disease, Parkinson's, disease and schizophrenia, as well targets to treat alcohol and nicotine dependence (Dineley *et al.*, 2015; Dwoskin *et al.*, 2009; Posadas *et al.*, 2013). A total of 17 nAChR subunits have been identified in vertebrates (Millar & Gotti, 2009). This number is less than the 32 subunits identified in *C. elegans*. Vertebrate nAChRs can be divided into two groups based on their primary site of expression as muscle and neuronal nAChRs. Muscle nAChRs are expressed at the neuromuscular junction and are composed of the subunits $\alpha 1$,

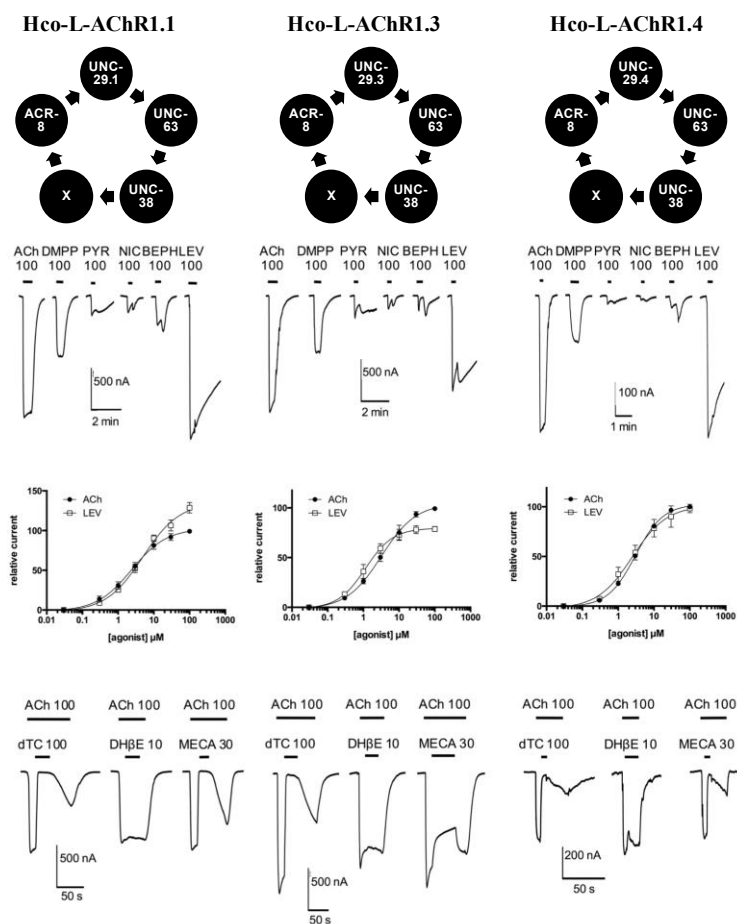


Figure 2.14 Pharmacological profile of *Hemonchus contortus* reconstituted receptors in *Xenopus* oocytes. *Hco-unc-29.1*, *Hco-unc-29.3* and *Hco-unc-29.4* were individually combined with *Hco-unc-63*, *Hco-unc-38* and *Hco-acr-8* and co-expressed with the three ancillaries *Hco-unc-3.1*, *Hco-unc-50* and *Hco-unc-74*. All responses were normalized to 100 μM acetylcholine to generate the acetylcholine and levamisole concentration-response curves. Modified from Duguet *et al.*, 2016, pp. 12/26.

$\beta 1$, δ , and either γ and ϵ . The five muscle nAChRs co-assemble into only two nAChR subtypes, embryonic and adult. Embryonic muscle nAChRs are composed of $(\alpha 1)_2$, $\beta 1$, γ and δ subunits whereas adult muscle nAChRs are composed of $(\alpha 1)_2$, $\beta 1$, δ and ϵ . Neuronal nAChRs are more diverse than muscle nAChRs and comprise of various homomeric or heteromeric combinations of twelve subunits: $\alpha 2 - \alpha 10$ and $\beta 2 - \beta 4$ (Kalamida *et al.*, 2007; Millar, 2003). Most vertebrate neuronal nAChRs are heteromeric, containing at least one α

and one β subunit (most commonly $(\alpha)_2(\beta)_3$). Only $\alpha 7$, $\alpha 8$ and $\alpha 9$ subunits reconstitute functional homomeric nAChRs in *Xenopus* oocytes (Couturier *et al.*, 1990; Elgoyhen *et al.*, 1994; Gerzanich *et al.*, 1994). Evidence for co-assembly and subunit diversity of vertebrate nAChRs has been revealed in the insect *Drosophila* and *C. elegans* models. In *Drosophila*, 10 nAChR subunits have been identified and 42 possible nAChR subunits have been predicted in *C. elegans* (Bargmann, 1998; Littleton & Ganetzky, 2000). Table 2.2 provides a summary of vertebrate nAChR subunit combinations from studies of native nAChRs and heterologous expression studies.

2.4 Medicinal plants

Broadly, medicinal plants are defined as plants which have similar therapeutic properties with conventional pharmaceutical drugs. Humans have used medicinal plants to cure or lessen disease symptoms since ancient times. Even today, a large proportion of the population in developing nations still rely on phytomedicine for primary health care and treatment of diseases in animals (Githiori *et al.*, 2005; Tagboto & Townson, 2001). Medicinal plants are frequently preferred because they are perceived to be well-tolerated and have fewer side effects compared to conventional pharmaceuticals (Petrovska, 2012). It is also important to remember that many drugs used in modern medicine today are modeled from medicinal plant products. Use of medicinal plants to treat anthelmintic infections in livestock and humans continues to be exploited as an alternative to pharmaceutical products (Githiori *et al.*, 2004). Remarkably, use of plants to treat worm infections in animals is no longer limited to developing nations. The developed world is experiencing a widespread reawakening in phytomedicine. This is driven in part by the limited availability of pharmaceutical anthelmintic drugs and the widespread occurrence of multidrug resistance

Table 2.2 Assembly and subunit diversity of vertebrate nicotinic acetylcholine receptors.
(Modified from Millar, 2003, p. 871.)

Receptor subtype	Subunits	Subunit combinations
Muscle-type	$\alpha 1, \beta 1, \gamma, \delta, \epsilon$	$\alpha 1, \beta 1, \gamma, \delta \ddagger$ $\alpha 1, \beta 1, \epsilon, \delta \ddagger$
Neuronal (α BTX-insensitive)	$\alpha 2-\alpha 6, \beta 2-\beta 4$	$\alpha 2\beta 2$ $\alpha 2\beta 4$ $\alpha 3\beta 2$ $\alpha 3\beta 4$ $\alpha 4\beta 2$ $\alpha 4\beta 4$ $\alpha 6\beta 2 \S$ $\alpha 6\beta 4$ $\alpha 2\alpha 5\beta 2$ $\alpha 3\alpha 5\beta 2$ $\alpha 3\alpha 5\beta 4$ $\alpha 3\alpha 6\beta 2$ $\alpha 3\alpha 6\beta 4$ $\alpha 3\beta 3\beta 4$ $\alpha 4\alpha 5\beta 2$ $\alpha 5\alpha 6\beta 2$ $\alpha 6\beta 3\beta 4$ $\alpha 3\alpha 5\beta 2\beta 4$ $\alpha 3\alpha 6\beta 3\beta 4$ $\alpha 4\alpha 5\alpha 6\beta 2$ $\alpha 4\beta 2\beta 3\beta 4$
Neuronal (α BTX-sensitive)	$\alpha 7, \alpha 8 \P$	$\alpha 7$ $\alpha 8$ $\alpha 7\beta 2$ $\alpha 7\beta 3$ $\alpha 7\alpha 8$ $\alpha 5\alpha 7\beta 2$ $\alpha 5\alpha 7\beta 4$
Sensory epithelia	$\alpha 9, \alpha 10$	$\alpha 9$ $\alpha 9\alpha 10$

(Waller *et al.*, 2001). Although the bioactive compounds in medicinal plants have not been fully identified, scientific validation of the anthelmintic activity of several of these plant species have been reported (Al-Abd *et al.*, 2013; Githiori *et al.*, 2006). Interaction between additional healers and scientists as well as research aiming to identify the bioactive compounds in plants with anthelmintic activity should therefore be promoted as this could accelerate anthelmintic drug discovery and development.

2.4.1 *Daniellia oliveri*

Daniellia oliveri is a deciduous, medium-sized tree of the family Caesalpinaceae up to 25 – 35 m tall. The genus *Daniellia* comprises 10 species which are all confined to the forest areas of West and Central Africa. Only *D. oliveri* extends to Sudan and Uganda. *D. oliveri* flowers during the dry season from October to March and fruits from January to June. Various biological activities for *D. oliveri* have been reported. Cardiac glycosides present in the methanol extract of the bark showed non-competitive antagonism on muscarinic receptors on isolated rat bladder smooth muscle (Onwukaeme *et al.*, 1999a). Methanol extracts of the leaves and stem bark were showed to possess neuromuscular blocking properties on rat skeletal muscle (Onwukaeme *et al.*, 1999b). The smoke of the bark of *D. oliveri* is traditionally used to repel mosquitoes in Guinea Bissau, West Africa, and may significantly contribute to reducing prevalence of diseases transmitted by these mosquitoes (Palsson & Jaenson, 1999a; Palsson & Jaenson, 1999b). The leaves of *D. oliveri* are traditionally used to treat diarrhea in Northern Nigeria (Ahmadu *et al.*, 2007). Ahmadu *et al.* (2007), showed the n-butanol extract of *D. oliveri* leaves to protect against castor oil-induced diarrhea in mice. The anti-diarrheal effect of this extract was dose-dependent; 200 mg/kg of the extract provided 80% while 100 mg/kg and 50 mg/kg provided 60% protection against

diarrhea. Various aqueous and ethanol extracts of the leaves, bark and roots showed *in vitro* antibacterial activity against a range of pathogenic bacteria including *Staphylococcus aureus*. The ethanol extract of the leaves also showed significant antifungal activity against *Tricophyton rubrum* (Ahmadu *et al.*, 2004). Fodders supplemented with *D. oliveri* foliage improved performance of buckling goats fed threshed sorghum top basal diet (Isah *et al.*, 2015; Okunade *et al.*, 2016).

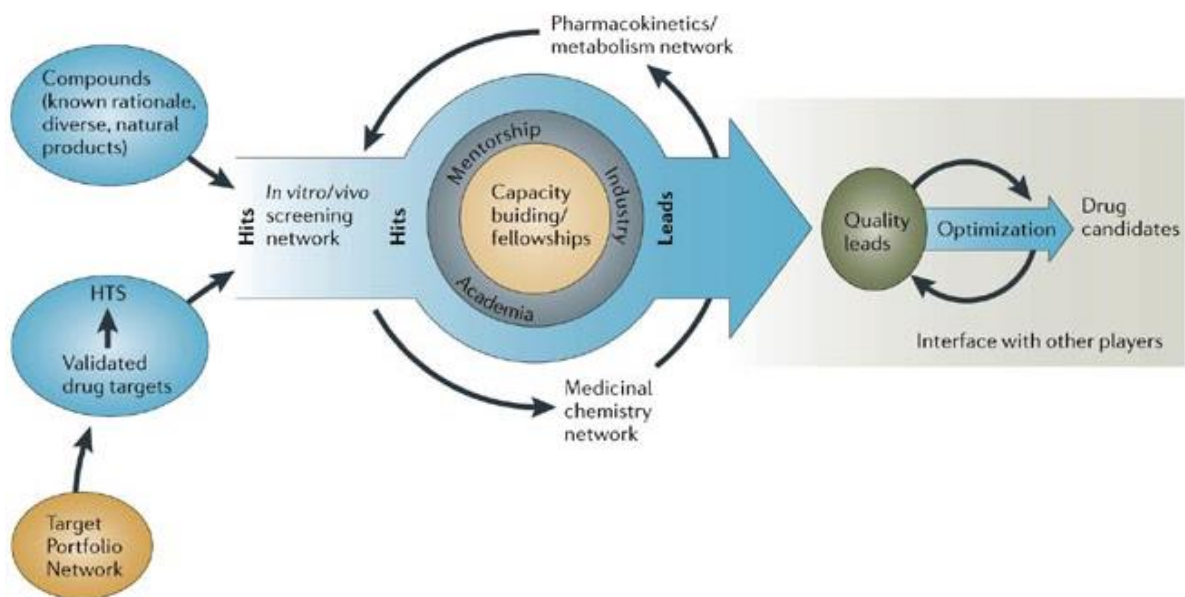
2.4.2 *Psorospermum febrifugum*

Psorospermum febrifugum (family Hypericaceae) is a flowering shrub or tree up to 4 m high that is widespread in tropical Africa but grows predominantly in the savanna from Guinea to West Cameroon. *P. febrifugum* as the name implies is known for its febrifugal action. The bark and roots are used to treat all sorts of skin infections including ‘craw-craw’ and other parasitic skin diseases. The bark is used in Bukoba Rural district in Tanzania for the traditional treatment of skin infections including body sores and Herpes zoster (Kisangau *et al.*, 2007). These authors showed the petroleum ether, dichloromethane and water extract of *P. febrifugum* bark to have antimicrobial activity against *Escherichia coli*. *P. febrifugum* is rich in antioxidants. Xanthonenes and emodines have been isolated from *P. febrifugum* and showed to possess antioxidant, anticancer, antiviral and antimicrobial potential (Permana *et al.*, 1994; Tsaffack *et al.*, 2009). The leaves, stem bark and root bark of *P. febrifugum* are used for traditional treatment of HIV/AIDS and its associated symptoms in some districts in Uganda (Lamorde *et al.*, 2010).

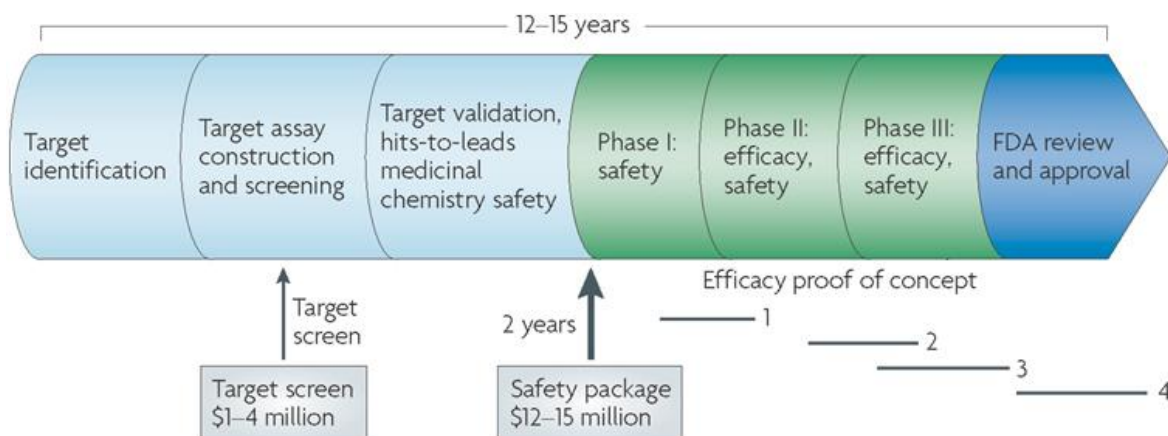
2.4.3 The drug development pipeline

The demand for new antiparasitic therapeutic agents to complement or replace existing ones is on the rise as resistance is likely to compromise every drug over time. Use of

existing drugs is also limited by their side effects, poor compliance and limited efficacy (Renslo & McKerrow, 2006). Therefore, a drug development pipeline is essential for securing the availability of new therapies should existing ones fail. The drug development pipeline represents the series of activities involved in the discovery and production of a new therapeutic product (Figure 2.15). For NTDs, this usually requires cross-sector partnerships with pharmaceutical companies, academic and nonprofit research institutions worldwide (Ramamoorthi *et al.*, 2014a; Ramamoorthi *et al.*, 2014b). Unfortunately, development of the drugs for NTDs is a low priority to pharmaceutical companies, causing the drug development pipeline for these diseases to dry up (Trouiller & Olliario, 1998; Trouiller & Olliario, 1999). Collaboration between nonprofit private and public research institutions in both developed and developing countries should therefore be promoted to significantly accelerate development of new drugs (McKerrow, 2005; Trouiller *et al.*, 2002). The very first step in pipeline is the identification and validation of targets. This is followed by high-throughput screening efforts for identification of hits. Hits are further screened to identify leads which show potentials for improvement via development of structure-activity relationships (Nwaka & Hudson, 2006). Lead compounds are screened for activity and toxicity, and those with pharmacological and toxicity profiles within acceptable limits are considered drug candidates and will undergo clinical trials (phases I, II and III) to ascertain their efficacy and safety in humans. Lastly, drug candidates that pass all 3 clinical trial phases are submitted to the Food and Drug Administration (FDA) for review and approval (Roses, 2008). Since it takes at least 15 years for a drug to go through the development pipeline to when it becomes available in the drug market, research leading to discovery of lead compounds must continue so that



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Source: Nwaka & Hudson, 2006, p. 944; Roses, 2008, p. 808.

Figure 2.15 Drug candidate and development pipeline. Top: Lead discovery strategy for tropical diseases. Bottom: Summary of steps involved in drug discovery and development.

compounds will always be available for further development should those in clinical trials or under review fail (Figure 2.15).

2.5 Anthelmintics and anthelmintic resistance

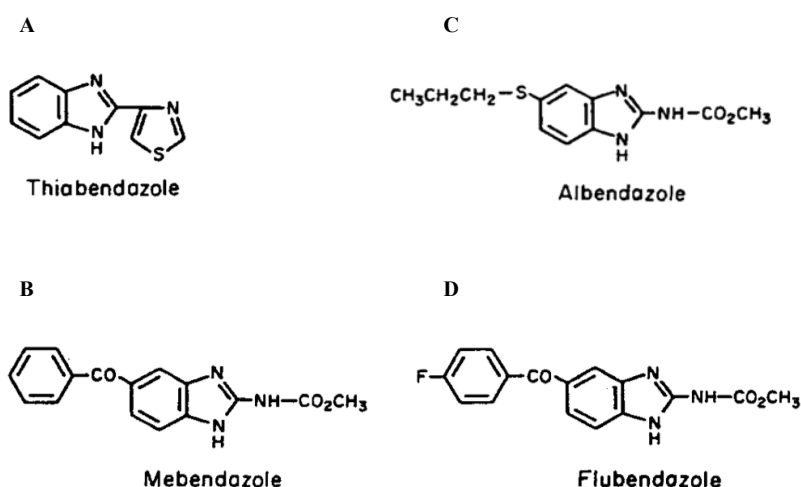
2.5.1 Anthelmintics

Anthelmintics are drugs that are used to treat infections caused by parasitic worms (helminths) (Holden-Dye & Walker, 2007). There are three major groups of helminths namely: nematodes (roundworms), trematodes (flukes) and cestodes (tapeworms) (Castro, 1996). These groups of helminths are divided into two phyla; nematodes (roundworms) and platyhelminths (trematodes and cestodes) (Hotez *et al.*, 2008; Wang *et al.*, 2008).

Anthelmintics either kill worms or cause their expulsion from the body, without causing any significant damage to the host (Martin *et al.*, 1997). Although there is a high prevalence of parasitic worms, the progress of anthelmintic drug discovery and development by pharmaceutical companies has been slow over the years. One contributing factor is that the majority of those suffering from helminth infections live in developing nations who lack the resources to support a profitable drug market (Pink *et al.*, 2005). Development of new anthelmintics is limited by high costs and modest global markets for antiparasitic drugs and chemicals. The cost of development of a new drug is estimated at US \$40 million for livestock use, and more than US \$800 million for human use. The global market for antiparasitic drugs and chemicals are estimated at US \$12 billion for plant pathogens, \$11 billion for livestock and companion animals, and \$0.5 for human health (DiMasi *et al.*, 2003; Evans & Chapple, 2002; Martin & Robertson, 2010; Morgan *et al.*, 2011). Many anthelmintic drugs used to treat humans were first developed and marketed as veterinary drugs (Crump & Omura, 2011; Geary, 2005; Omura, 2008). There are only a few classes of

anthelmintics including; benzimidazoles, imidazothiazoles, tetrahydropyrimidines, macrocyclic lactones, amino-acetonitrile derivatives, spiroindoles and cyclooctadepsipeptides.

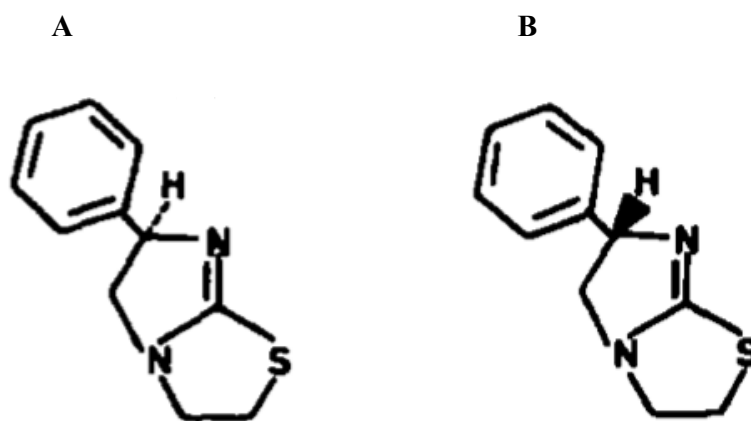
2.5.1.1 Benzimidazoles (BZs). Thiabendazole was the first benzimidazole anthelmintic agent produced. Since the introduction of thiabendazole in 1961, a number of benzimidazoles with improved efficacy and extended spectrum of action have been developed (McKellar & Scott, 1990). These include mebendazole, albendazole and flubendazole (Figure 2.16). The initial mode of action of benzimidazoles was thought to be inhibition of various parasite metabolic enzymes including fumarate reductase and malate dehydrogenase (Prichard, 1970; Tejada *et al.*, 1987). However, it is now established that benzimidazoles selectively bind with high affinity to parasite β -tubulin and inhibit microtubule polymerization. This results in the destruction of cell structure and consequent death of the parasite (Lacey, 1990).



Source: McKellar & Scott, 1990, p. 227.

Figure 2.16 Chemical structures of thiabendazole (A), mebendazole (B), albendazole (C) and flubendazole (D).

2.5.1.2 Imidazothiazoles. Imidazothiazoles act as nicotinic acetylcholine receptor (nAChR) agonists. They bind to nAChRs on body wall muscles, causing spastic paralysis of the worm, and hence, its expulsion from the host (Aceves *et al.*, 1970). Tetramisole (Figure 2.17), an aminothiazol derivative, was the first member of this class of anthelmintics, and constitutes a racemic mixture of 50% L- or S- and D- or R-isomers (Raeymaekers *et al.*, 1966; Raeymaekers *et al.*, 1967; Thienpont *et al.*, 1966). The L-isomer was later demonstrated to be more potent than the racemic mixture or the the D-isomer (Thienpont *et al.*, 1969; Van den Bossche & Janssen, 1967). Consequently, the D-isomer was removed from the racemic mixture and this led to the development of the L-isomer as levamisole. The detailed mode of action of levamisole, the only existing drug in this class, has been carefully studied at the single-channel level in nematode body wall muscles (Qian *et al.*, 2006; Robertson *et al.*, 1999; Robertson & Martin, 1993). Robertson & Martin (1993), showed using the patch-clamp technique that at the single-channel level in *A. suum* muscles. Levamisole (1 – 90 μM concentrations) causes activation of cation-selective channels, in

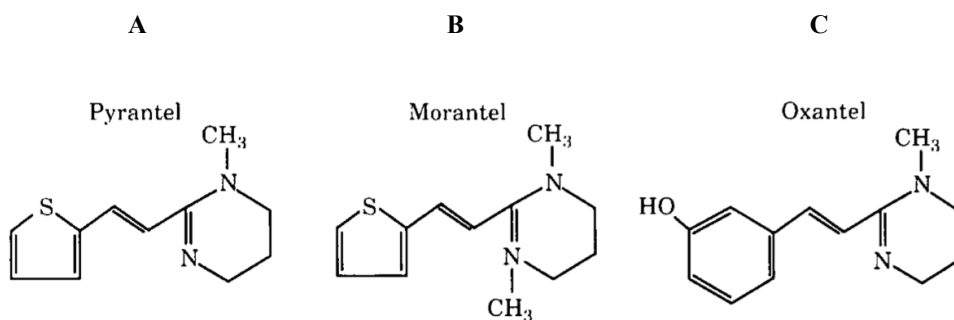


Source: Van den Bossche & Janssen, 1967, p. 1781.

Figure 2.17 Chemical structures of R (+)-tetramisole (A) and S (-)-tetramisole (levamisole) (B)

addition to voltage-sensitive open channel-block and desensitization. The mean open-times for single-channel currents activated by levamisole were 0.80 – 2.85 ms and the conductance levels were 19 – 46 pS, with a mean of 32.9 ± 1.23 pS. This corresponded to the levamisole-sensitive, L-subtype nAChR with a channel conductance of 35 pS, as revealed by Qian *et al.* (2006). Robertson *et al.* (1999) later revealed the presence of a similar nAChR subtype in levamisole-sensitive *O. dentatum* muscle patches which was absent in the levamisole-resistant muscle patches. In subsequent oocyte expression studies, the reconstituted *O. dentatum* L-subtype nAChR (UNC-29, UNC-38, UNC-63 and ACR-8) was preferentially sensitive to levamisole and also had a single channel conductance of ~35 pS (Buxton *et al.*, 2014). Levamisole not only causes spastic paralysis but it also stimulates egg-laying in wild-type *C. elegans* (Trent *et al.*, 1983).

2.5.1.3 Tetrahydropyrimidines. Tetrahydropyrimidines share a similar mode of action to imidazothiazoles and are commonly grouped together as nicotinic agonists (Aubry *et al.*, 1970; Martin, 1997). Examples of this anthelmintic drug class include pyrantel, oxantel and morantel (Figure 2.18). Pyrantel is an imidazothiazole-derived tetrahydropyrimidine that was discovered in 1966 as an anthelmintic agent with broad spectrum activity against roundworms and hookworms in domestic animals (Austin *et al.*, 1966; Howes & Lynch, 1967). Pyrantel however lacks activity against whipworms (McFarland & Howes, 1972). Studies on the mode of action of pyrantel at the single-channel level identified the L-subtype nAChR in *A. suum* as also preferentially activated by pyrantel (Martin *et al.*, 2005). Pyrantel, like levamisole, also causes open channel-block (Robertson *et al.*, 1994). Although not characterized at the single-channel level, the *O. dentatum* nAChR receptor subunits UNC-29, UNC-38 and UNC-63 reconstitute a pyrantel/tribendimidine- but not levamisole-sensitive

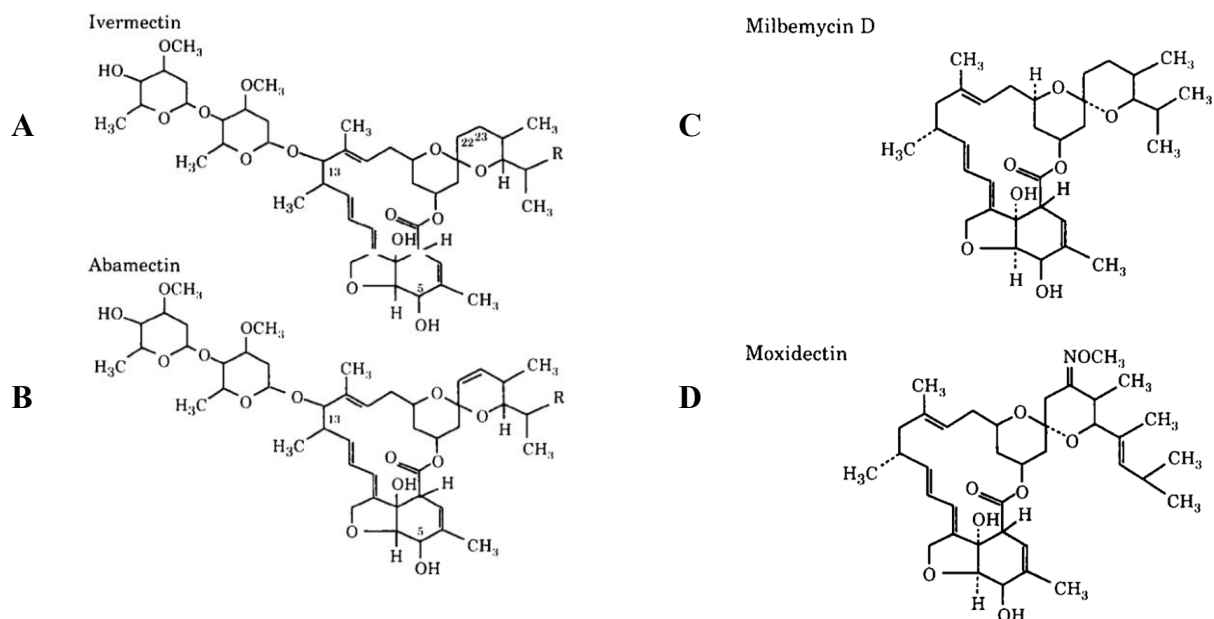


Source: Martin, 1997, p. 13.

Figure 2.18 Chemical structures of pyrantel (A), morantel (B) and oxantel (C).

nAChR subtype in *X. laevis* oocytes (Buxton *et al.*, 2014). The search for an agent with activity against whipworms led to the development of oxantel, an m-oxyphenol derivative of pyrantel (Howes 1972). Contrary to pyrantel, oxantel preferentially activates the N-subtype nAChRs in *A. suum* (Martin *et al.*, 2004). Oxantel, like levamisole and pyrantel, also causes open channel-block in *A. suum* (Dale & Martin, 1995). Morantel is a methyl ester analog of pyrantel which also targets the L-subtype nAChR in *A. suum* (Bamgbose *et al.*, 1973; Cornwell & Blore, 1970). At the single-channel level, morantel causes the activation and block of this receptor subtype (Evans & Martin, 1996). Recently, morantel was shown to act as an agonist of the nAChR subtype comprising ACR-26/ACR-27 subunits from *H. contortus* or *Parascaris equorum* expressed in *X. laevis* oocytes (Courtot *et al.*, 2015). In oocyte expression studies, morantel was seen to cause a non-competitive voltage-sensitive open channel block of the newly characterized *A. suum* ACR-16 receptor (Abongwa *et al.*, 2016a).

2.5.1.4 Macrocyclic lactones (MLs). Macrocyclic lactones (avermectins and milbemycins) are a group of chemical compounds derived from soil microorganisms of the genus *Streptomyces* (Burg *et al.*, 1979; Takiguchi *et al.*, 1980; Takiguchi *et al.*, 1983). MLs were introduced in the 1980s as antiparasitic agents with broad spectrum activity against



Source: Martin, 1997, p. 19.

Figure 2.19 Chemical structures of ivermectin (A), abamectin (B), milbemycin D (C) and moxidectin (D).

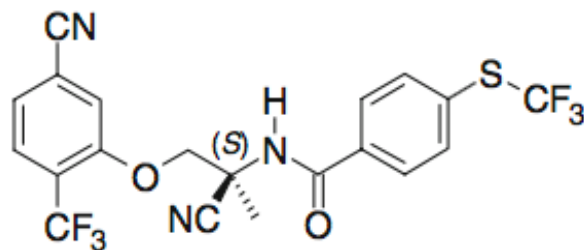
nematodes and arthropods (Davies & Green, 1986; McKellar & Benchaoui, 1996). Examples of commercially available avermectins are ivermectin, abamectin, doramectin and selamectin, while milbemycin oxime and moxidectin, are examples of commercially available milbemycins (Figure 2.19). MLs are selective agonists of glutamate-gated chloride channels (GluCl) which are present in neurons and pharyngeal muscles of nematodes and arthropods, but absent in humans. ML activation of GluCl inhibits movement and pharyngeal pumping (Cully *et al.*, 1994; Wolstenholme & Rogers, 2005). In addition to GluCl effects, the avermectins also act as antagonists of 4-aminobutyric acid (GABA) and nicotinic receptors expressed on somatic muscle cells of parasitic nematodes (Abongwa *et al.*, 2016b; Holden-Dye & Walker, 1990; Puttachary *et al.*, 2013). Ivermectin, the first member of the avermectins, although originally developed as a veterinary drug, was later

approved for use in humans for the control of onchocerciasis and lymphatic filariasis (Crump & Omura, 2011; Geary, 2005; Omura, 2008; Ottesen & Campbell, 1994). Also, ivermectin was shown to act as an irreversible agonist of recombinant human glycine receptors at higher concentrations $>0.3 \mu\text{M}$, but at lower concentrations (30 nM), it acted as a positive allosteric modulator (Shan *et al.*, 2001). Ivermectin showed a similar positive allosteric modulation effect on the vertebrate neuronal $\alpha 7$ nicotinic acetylcholine receptor (Krause *et al.*, 1998).

2.5.1.5 Amino-acetonitrile derivatives (AADs). The AADs are a new class of synthetic anthelmintics with high broad spectrum activity against nematodes that are resistant to the benzimidazoles, imidazothiazoles and macrocyclic lactones (Ducray *et al.*, 2008; Kaminsky *et al.*, 2008a; Kaminsky *et al.*, 2008b). Monepantel, also known as AAD 1556, is the first member of this class to be developed for the control of a broad range of parasitic nematodes in sheep (Figure 2.20) (Kaminsky *et al.*, 2008b). Genetic screens of *C. elegans* identified ACR-23, which belongs to the nematode-specific DEG-3 subfamily of nAChRs, as the target of AADs (Kaminsky *et al.*, 2008a). Further studies on the mode of action of the AADs have led to the confirmation of ACR-23 as the principal target for monepantel in *C. elegans*, as well as the identification of other DEG-3-like nAChR target genes; *H. contortus* monepantel-1 (*Hco-mptl-1*, formerly *Hc-acr-23*), *Hco-des-2*, *Hco-deg-3* and *C. elegans* *acr-20* (Baur *et al.*, 2015; Lecova *et al.*, 2014; Rufener *et al.*, 2013; Rufener *et al.*, 2009). Baur *et al.*, 2015, also demonstrated that at low concentrations ($<1 \text{ nM}$), monepantel acts as a positive allosteric modulator of *H. contortus* MPTL-1 and *C. elegans* ACR-20 receptors, and at high concentrations ($>0.1 \mu\text{M}$), it acts as a direct agonist of these receptors. In a different study, monepantel by itself did not activate *H. contortus* DEG-3/DES-2 receptors expressed

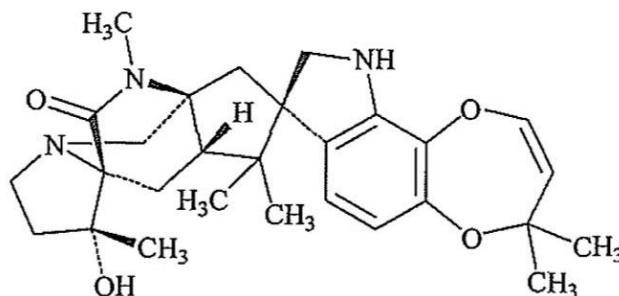
in *X. laevis* oocytes, but did cause a potentiation in the receptors' current responses when co-applied with choline (Rufener *et al.*, 2010).

2.5.1.6 Spiroindoles. Derquantel (2-deoxy-paraherquamide or PNU-141962) is the first semi-synthetic member of this new class of anthelmintics (Figure 2.21) (Lee *et al.*, 2002). Derquantel which is also the first commercial member of the spiroindoles, was introduced in 2010 for use in combination with the macrocyclic lactone, abamectin, under the trade name STARTECT[®], for the control of parasitic nematodes in sheep. Derquantel acts as an antagonist of nAChRs to cause flaccid paralysis which results in the expulsion of parasites from the host (Robertson *et al.*, 2002). The combination of derquantel and abamectin has an



Source: Kaminsky *et al.*, 2008b, p. 935.

Figure 2.20 Chemical Structure of monepantel.

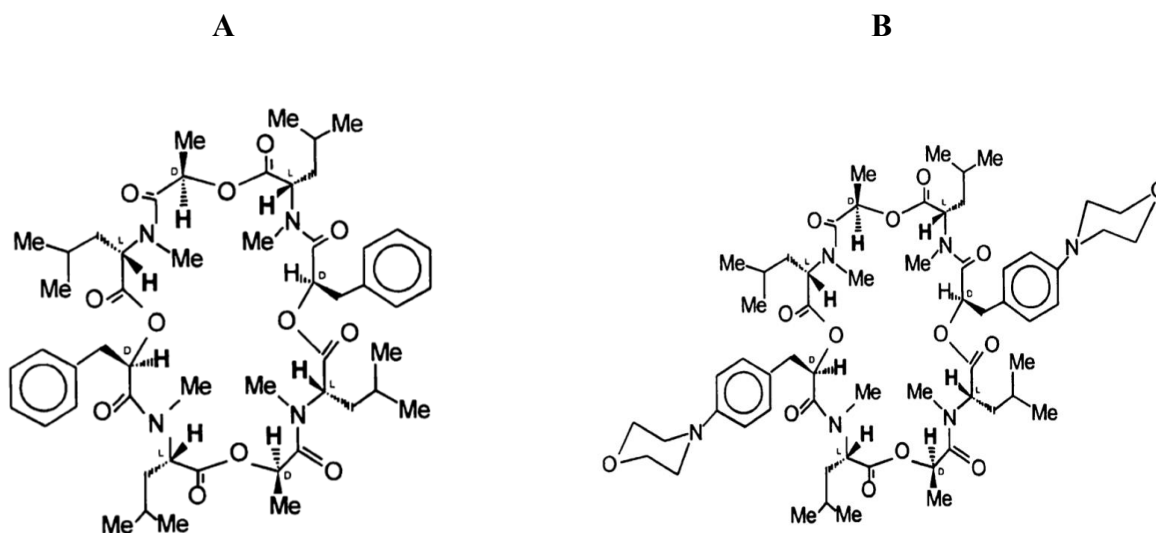


Source: Little *et al.*, 2011, p. 182.

Figure 2.21 Chemical structure of derquantel.

excellent broad spectrum efficacy against several parasitic nematodes in sheep, including those resistant to benzimidazoles, levamisole and macrocyclic lactones (Geurden *et al.*, 2012; Little *et al.*, 2011). The efficacy of the derquantel and abamectin combination has also been shown in muscle contraction and electrophysiological studies on *A. suum* muscle flaps. Derquantel or abamectin alone inhibited responses to acetylcholine, and the inhibition was greater when a combination of derquantel and abamectin was used, producing a synergistic (greater than additive) effect (Puttachary *et al.*, 2013). Also, the derquantel and abamectin combination was shown to produce a greater inhibition of acetylcholine- or pyrantel-induced current responses from expressed pyrantel/tribendimidine *O. dentatum* receptors compared to derquantel or abamectin alone (Abongwa *et al.*, 2016b). The introduction of combination anthelmintics provides a useful tool to increase anthelmintic drug efficacy, overcome resistance to other anthelmintic classes and delay resistance development (Anderson *et al.*, 1988; Bartram *et al.*, 2012).

2.5.1.7 Cyclooctadepsipeptides. Cyclooctadepsipeptides were discovered in the early 1990s. In 1992, PF1022A, the parent compound, was isolated from the fungus, *Mycelia sterilia*, which grows on the leaves of the plant, *Camellia japonica* (Sasaki *et al.*, 1992). PF1022A is made up of four N-methyl-L-leucine, two D-lactate and two D-phenyllactate residues that are arranged as a cyclic octadepsipeptide with an alternating L-D-L configuration (Figure 2.22) (Harder *et al.*, 2003). Emodepside, formerly PF1022-221 and BAY 44-4400, is a semisynthetic derivative of PF1022A, produced by attaching a morpholine ring at the para position of the two D-phenyllactic acids (Harder *et al.*, 2005). This modification resulted in improved pharmacokinetic properties. The anthelmintic potential of PF1022A and emodepside has been reported in numerous *in vitro* and *in vivo*



Source: Harder *et al.*, 2003, p. 320.

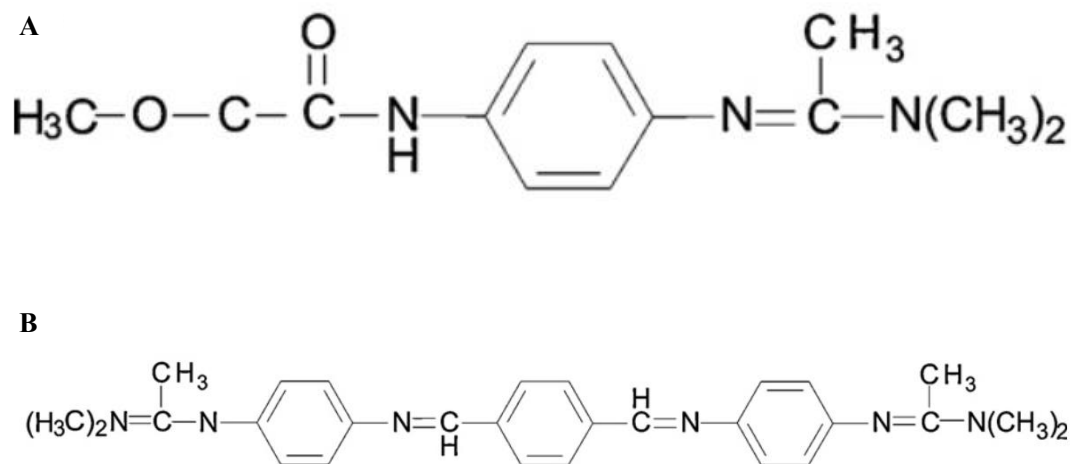
Figure 2.22 Chemical structure of PF1022A (A) and emodepside (B).

studies (Harder & von Samson-Himmelstjerna, 2001; Kulke *et al.*, 2013a; Kulke *et al.*, 2013b; Kulke *et al.*, 2014; Zahner *et al.*, 2001a; Zahner *et al.*, 2001b). Interestingly, PF1022A and emodepside have a broad spectrum of activity against several nematode species including those that are resistant to benzimidazoles, levamisole and ivermectin (von Samson-Himmelstjerna *et al.*, 2005). This indicated that the mode of action of the cyclooctadepsipeptides is different and that this class of anthelmintics possess ‘resistance-busting’ properties.

Studies on the mode of action suggest that emodepside targets the calcium-activated potassium channel (SLO-1), there is also evidence for the involvement of the latrophilin (LAT-1) receptor (Holden-Dye *et al.*, 2007; Krucken *et al.*, 2012; Martin *et al.*, 2012a). Mutagenesis screens in *C. elegans* revealed a lack of sensitivity of *slo-1* null mutants to emodepside’s inhibitory effects on locomotion and feeding. Inhibition of locomotion was

achieved via the action of emodepside on SLO-1 expressed in body wall muscles or neurons, whereas inhibition of feeding was achieved via the action of emodepside on SLO-1 expressed in neurons but not muscle (Guest *et al.*, 2007). RNAi studies implicated a role for LAT-1 in mediating emodepside's inhibitory effect on pharyngeal pumping in the pharynx (Willson *et al.*, 2004). Guest *et al.* (2007) showed *C. elegans lat-1* null mutants had an estimated five-fold reduction in sensitivity to emodepside. These studies suggest that the inhibitory effect of emodepside on feeding is both SLO-1 and latrophilin-dependent. However, emodepside treatment inhibited locomotion in both wild type and *lat-1:lat-2* null *C. elegans*, implying that the inhibitory effect of emodepside on locomotion is latrophilin-independent (Guest *et al.*, 2007). The sensitivity of nematode SLO-1 channels to calcium is different from that of insects and humans (Crisford *et al.*, 2015).

2.5.1.8 Tribendimidine. Tribendimidine is a symmetrical diamidine derivative of amidantel (Figure 2.23). It was developed in the mid 1980s by the National Institute of Parasitic diseases in Shanghai, China, as a broad spectrum anthelmintic drug (Ren *et al.*, 1987). In 2004, tribendimidine was approved by the Chinese Food and Drug Administration for treatment of helminth infections in humans (Xiao *et al.*, 2005). It is the only new anthelmintic drug that has been approved for human use within the past 3 decades (Bergquist, 2016). Tribendimidine has been shown in laboratory and clinical studies to have a broad spectrum of activity against several nematode, trematode and cestode species (Keiser *et al.*, 2007; Kulke *et al.*, 2012; Steinmann *et al.*, 2008; Wu *et al.*, 2006; Xiao *et al.*, 2009; Xu *et al.*, 2014). The activity of tribendimidine against 20 helminth parasites has been documented (Xiao *et al.*, 2013). Earlier studies on the mode of action of tribendimidine in the nematode model *C. elegans* demonstrated that tribendimidine acts as an agonist of the L-



Source: Kulke *et al.*, 2012, p. 79.

Figure 2.23 Chemical structure of amidantel (A) and tribendimidine (B).

subtype nAChR in this species, similar to levamisole and pyrantel (Hu *et al.*, 2009). Parasitic nematodes however, show different nAChR subtype selectivity from *C. elegans*, and this varies across nematode species. Buxton *et al.* (2014), showed in oocyte expression studies that tribendimidine, just like pyrantel, is more selective for the reconstituted pyrantel/tribendimidine nAChR subtype comprising of UNC-29, UNC-38 and UNC-63 subunits from *O. dentatum* and had little effect on the levamisole-sensitive subtype. In *A. suum*, the action of tribendimidine is pharmacologically similar to that of buphenium rather than levamisole, leading to the conclusion that tribendimidine selectively acts on the buphenium-sensitive, B-nAChR subtype, not the L-subtype nAChR in *Ascaris* (Robertson *et al.*, 2015). Robertson *et al.* (2015), further showed tribendimidine to cause a more potent inhibition of migration of *O. dentatum* levamisole-resistant larvae (LEVR) than levamisole-sensitive larvae (SENS). Thus, confirming their hypothesis that unlike in *C. elegans*, tribendimidine does not act on the L-subtype nAChR in parasitic nematodes.

2.5.2 Anthelmintic resistance

In broad terms, anthelmintic resistance is referred to as the decline in the efficacy of an anthelmintic drug in a population of parasites that were once susceptible to the drug. The repeated and improper use of currently available anthelmintics has led to the development of resistance in numerous veterinary parasite species worldwide, with increasing concerns that this may extend to human parasites (Coles *et al.*, 2006; Geerts & Gryseels, 2000; Geerts & Gryseels, 2001). Since anthelmintics within each drug class act in a similar manner, resistance to one anthelmintic in a given drug class is likely to be accompanied by resistance to other anthelmintics of that same class (side resistance). There is also the likelihood for the development of cross resistance from anthelmintics of one drug class to those of another, if the two drug classes share similar targets (Sangster, 1999). Hence, the widespread occurrence of resistance across the majority of anthelmintic drug classes (Tables 2.3 & 2.4). Sadly, the onset of anthelmintic resistance development can be rapid, thiabendazole resistance occurred 3 years after its introduction to the market (Conway, 1964).

Reports of resistance to anthelmintics in various parts of the world have been well-documented (Kaplan, 2004; Kaplan & Vidyashankar, 2012; Waller, 1997). In spite of the numerous reports of anthelmintic resistance, the mechanisms by which resistance occurs remain to be fully elucidated (Table 2.3). Resistance mechanisms include: (i) mutation or deletion of one or more amino acids in the target genes, (ii) reduction in the number of receptors, (iii) decreased affinity of receptors for drugs, and (iv) absence of bioactivating enzymes (Gilleard, 2006; Jabbar *et al.*, 2006; James *et al.*, 2009; Sangster & Gill, 1999; Wolstenholme *et al.*, 2004). Management practices can also delay or overcome

Table 2.3 Anthelmintic resistance and mechanisms of resistance to the major anthelmintic drug classes. (Modified from Kaplan, 2004, p. 478; Sangster & Gill, 1999, p. 141; & Wolstenholme *et al.*, 2004, p. 471.)

Anthelmintic class	Host	Year of initial approval	Year of first published report of resistance	Potential mechanism of resistance
Benzimidazoles				Mutations in β -tubulin; Phe200Try, Phe167Try or Glu198Ala.
Thiabendazole	Sheep	1961	1964	
	Horse	1962	1965	
Imidothiazoles-tetrahydropyrimidines				Changes in nicotinic acetylcholine receptors
Levamisole	Sheep	1970	1979	
Pyrantel	Horse	1974	1996	
Avermectin-milbemycins				Reduced sensitivity of GluCl/GABA receptors
Ivermectin	Sheep	1981	1988	
	Horse	1983	2002	
Moxidectin	Sheep	1991	1995	
	Horse	1995	2003	

anthelmintic resistance (Shalaby, 2013). Anthelmintic resistance can be delayed or overcome by: (i) identifying new drug targets with different pharmacological profiles from those of existing drugs, (ii) introducing new anthelmintics with different modes of action from those of existing anthelmintics, (iii) combination therapy, with members of the combination from different drug classes, (iv) rotating drugs with different modes of action between dosing seasons, and (v) keeping some parasites in untreated refugia (Coles, 2005; Leathwick *et al.*, 2009; Shalaby, 2013). A detailed understanding of the biochemical and genetic basis of

Table 2.4 Worldwide reports of anthelmintic resistance. (Modified from Jabbar *et al.*, 2006, pp. 2415-2416)

Species/genus of nematodes	Resistant to anthelmintic	Country
<i>O. circumcincta</i>	TBZ, LEV, Morantel	Australia
<i>H. contortus</i>	TBZ	Australia
<i>H. contortus</i>	BZ, Non-BZ, Organophosphorus Anthelmintics	Australia
<i>Haemonchus, Trichostrongylus, Ostertagia</i> spp.	FEN, LEV	Australia
<i>T. colubriformis</i>	OXF, LEV	Australia
<i>Haemonchus, Trichostrongylus, Ostertagia, Nematodirus</i>	TBZ, LEV	Australia
<i>Trichostrongylus, Ostertagia</i> spp.	TBZ, LEV, ALB, OXF, Morantel	Australia
<i>H. contortus, Trichostrongylus, Ostertagia</i> spp.	TBZ, LEV	Australia
Sheep nematodes	TBZ, LEV	Australia
<i>H. contortus, T. colubriformis, O. circumcincta</i>	OXL, LEV, Closantel, Morantel	Australia
<i>H. contortus</i>	BZ	Belgium
<i>T. circumcincta</i>	TBZ, IVM, LEV	Brazil
<i>O. circumcincta</i>	LEV	Denmark
<i>Ostertagia, Trichostrongylus</i> spp.	T5BZ, LEV, IVM	Denmark
Goat nematodes	BZ	France
<i>H. contortus</i>	BZ	France
<i>H. contortus, Trichostrongylus, Ostertagia</i> spp.	BZ, LEV	France
<i>H. contortus</i>	BZ	Germany
Gastrointestinal nematodes	TBZ, MBZ, FEN, ALB, OXF, IVM LEV, Febantel, Pyrantel Tartrate	Germany
Nematodes	BZ, LEV, Morantel	Greece
Nematodes	BZ	Ireland
<i>H. contortus</i>	BZ	India
<i>H. contortus</i>	BZ, LEV, IVM, Thiophanate, Morantel, Closantel	India
<i>H. contortus</i>	FEN, LEV, IVM, Closantel, Morantel	India
Gastrointestinal nematodes	ALB, LEV, IVM	India
<i>H. contortus</i>	FEN, LEV, IVM, Morantel	India
Sheep and goat nematodes	BZ	Italy
<i>H. contortus Trichostrongylus</i> spp.	BZ, FEN, LEV	Kenya
Gastrointestinal nematodes	BZ, LEV, IVM	Kenya
<i>H. contortus</i>	Thiophanate, Closantel, ALB, LEV, IVM	Kenya
<i>H. contortus, Trichostrongylus, Oesophagostomum</i> spp.	BZ, LEV, IVM, RAF	Kenya
Goat nematodes	TBZ	Malaysia
<i>H. contortus, T. colubriformis</i>	BZ, LEV, IVM, Closantel, Moxidectin	Malaysia
<i>Trichostrongylus</i> spp.	BZ	Netherlands
<i>H. contortus, C. curticei, Ostertagia, Trichostrongylus</i> spp.	OXF, IVM, LEV	Netherlands
<i>H. contortus, O. circumcincta</i>	BZ, LEV, IVM	Netherlands
Sheep nematodes	BZ, Non BZ	New Zealand
<i>Cooperia oncophora</i>	OXF	New Zealand
<i>H. contortus, Trichostrongylus</i> spp.	BZ, LEV, IVM	New Zealand
Sheep nematodes	BZ, LEV, IVM	New Zealand
<i>Trichostrongyles</i>	BZ	North West Cameroon
Sheep gastrointestinal nematodes	BZ, LEV	Pakistan
<i>H. contortus</i>	OXF	Pakistan
Sheep gastrointestinal nematodes	OXF, LEV	Pakistan

Table 2.4 (Continued)

Species/genus of nematodes	Resistant to anthelmintic	Country
<i>Trichostrongylus</i> spp.	BZ	Slovakia
<i>Ostertagia</i> , <i>Trichostrongylus</i> spp.	BZ, LEV, TMZ	Slovakia
<i>H. contortus</i>	IVM, BZ, CLOST, Rafoxanide	South Africa
<i>H. contortus</i> , <i>Ostertagia</i> , <i>Trichostrongylus</i> spp	BZ, LEV, IVM, Closantel	Southern Latin America, Brazil
<i>H. contortus</i> <i>Trichostrongylus</i> , <i>Oesophagostomum</i>	BZ, LEV, IVM	South Latin America, Argentina
<i>H. contortus</i> <i>Trichostrongylus</i> , <i>Oesophagostomum</i>	BZ, LEV	Southern Latin America
<i>H. contortus</i> , <i>Ostertagia</i> spp.	BZ, LEV, IVM	Southern Latin America, Uruguay
<i>T. circumcincta</i>	Netobimin, BZ	Spain
<i>H. contortus</i>	TBZ	United Kingdom
<i>O. circumcincta</i>	TBZ	United Kingdom
<i>H. contortus</i>	FEN, IVM	United Kingdom
<i>H. contortus</i> , <i>O. circumcincta</i>		United Kingdom
<i>H. contortus</i> , <i>O. circumcincta</i>	BZ, IVM	United Kingdom
<i>O. circumcincta</i>	BZ	United Kingdom
Sheep nematodes	BZ	United Kingdom
Sheep and goat nematodes	BZ, LEV, IVM	United Kingdom
Sheep nematodes	BZ, LEV, IVM	United Kingdom
<i>H. contortus</i>	TBZ	United States of America
<i>H. contortus</i> , <i>O. circumcincta</i>	TBZ	United States of America
<i>H. contortus</i>	FEN, LEV, IVM, Pyrantel pamoate	United States of America
<i>H. contortus</i>	BZ, LEV, FEN, RAF	Zimbabwe

C. – Cooperia; H. – Haemonchus; O. – Ostertagia, T. – Trichostrongylus; T. – Teladorsagia; BZ – Benzimidazole; MBZ – Mebendazole; FEN – Fenbendazole; TBZ – Thiabendazole; ALB – Albendazole; OXF = Oxfendazole; Lev = Levamisole; IVM = Ivermectin; RAF = Rafoxanide; TMZ = Tetramizole; CLOST = Closantel.

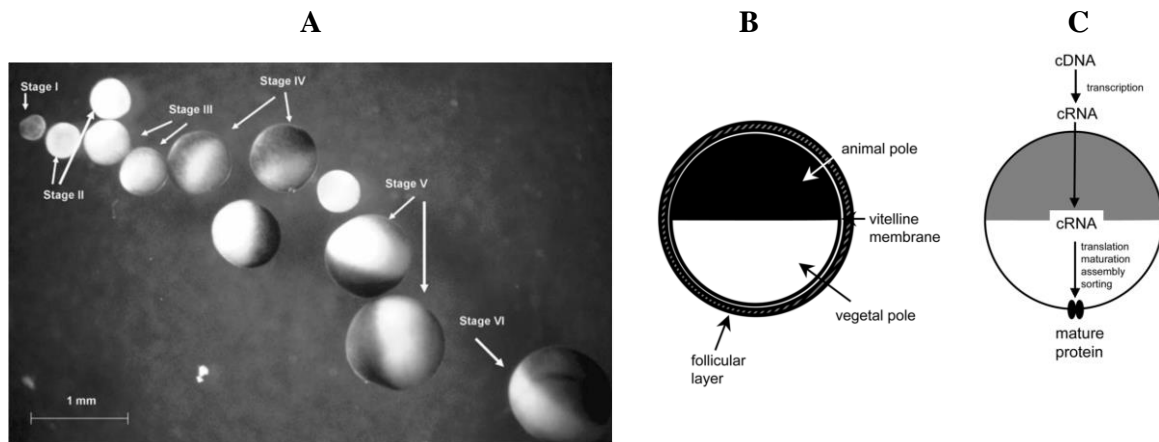
anthelmintic action is, therefore, imperative as this will allow for the development of sensitive assays for early detection and, hence, more efficient management of anthelmintic resistance.

2.6 *Xenopus laevis* oocytes heterologous expression system

Oocytes of the South African clawed toad, *Xenopus laevis*, are an efficient and widely employed heterologous expression system for protein expression, including ion channels and membrane receptors (Broer, 2010; Buckingham *et al.*, 2006; Dascal, 1987; Sigel, 1990). The oocytes have 6 growth stages, namely, stages I – VI, which are distinguished based on size and level of pigmentation (Dumont, 1972). All 6 developmental stages of the oocytes are

contained in the ovaries of the adult female *Xenopus*. These oocytes, which are usually in thousands, can be surgically removed after blocking hormonal stimulation such that the oocytes are retained in the ovaries and do not pass into the oviduct (Bossi *et al.*, 2007; Theodoulou & Miller, 1995). Stages V and VI *Xenopus* oocytes are the largest and measure 1.0 – 1.2 and 1.2 – 1.3 mm in diameter respectively. Stages V and VI *Xenopus* oocytes are typically used as a system for expression and electrophysiological analysis of ion channels and membrane receptors, although the smaller stage IV oocytes are used for studying currents with very fast kinetics (Bianchi & Driscoll, 2006). The oocytes have two clearly distinct poles; the yellow vegetal pole, and the darker animal pole, surrounded by a vitelline membrane and a layer of follicle cells containing ion channels which are electrically coupled to the oocytes through gap junctions (Figure 2.24). Therefore, the oocytes must be defolliculated prior to conducting electrophysiological studies to prevent recording endogenous current responses. Additionally, for single channel studies where the patch clamp technique is used, the vitelline membrane must be removed prior to recordings. This is because interferes with the formation of high resistance gigaseal between the patch electrode and the oocyte membrane (Bianchi & Driscoll, 2006; Choe & Sackin, 1997). This gigaseal is crucial for improving signal-to-noise ratio during patch clamp recordings.

During oogenesis, *Xenopus* oocytes accumulate massive amounts of enzymes and organelles which after fertilization can be used for DNA transcription and RNA translation (Dumont, 1972). The introduction of *Xenopus* oocytes as an expression system can be traced as far back as 1971 when John B. Gurdon observed that mRNA injected into *Xenopus* oocytes were translated to the appropriate proteins after a period of incubation (Gurdon *et al.*, 1971). Nevertheless, it was only in 1982 that *Xenopus* oocytes came to the spotlight as a



Source: Bossi *et al.*, 2007, p. 124 and Bianchi & Driscoll, 2006, p. 3.

Figure 2.24 Structures of *Xenopus laevis* oocytes showing different stages of development (A), annotated anatomical features (B) and cartoon representation of protein expression (C).

system for the expression of membrane proteins such as nicotinic acetylcholine receptors (Barnard *et al.*, 1982; Miledi *et al.*, 1982). Subsequently, *Xenopus* oocytes have been greatly utilized for expression of nicotinic acetylcholine receptors, allowing for the characterization of these receptors using different electrophysiology techniques such as two-electrode voltage clamp and patch clamp (Papke & Smith-Maxwell, 2009; Wagner *et al.*, 2000). The two-electrode voltage clamp technique is usually employed for studying expressed nicotinic acetylcholine receptors as it is more suitable for clamping large cells like *Xenopus* oocytes (Dascal, 2001; Guan *et al.*, 2013). RNA or DNA is injected into the oocyte cytoplasm or nucleus respectively, and the injected oocytes to allow for functional protein expression. Cytoplasmic injection of RNA is preferred over nuclear injection of DNA because of the technical difficulties associated with locating the nucleus (Miller & Zhou, 2000).

The ability of *Xenopus* oocytes to initiate protein synthesis, in addition to their abundance, large size and relative ease of manipulation make *Xenopus* oocytes a popular

heterologous expression system compared to *Escherichia coli*, yeast, or some eukaryotic cell lines (Lin-Moshier & Marchant, 2013; Markovich, 2008). For studies involving parasitic nematode ion channels, the *Xenopus* oocyte has two specific advantages; (i) electrophysiology requires a steady supply of viable parasites which is often problematic, and (ii) the *Xenopus* system allows expression of a single type (or subtype) of channels whereas *in vivo* recordings from nematode cells can be confounded by the presence of multiple channel types and subtypes.

There are also limitations of the *Xenopus* oocyte expression system which should be taken into consideration when interpreting results and these include: (i) oocytes are not the native cells the proteins are normally expressed in so results may be different from those obtained in native cells, (ii) seasonal variations in oocyte quality and alterations in protein expression ability, and (iii) oocytes are temperature sensitive; they can only survive at room temperature (18 – 22 °C) and will deteriorate at higher temperatures (Stuhmer, 1992).

**CHAPTER 3. PHARMACOLOGICAL PROFILE OF *ASCARIS SUUM* ACR-16, A
NEW HOMOMERIC NICOTINIC ACETYLCHOLINE RECEPTOR WIDELY
DISTRIBUTED IN *ASCARIS* TISSUES**

A paper published in the *British Journal of Pharmacology* (2016)¹

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3.1 Summary

3.1.1 Background and Purpose

Control of nematode parasite infections relies largely on anthelmintic drugs, several of which act on nicotinic ACh receptors (nAChRs), and there are concerns about the development of resistance. There is an urgent need for development of new compounds to overcome resistance and novel anthelmintic drug targets. We describe the functional expression and pharmacological characterization of a homomeric nAChR, ACR-16, from a nematode parasite.

3.1.2 Experimental Approach

Using RT-PCR, molecular cloning and two-electrode voltage clamp electrophysiology, we localized *acr-16* mRNA in *Ascaris suum* (*Asu*) and then cloned and

expressed *acr-16* cRNA in *Xenopus* oocytes. Sensitivity of these receptors to cholinergic anthelmintics and a range of nicotinic agonists was tested.

3.1.3 Key Results

Amino acid sequence comparison with vertebrate nAChR subunits revealed ACR-16 to be most closely related to $\alpha 7$ receptors, but with some striking distinctions. *acr-16* mRNA was recovered from *Asu* somatic muscle, pharynx, ovijector, head and intestine. In electrophysiological experiments, the existing cholinergic anthelmintic agonists (morantel, levamisole, methyridine, thenium, bphenium, tribendimidine and pyrantel) did not activate *Asu*-ACR-16 (except for a small response to oxantel). Other nAChR agonists: nicotine, ACh, cytosine, 3-bromocytosine and epibatidine, produced robust current responses which desensitized at a rate varying with the agonists. Unlike $\alpha 7$, *Asu*-ACR-16 was insensitive to α -bungarotoxin and did not respond to genistein or other $\alpha 7$ positive allosteric modulators. *Asu*-ACR-16 had lower calcium permeability than $\alpha 7$ receptors.

3.1.4 Conclusions and Implications

We suggest that ACR-16 has diverse tissue-dependent functions in nematode parasites and is a suitable drug target for development of novel anthelmintic compounds.

3.2 Abbreviations

α -BTX, α -bungarotoxin; BAPTA-AM, 1,2-bis(2-aminophenoxy)ethane-*N,N,N',N'*-tetraacetic acid tetrakis (acetoxymethyl ester); blastP, protein–protein blast; DH β E, dihydro- β -erythroidine; DMPP, dimethyl-4-phenylpiperazinium iodide; dTC, d-tubocurarine; GHK, Goldman Hodgkin Katz; MLA, methyllycaconitine; nAChR, nicotinic ACh receptor; PAM, positive allosteric modulator.

3.3 Table of Links

Table 3.0 Key protein targets and ligands.

TARGETS
Ligand-gated ion channels
Asu-ACR-16
ACR-16
Nicotinic ACh receptor $\alpha 7$ subunit

LIGANDS		
A844606	Dimethyl-4-phenylpiperazinium	Morantel
Acetylcholine	Epibatidine	Nicotine
Bephenium	Genistein	Oxantel
Betaine	Hexamethonium	Parahequamide
Bromocytisine	Ivermectin	PNU120596
α -Bungarotoxin	Levamisole	Pyrantel
Choline	Lobeline	Thenium
Cytisine	Mecamylamine	Tribendimidine
Derquantel	Methyllycaconitine	d-Tubocurarine
Dihydro- β -erythroidine	Methyridine	

These Tables list key protein targets and ligands in this article which are hyperlinked to corresponding entries in <http://www.guidetopharmacology.org>, the common portal for data from the IUPHAR/BPS Guide to PHARMACOLOGY (Southan *et al.*, 2016) or the PubChem or Wormbase databases. Entries in the IUPHAR database are permanently archived in the Concise Guide to PHARMACOLOGY 2015/16 (Alexander *et al.*, 2015).

3.4 Introduction

Soil-transmitted helminths (gastrointestinal nematode parasites) cause significant global health problems in humans and animals. It is estimated that at least one-quarter of the world's human population (Brooker, 2010) and most animal species are infected with parasitic worms. Nematode parasite infections have a high morbidity and cause debilitating conditions such as weight loss, anaemia, compromised immunity, impaired learning ability and, in severe cases, death (Hotez *et al.*, 2007). No current vaccine against nematode parasite infections of humans is effective (Hewitson and Maizels, 2014), so control of these infections relies on chemotherapy. Regrettably, there are a limited number of classes of anthelmintics (Martin, 1997; Kaminsky *et al.*, 2008), which, with the repeated large scale use of the drugs, has led to the development of resistance in animals (Wolstenholme *et al.*, 2004), and concerns about the development of resistance in humans (Taman and Azab, 2014). The increasing resistance means that novel drug targets are required to overcome this resistance.

Nicotinic ACh receptors (nAChRs) of vertebrates and invertebrates serve a very wide range of functions. For example, in excitable cells, they are involved in neuronal and neuromuscular transmission and, in non-excitabile cells, are involved in modulation, development of growth and differentiation (Wessler and Kirkpatrick, 2008). Nematode parasite nAChRs are pharmacologically different to their host nAChRs and are validated and exploited anthelmintic drug targets (Gopalakrishnan *et al.*, 2007). All nAChRs are five-subunit ligand-gated ion channels which open in the presence of ACh or choline, and are found on muscles, nerves, secretory cells and a wide range of non-excitabile tissues in both vertebrates and invertebrates. The pharmacology of individual nAChRs depends on key amino acid sequences of each nAChR subunit of the pentamer and the composition of the subunits that form the receptor. The subunits that make up vertebrate nAChRs are derived from at least 17 genes ($\alpha 1$ – $\alpha 10$, $\beta 1$ – $\beta 4$, γ , δ , ϵ) (Karlin, 1993; Millar and Gotti, 2009) and from 29 genes in the free-living nematode, *Caenorhabditis elegans* (Jones *et al.*, 2007). The subunits of the pentameric receptor channel may be composed of five identical subunits (homomeric) or a mixture of different subunits (heteromeric) arranged around a central ion conducting pore (Chen, 2010).

The older, cholinergic anthelmintics, levamisole and pyrantel, and the more recently introduced anthelmintics, tribendimidine and derquantel, activate heterogeneous pentameric nAChRs composed of a mixture of UNC-29, UNC-38, ACR-8 or UNC-63 subunits (Buxton *et al.*, 2014). The more recently introduced cholinergic anthelmintic, monepantel, activates nAChRs composed of a mixture of DEG-3-like subunits, including ACR-23, ACR-20 and MPTL-1 (Baur *et al.*, 2015). Resistance to some of these anthelmintics has been observed in animal parasites (McMahon *et al.*, 2013; Scott *et al.*, 2013), and although the mechanism(s)

of field resistance have not been well characterized, there is evidence that the resistance can involve altered subunit sequence or subunit truncation (Fauvin *et al.*, 2010; Neveu *et al.*, 2010).

Here, we have cloned and expressed, in *Xenopus* oocytes, *acr-16* cRNA from *Ascaris suum*, a clade III nematode parasite, which is very similar to the significant human parasite, *A. lumbricoides*. This receptor was expressed as a homomeric receptor in *Xenopus* oocytes, and transcripts are found in muscle, intestine, reproductive tract and other tissues of the *Ascaris* body, suggesting diverse physiological functions in addition to neuromuscular transmission. Knowing that ACR-16 is a nicotine-sensitive nAChR and that nicotine has in the past been used as the drug of choice for treatment of *Ascaridia galli* infections (Kerr and Cavett, 1952), a selective drug targeted against ACR-16 could affect motility, digestion and reproduction of parasites and be an effective anthelmintic.

3.5 Methods

3.5.1 Animals

No vertebrate animals were used directly in the study. Adult female *A. suum* worms were collected from Marshalltown Pork Plant, Marshalltown, IA, USA. Defolliculated *Xenopus laevis* oocytes were obtained from Ecocyte Bioscience (Austin, TX, USA).

3.5.2 Sequence analysis

For convenience, the sources of the AChR subunits are indicated, in this article, by three letter prefixes. Thus, *Ace*, *Asu*, *Cel*, *Hco*, *Llo*, *Nam*, *Sra*, *Tca* and *Xle*, refer to *Ancylostoma ceylanicum*, *Ascaris suum*, *Caenorhabditis elegans*, *Haemonchus contortus*, *Loa loa*, *Necator americanus*, *Strongyloides ratti*, *Toxocara canis* and *Xenopus laevis* respectively.

Database searches around the sequence of *Asu*-ACR-16 were performed with the blast Network Service (NCBI), using the protein–protein blast (blastP) algorithm (Altschul *et al.*, 1997). Signal peptide predictions were carried out using the SignalP 4.0 server (Bendtsen *et al.*, 2004), and membrane-spanning regions were predicted using TMPred (Hofmann and Stoffel, 1993). Distance trees were generated on the full-length deduced amino acid sequences aligned with the MUSCLE programme (Edgar, 2004). The alignment was analysed using the SEAVIEW suite (Gouy *et al.*, 2010) with the neighbour-joining method and bootstrapped with 1000 replicates. The resulting tree was visualized and edited using FigTree 1.4 (<http://tree.bio.ed.ac.uk/software/figtree/>).

3.5.3 *Asu*-ACR-16 receptor localization

Total RNA was extracted with TRIzol (Invitrogen™, Carlsbad, CA, USA) from different body tissues of five dissected adult female *Asu* worms. The tissues were the gut, ovijector, head, single muscle cells (RNA extracted via micropipette), bulk somatic muscle, single muscle cells of the pharynx (RNA extracted via micropipette) and bulk muscle cells of the pharynx. Specific primers were designed for PCR for *acr-16* (forward primer GACTTGCAACCAGGCAAAGG; reverse primer ACGGGTCGTTATGCCCATTT) and *gapdh* (positive control) (forward primer CTGCTGGACCAATGAAGGGT; reverse primer CACTCCACTCACAGCCACTT) using the online Primer-blast tool. With these primer sets, the expected product size for *acr-16* was 468 and 411 bp for *gapdh*. The presence or absence of *acr-16* in the RNA samples was detected using RT-PCR and single-cell RT-PCR (QIAGEN OneStep RT-PCR Kit; Valencia, CA, USA) at an annealing temperature of 55°C and for 45 PCR cycles. The PCR products from both RT-PCR and single-cell RT-PCR were run on a 1% agarose gel, at the end of which the gel was viewed and captured on a UVP

BioSpectrum Multi Spectral Imaging System (UVP LLC, Upland, CA, USA). Representative bands were sequenced to confirm the identity of *acr-16*.

3.5.4 cRNA preparation

Total RNA samples were extracted with TRIzol (Invitrogen™) from a 1 cm muscle flap and dissected whole pharynx of *Asu*. RT-PCR was used to synthesize first-strand cDNA from muscle and pharynx total RNA with both oligo (dT) RACER primer and Random Hexamer, and superscript III reverse transcriptase (Invitrogen). To amplify the full-length coding sequence of *Asu-ACR-16*, specific primer pairs were designed on the putative 5'- and 3'-UTRs mRNA sequence deduced from *Asu* whole genome shotgun contig N°AEUI02000378 (*Asu-acr-16-F0* ATCACGCATTACGGTTGATG, *Asu-acr-16-F1* TTGATGTAGTGGCGTCGTGT, *Asu-acr-16-R0* ATTAGCGTCCCAAGTGGTTG, *Asu-acr-16-R1* GCATTGATGTTCCCTCACCT) for a first round of PCRs. We used a classical nested PCR approach with F0/R0, F0/R1, F1/R0 and F1/R1 respectively to perform four separate PCR reactions for the first round to increase the chance of amplification success. These four PCR products were subsequently used as templates for a second round of four separate PCR reactions using the following specific primers containing *HindIII* and *ApaI* restriction enzyme sites (*Asu-acr-16-F-Hind3* AAAAAAGCTTATGAGCGTGCAGCGGGCATT, *Asu-acr-16-R-ApaI* TTTGGGCCCTAGAGTGCTGATGATGTGCTA) to facilitate directional cloning into the PTB-207 expression vector. PCR products were then digested with *HindIII* and *ApaI* restriction enzymes, purified using the NucleoSpin® Gel and PCR Clean-up kit (Macherey-Nagel Inc. Bethlehem, PA, USA), cloned into PTB-207 as previously described (Boulin *et al.*, 2011) and sequenced. A positive clone was selected and linearized with *NheI* for

subsequent *in vitro* transcription with the mMessage mMachine T7 transcription kit (Ambion). The cRNA was precipitated with lithium chloride, resuspended in RNase-free water, aliquoted and stored at -80°C .

3.5.5 Oocyte microinjection

The *Xenopus* oocytes were kept at 19°C for ~ 3 h prior to injections in incubation solution (100 mM NaCl, 2 mM KCl, 1.8 mM $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 1 mM $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$, 5 mM HEPES, 2.5 mM Na pyruvate, $100 \text{ U} \cdot \text{mL}^{-1}$ penicillin and $100 \mu\text{g} \cdot \text{mL}^{-1}$ streptomycin, pH 7.5). Depending on the cRNA mix, 10–25 ng of *acr-16* cRNA either alone or in combination with 2.5–15 ng of each ancillary (*ric-3*, *unc-50* and *unc-74*), in a total volume of 50 nL in RNase-free water, was injected into the animal pole of the oocytes using a nanoject II microinjector (Drummond Scientific, Broomall, PA, USA). The injected oocytes were transferred into 96-well culture plates containing 200 μL incubation solution per well; each well contained one oocyte. Oocytes were incubated at 19°C for 2–7 days to allow for receptor expression; incubation solution was changed daily. Oocytes with membrane potentials less than -15 mV were excluded from recording. Oocyte recordings that failed (shown by a change in the holding current following wash) before the complete series of drug applications were excluded from the analysis.

3.5.6 Two-electrode voltage clamp electrophysiology (TEVC) in *Xenopus* oocytes

Two-electrode voltage clamp electrophysiology was used to record currents produced by activation of the expressed *Asu-ACR-16* receptor (Buxton *et al.*, 2014). Four hours prior to recording, 100 μM BAPTA-AM (final concentration), a cell-permeant calcium chelator, was added to the oocyte incubation solution to prevent activation of endogenous calcium-activated chloride channels during recordings. Recordings from non-injected oocytes served

as control experiments. Recordings were made using an Axoclamp 2B amplifier (Warner Instruments, Hamden, CT, USA) with the oocytes voltage clamped at -60 mV and data acquired on a computer with Clampex 9.2 (Molecular Devices, Sunnyvale, CA, USA). The microelectrodes used to impale the oocytes were pulled using a Flaming/Brown horizontal electrode puller (Model P-97; Sutter Instruments, Novato, CA, USA) set to pull micropipettes that when filled with 3 M KCl had a resistance of 20–30 M Ω . The micropipettes tips were carefully broken with a piece of tissue paper in order to achieve a resistance of 2–5 M Ω in recording solution (100 mM NaCl, 2.5 mM KCl, 1 mM CaCl₂·2H₂O and 5 mM HEPES, pH 7.3). The low resistance pipettes allowed large currents to be passed to maintain adequate voltage clamp.

3.5.7 Assessment of agonists and antagonists

Except where indicated, agonists were used at a final concentration of 100 μ M, while the antagonists were used at a final concentration of 10 μ M for rank order potency experiments and 1 μ M for the dose–response experiments. Effects of the positive allosteric modulators (PAMs): ivermectin (10 μ M), genistein (3 μ M) and PNU120596 (3 μ M), were tested. Control responses were obtained first with agonists applied for 10 s. Responses were again observed after the antagonists or PAMs were applied for 2 min and observed in the continued presence of antagonist or PAM. In the case of the antagonist rank order potency experiments, a control application of 100 μ M ACh was first applied for 10 s, immediately followed by a test 10 s application of antagonist in the continued presence of 100 μ M ACh and then a final 10 s application of 100 μ M ACh. Note that, with this approach, the potency for each antagonist is likely to be slightly underestimated due to the short time of drug

application. In order to minimize desensitization effects, at least 2 min was allowed for drug wash off between applications.

Dose–response studies were conducted in ascending order of concentrations and were not presented randomly. This approach minimizes desensitization by high concentrations of agonist. The application of the sequence of agonists for determining the potency series was random and not predetermined.

Blinding was not used because it was necessary to allow the appropriate technique and study methods to be used to test if the drug was a potential agonist, potential antagonist or potential PAM. In all our recordings, we applied an initial 100 μM ACh control, and all other responses were normalized to this control 100 μM ACh current. The normalized ACh current (100%) was not used for statistical analysis. Log dose–response plots are used for display and determination of the EC_{50} , nH and maximum response.

3.5.8 Permeability of receptors to calcium

Calcium permeability experiments were conducted by increasing the external Ca^{2+} concentration from 1 to 10 mM in the recording solution without changing the concentration of other cations. Oocytes were challenged with 30 μM ACh in the recording solution, with the membrane of the oocytes held at different potentials between -60 and $+30$ mV. The Goldman Hodgkin Katz (GHK) constant field equation was used to calculate the permeability ratio, $P_{\text{Ca}}/P_{\text{Na}}$. Because the oocytes were BAPTA-treated prior to recording, the assumptions made in calculating the permeability ratio of the expressed *Asu*-ACR-16 receptor were that the internal $[\text{Ca}^{2+}]$ is negligible and permeability of Na and K, P_{Na} and P_{K} is equal. Ionic activity coefficients used for the calculations were 0.56 for Ca^{2+} and 0.72 for

Na⁺ and K⁺. The GHK equation (with ionic activity inserted) used in calculating the P_{Ca}/P_{Na} was:

$$E_{rev} = RT/F \ln \left\{ \frac{(P_{Na} * 0.72 [Na]_o + P_K * 0.72 [K]_o + 4P' * 0.56 [Ca]_o)}{P_{Na} * 0.72 [Na]_i + P_K * 0.72 [K]_i} \right\},$$

where E_{rev} is the reversal potential (potential at which current changes direction), R is the universal gas constant (8.314 J·K⁻¹·mol⁻¹), T is room temperature in Kelvin (298 K), F is Faraday's constant (96 485 C·mol⁻¹) and $P' = P_{Ca}/P_{Na} \{ 1/(1 + e^{FE_{rev}/RT}) \}$.

3.5.9 Data and statistical analysis

The data and statistical analysis comply with the recommendations on experimental design and analysis in pharmacology (Curtis *et al.*, 2015). The acquired data from electrophysiological recordings were analysed with Clampfit 9.2 (Molecular Devices, Sunnyvale, CA, USA) and GraphPad Prism 5.0 (Graphpad Software Inc., La Jolla, CA, USA). In all recordings, the peak currents in response to applied drugs were measured, and except where otherwise indicated, peak current values obtained were normalized to 100 μM ACh and expressed as mean ± SEM. Dose–response relationships were analysed by fitting log dose–response data points with the Hill equation as previously described (Boulin *et al.*, 2008), while desensitization kinetics in response to the potent agonists were fitted using a single exponential decay fit:

$$f(t) = \sum_{i=1}^n A_i e^{-t/\tau_i} + C$$

where n is the number of components, A the amplitude, t the time, τ the time constant and C the constant y-offset for each i component.

The group sizes varied with the type of experiment performed, as described below. To optimize our expression and recording conditions, we injected 10 ng of *Asu-acr-16* alone and with 1.8 ng each of the ancillary factors, *ric-3*, *unc-50* and *unc-74* from *A.suum*, *H. contortus* and *X.laervis* ($n = 21$ for *Asu-acr-16* alone; $n = 15$ for *Asu-acr-16* + *Hco-ric-3*, *Hco-unc-50* and *Hco-unc-74*; $n = 15$ for *Asu-acr-16* + *Asu-ric-3*, *Asu-unc-50* and *Asu-unc-74*; $n = 17$ for *Asu-acr-16* + *Hco-ric-3*; $n = 20$ for *Asu-acr-16* + *Xle-ric-3*; and $n = 23$ for *Asu-acr-16* + *Asu-ric-3*). We found that *Asu-unc-50* and *Asu-unc-74* were not required for expression and that *Asu-acr-16* + *Asu-ric-3* produced the large robust currents (290.6 ± 63.7 , $n = 23$). We also tested different amounts of *Asu-acr-16* and *Asu-ric-3* ($n = 6$ for 25 ng *Asu-acr-16* + 5 ng *Asu-ric-3*, $n = 6$ for 10 ng *Asu-acr-16* + 5 ng *Asu-ric-3*, $n = 6$ for 10 ng *Asu-acr-16* + 10 ng *Asu-ric-3* and $n = 6$ for 15 ng *Asu-acr-16* + 15 ng *Asu-ric-3*) and observed that the size of the currents depended on the amount of *Asu-acr-16* and *Asu-ric-3* injected.

Thereafter, we injected 25 ng *Asu-acr-16* + 5 ng *Asu-ric-3* (which produced the biggest currents) for all subsequent experiments. For nAChR agonists and cholinergic anthelmintics, we tested larger numbers of oocytes ($n = 21$ for nicotine, $n = 21$ for cytisine, $n = 15$ for 3-bromocytisine, $n = 15$ for epibatidine, $n = 21$ for DMPP, $n = 36$ for oxantel, $n = 15$ for choline, $n = 15$ for betaine, $n = 15$ for lobeline, $n = 15$ for A844606, $n = 21$ for morantel, $n = 21$ for levamisole, $n = 15$ for methyridine, $n = 15$ for thenium, $n = 15$ for buphenium, $n = 15$ for tribendimidine and $n = 15$ for pyrantel) to measure and examine variability of responses between oocytes. Once we had confirmed the reproducible nature of the responses (the mean and standard errors for each of the nAChR agonist and cholinergic anthelmintics shown in Figure 3.3), we reduced our n number to 6 for all other experiments, except the antagonist experiment where the n number was 5.

Data were analysed statistically as follows. All completed drug application sequences on the oocytes were used for analysis without exclusion. If the recording became unstable, indicated by a change in the baseline holding current, all of that recording was rejected for analysis. Statistical analyses were performed on groups of values using ANOVA to determine if the group means are similar and if there was variance inhomogeneity (Bartlett's test). *Post hoc* tests (Tukey's multiple comparison test for Figures 3.2B, 3.3 and 3.6A; Dunnett's test to compare with control, for Figure 3.4) were used to determine significance of differences between groups. We analysed the effects of PAMs on *Asu*-ACR-16 using two-way ANOVA. We defined $P < 0.05$ as showing statistical significance.

3.6 Materials

The drugs used in this study, with the exception of paraherquamide, tribendimidine and derquantel were purchased from Sigma-Aldrich (St Louis, MO, USA), Tocris Bioscience (Ellisville, MO, USA) or Calbiochem (San Diego, CA, USA). The drugs were solubilized in recording solution, DMSO or ethanol. Paraherquamide and derquantel were gifts from Zoetis (Kalamazoo, MI, USA) and tribendimidine was a gift of Prof Shu Hua Xiao (National Institute of Parasitic Diseases, China).

3.7 Results

3.7.1 Identification of *Asu*-ACR-16 sequence

We used the *Cel*-ACR-16 sequence (Supporting Information Figure S3.0) as a query in a blastP search in protein databases from nematodes which allowed the identification of a potential complete coding sequence of an ACR-16 homologue in the pig parasite *Asu* (ERG81952.1). RT-PCR experiments using primers designed using this predicted sequence

led to the amplification of a full coding sequence (Figure 3.0A), which was submitted to GenBank under the accession number KP756901.

When we used the *Asu-acr-16* transcript sequence as a query, a blastP search resulted in the identification of highly conserved (complete or partial) homologous sequences from other parasitic nematode species belonging to Clade III (*T. canis* and *L. loa*), Clade IV (*S. ratti*) and Clade V (*H. contortus*, *A. ceylanicum* and *Necator americanus*) (Figure 3.0B and Supporting Information S3.1). The distance tree presented in Figure 3.0B indicates the orthologous relationship of the ACR-16 sequences from parasitic nematodes with the *Cel-ACR-16* sequence and also shows the orthologous relationship to the other nAChR subunits of *C. elegans*. The predicted complete sequences corresponding to ACR-16 orthologues in parasitic nematodes from Clade III and V were further analysed in a structural alignment. All amino acid sequences were found to share typical features of nAChR subunits including a predicted signal peptide, four transmembrane domains, a Cys-loop motif and a cysteine doublet in the potential agonist site defining them as α -subunits. Of note is that, despite their phylogenetic separation, ACR-16 sequences from Clade III and Clade V species were found to be highly conserved (i.e. 80% identities between *Asu-ACR-16* and *Hco-ACR-16*), suggesting that their pharmacology may also be similar.

3.7.2 *Asu-ACR-16* sequence suggests pharmacological differences to host mammalian $\alpha 7$ nAChRs

Alignment of the *Asu-ACR-16* amino acid sequence with that of human- $\alpha 7$ nAChRs using the Clustal Omega online alignment tool (Sievers *et al.*, 2011) showed *Asu-ACR-16* and human- $\alpha 7$ receptors share 44.90% identity in their amino acid sequences. Figure 3.0A shows the amino acid sequence alignment of *Asu-ACR-16*, which is compared with that of

A

Signal peptide

Asu-ACR-16 MSVQRALHYLLCSQLLHLHYAVEGSYHERRLYEDLMRDYNNLNERPVANHSQPVTYVLKVS 60
Human-α7 MRCSPGGVWLALAAASLLH-VSLAG-EFQRKLYKELVKNYNPLERPVANDSQPLTYVYFSLN 58
* : * * * : : * . . : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 LQQIIVDEKNQIVYVNAHLDYAMNDYKLRWDKEEYGNITDVRFPAGKIWKPDVLLYNSV 120
Human-α7 LLQIMDVDEKNQVLTNTNIWLQMSWTDHYLQWNVSEYPGVKTVRFPDGQIWKPDILLYNSA 118
* * : *

Asu-ACR-16 DATLDSTYPTNMVYVNTGDISWIIPGGIFKISKIDIKWPFDEQRCFFKFGSNTYDGFKL 180
Human-α7 DERFDATFHTNVLVNPSTGHCQYLPGGIFKSSCYIDVRWFPPDVQHCCLKFGSNTSYGGNSL 178
* : *

Asu-ACR-16 DLQPKGGFDISEYMPSGEWALPMTTVSRTEKFDCCPEYPDLTFYLMRRLTYYGFN 240
Human-α7 DLQMQE--ADISGYIPNGEWDLVGIPGKRSERFYCCKEYPDVTFTVMRRLTYYGLN 236
* * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 LIMPCILTTMTLLGGFTLPPDAGEKITLQITVLLSICFFLSIVSEISPTSEAVPLLGI 300
Human-α7 LLIPCVLISALALLVFLLPADSGEKISLGITVLLSLTVFMLLVAEIMPATSDSVPLIAQY 296
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 FSCCMIVVTASTVFTVYVNLHYRTPETHEMGITTRTLLLYWFPYILRMRPGVYLTWQT 360
Human-α7 FASTMIIVGLSVVTVIVLQYHHHDPDGGMKPKWTRVILLNWCWFLRMKRPGEKVRPA 356
* : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 LPPLFPCSKPKKHSESLIR-NVKDVET-GSSRSNSLDVERRVHQYMSGLTNGTGAPMCTV 418
Human-α7 -----CQHKQRR-CSLASVEMSAVAPPASNGNLLYIGFRGLDGVHCVPTPDSGVVVCGR 409
* . : : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 LNGGP-----ATVAGAPMDIGQQATLLVLQRIYQELKTI TRRMIEADREGAQSNNWKFAA 473
Human-α7 MACSPTHDEHLLHGGQPPE-G----DPDLAKILEEVRYIANRFRQDESEAVCSEWKFAA 464
: . * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Asu-ACR-16 MVVDR LCLYVFTVFI VASSCGILLSA PYTIA----- 504
Human-α7 CVVDR LCLMAFSVFTICTIGILMSA PNFVEAVSKDFA 502
* * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : * : *

Structural motifs: D, A, E, Cys loop, B, F, C, TM1, TM2, TM3, TM4. Arrows indicate conserved residues between Asu and Human sequences.

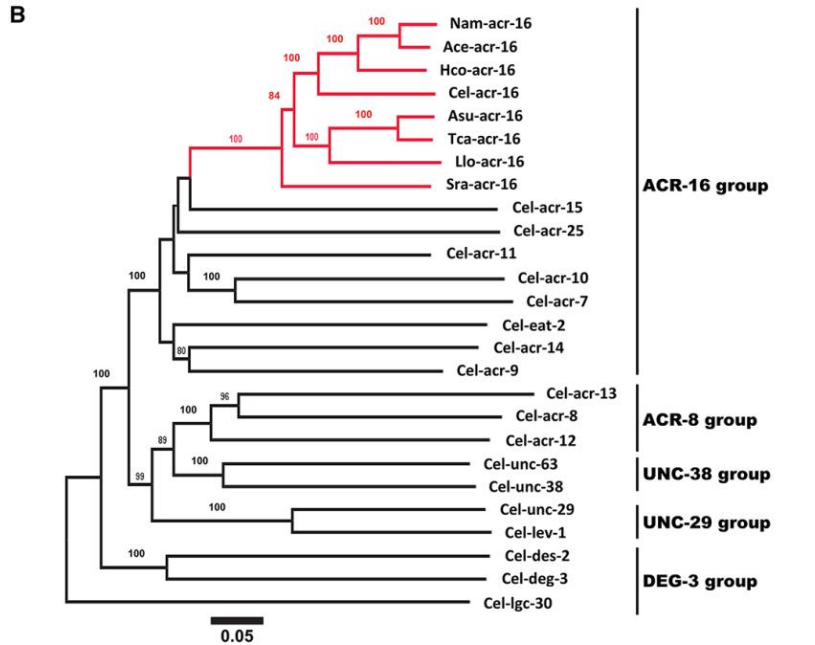


Figure 3.0 (A) Amino acid sequence alignment of *Asu*-ACR-16 and human- $\alpha 7$ nAChR subunits. The signal peptide (bright green box), ACh-binding loops A–F (pink boxes), cysteine loop (yellow box) and transmembrane regions TM1–TM4 (turquoise boxes) are indicated. The vicinal cysteines (black-edged box) that characterize an α -subunit are present in the C-binding loop. The blue-edged box between TM2 and TM3 represents the region where PNU120596 acts on $\alpha 7$ nAChRs. Green arrows are residues important for positive allosteric modulation of $\alpha 7$ receptors by ivermectin. Grey (and grey outline) arrows are residues important for permeability of $\alpha 7$ receptors to Ca^{2+} . Black (and black outline) arrows are residues affecting $\alpha 7$ receptor desensitization. Residues in C-binding loop of $\alpha 7$ nAChRs that bind α -BTX are highlighted in grey. (B) Distance tree showing relationships of ACR-16 homologues in parasitic nematode species with AChR subunit sequences from *C. elegans*. A neighbour joining tree was generated with deduced amino acid sequence from AChR subunits representative from the ACR-16, ACR-8, UNC-38, UNC-29 and DEG-3 group as defined by Mongan *et al.*, ([1]). Three letter prefixes in AChR subunit names: *Ace*, *Asu*, *Cel*, *Hco*, *Llo*, *Nam*, *Sra* and *Tca*, refer to *A. ceylanicum*, *A. suum*, *C. elegans*, *H. contortus*, *L. loa*, *N. americanus*, *S. ratti* and *T. canis* respectively. ACR-16 orthologues are highlighted in red. Numbers at each branch indicate percentage bootstrap values (>80%) corresponding to 1000 replicates. The scale bar represents substitutions per site. The *Cel-lgc-30* subunit sequence was used as an outgroup.

human- $\alpha 7$ receptors (Raymond *et al.*, 2000; Touroutine *et al.*, 2005). *Asu*-ACR-16 has the characteristic vicinal cysteine residues (Y-x-C-C) found in the C-loop of most nAChR α -subunits; these C-C residues play an essential role in ACh binding (Kao *et al.*, 1984).

Significantly, the Y-x-C-C residues of the C-loop of *Asu*-ACR-16 (Supporting Information S3.2) differ from the C-loop of the levamisole receptor α -subunits, *Cel*-UNC-38 and *Cel*-ACR-13, which have a Y-x-x-C-C motif (Mongan *et al.*, 1998); this C-loop difference encouraged our view that the *Asu*-ACR-16 nAChR would differ in its pharmacology from that of the levamisole receptors.

We were further encouraged to investigate the pharmacology of *Asu*-ACR-16 because of other significant differences in amino acid residues which are known to affect activation, desensitization and modulation in $\alpha 7$ nAChRs. For example, Figure 3.0A shows four amino acids (black and black outline arrows in the TM2 region known as L247, V251, L254 and

L255 when mature peptide numbering of $\alpha 7$ subunits is used) that change the desensitization of $\alpha 7$ receptors (Revah *et al.*, 1991; Bertrand *et al.*, 1992; Corringer *et al.*, 1999b). Note that only the first of these (L247) is conserved in *Asu*-ACR-16. Consequently, we chose to investigate the rate of desensitization of *Asu*-ACR-16. Other amino acid differences between the $\alpha 7$ and the levamisole α -receptor subunits, which we describe subsequently, suggest that the *Asu*-ACR-16 receptor pharmacology will be different.

3.7.3 Ubiquitous tissue and single-cell expression of ACR-16 in *Asu*

We examined the distribution of *Asu*-ACR-16 in dissected adult female *Asu* tissues using RT-PCR. We found reproducible and clear evidence of expression of *Asu*-ACR-16 message in strips of intestine (Figure 3.1A; g, gut), sections of the reproductive tract (Figure 3.1A; o, oviduct, uterus), whole dissected pharynx (Figure 3.1A; p), body muscle strips (Figure 3.1A; m) and head (Figure 3.1A; h) region. We observed similar expression patterns of *Asu*-ACR-16 message in the gut, oviduct, whole pharynx, body muscle strip and head from four other adult female *Asu*. The expression of *Asu*-ACR-16 in tissues other than nerves and body muscle tissue, like the non-excitabile tissues of the intestine and reproductive tract (uterus), was not anticipated. But it was reproducible and may be part of an ACh-mediated paracrine system (Proskocil *et al.*, 2004; Bschiepfer *et al.*, 2007) rather than part of a neurotransmitter process. The *Asu*-ACR-16 ACh receptor may serve multiple roles in reproduction, digestion, etc., as well as neuromuscular transmission in the parasite.

Single-cell RT-PCR was conducted to further investigate the localization of *Asu*-ACR-16 in the pharyngeal and somatic muscle cells of *A. suum*. We used intracellular micropipettes to collect cytoplasm from individual somatic and pharyngeal muscle cells for PCR analysis. We recovered *Asu*-ACR-16 message from single body muscle cells but not

from pharyngeal muscle cells (Figure 3.1B). The presence of *Asu*-ACR-16 positive bands in the whole pharynx and absence in single-cell RT-PCR samples suggests that *Asu*-ACR-16 is present in the neurons of the circum-pharyngeal nerve ring but not present on pharyngeal muscle cells. In contrast to the pharyngeal muscle cells, we observed that *Asu*-ACR-16 expression is widespread in somatic muscle as well as other tissues of the *Ascaris* body, implying tissue-related functions in addition to a neuromuscular function.

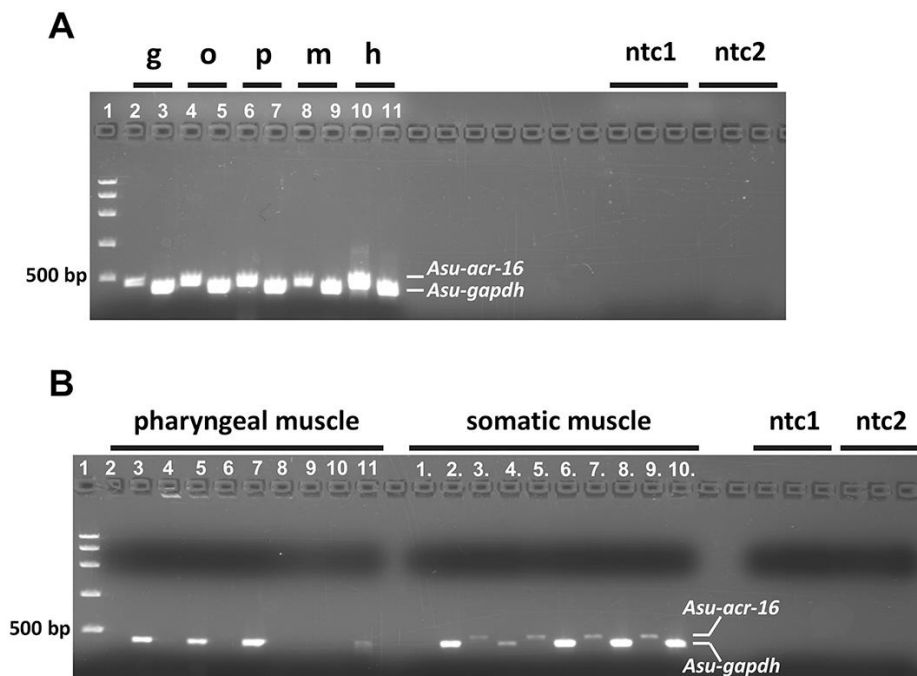


Figure 3.1 Localization of *Asu*-ACR-16 in different body tissues of the *A. suum* worm using RT-PCR and single-cell RT-PCR ($n = 5$). (A) RT-PCR analysis of *Asu-acr-16* (lanes 2, 4, 6, 8, 10) and *gapdh* control (lanes 3, 5, 8, 9, 11) in gut (g), oviduct (o), pharynx (p), somatic muscle strip (m) and head region (h). The PCR products size for *acr-16* and *gapdh* is 468 and 411 bp respectively. (B) Single-cell RT-PCR of *Asu*-ACR-16 in pharyngeal muscle (2, 4, 6, 8, 10) and in somatic muscle (1., 3., 5., 7., 9.). RT-PCR of *gapdh* control in pharyngeal muscle (3, 5, 7, 9, 11) and in somatic muscle (2., 4., 6., 8., 10.). 1, FastRuler High Range DNA ladder; ntc1, no-template controls for *acr-16*; ntc2, no-template controls for *gapdh*.

3.7.4 *ric-3* is required for functional expression of *Asu-ACR-16*

After we cloned *Asu-ACR-16*, we examined ancillary protein requirements for its expression in *Xenopus* oocytes. Figure 3.2 shows the effects of co-injecting the cRNA for the ancillary proteins: *ric-3*, *unc-50* and *unc-74* from *A.suum*; *ric-3*, *unc-50* and *unc-74* from *H.contortus*; and *ric-3* from *X. laevis*. We measured oocyte responses to 100 μ M ACh. Figure 3.2A shows representative traces of inward currents induced by the different combinations of ancillary proteins and *Asu-acr-16*. Figure 3.2B is a bar chart of the mean \pm SEM of the 100 μ M ACh responses. Oocytes injected with *Asu-acr-16* cRNA alone did not respond to 100 μ M ACh ($n = 21$). The largest currents ($I_{\max} = 290.6 \pm 63.7$ nA, $n = 23$) were seen in oocytes where just *ric-3* from *A. suum* was co-injected with *Asu-acr-16*: these oocytes had larger current responses to 100 μ M ACh than oocytes in which all three of the ancillaries (*ric-3*, *unc-50* and *unc-74* from either *H. contortus* or *A. suum*) were injected with *Asu-acr-16*. The currents were also larger than when just *Hco-ric-3* was co-injected with *Asu-acr-16*, suggesting that there is a species-selective interaction between *Asu-ACR-16* and *Asu-RIC-3*. Interestingly, *Xle-ric-3* produced mean currents that lay between those produced by *Ascaris* and *Haemonchus ric-3*. We concluded that the robust expression of *Asu-ACR-16* in *Xenopus* oocytes requires *ric-3*, but not *unc-50* and *unc-74*.

We also varied the amount of cRNA of *Asu-acr-16* (10–25 ng) and cRNA of *Asu-ric-3* (5–15 ng) injected to test the effects on expression. Supporting Information S3A, B shows representative current traces and bar charts of mean \pm SEM of the current responses. The largest response (1062 ± 94.1 nA, $n = 6$) was obtained from oocytes injected with 25 ng *Asu-acr-16* and 5 ng *Asu-ric-3*. We observed that the responses were dependent on the amounts of *Asu-acr-16* and *Asc-ric-3* injected and that increased *ric-3* did not overcome the effects of

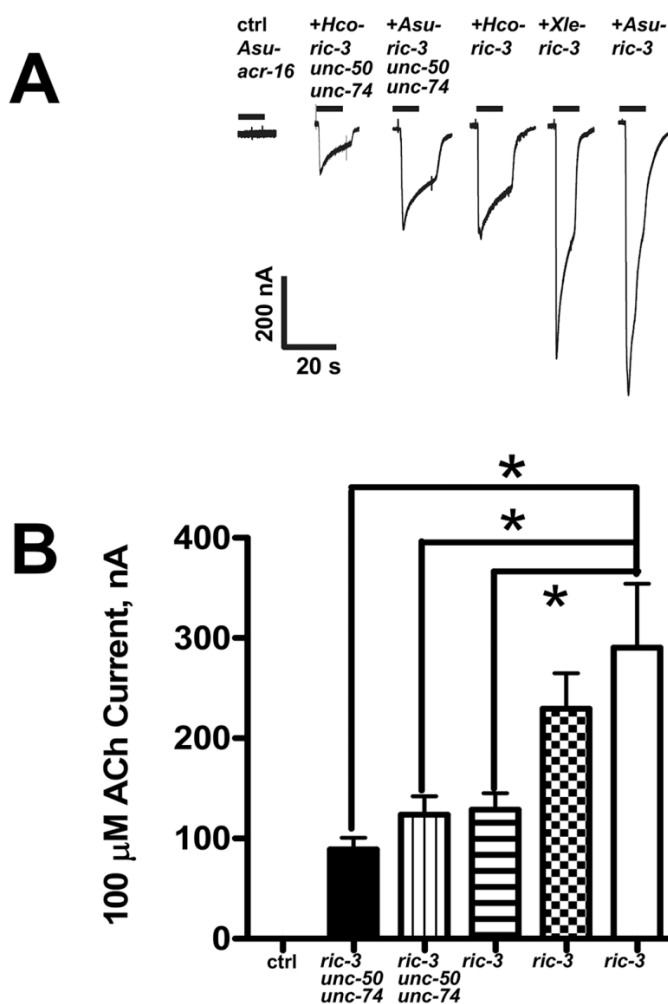


Figure 3.2 Effects of the ancillary proteins, RIC-3, UNC-50 and UNC-74, from different nematode species, on *Asu*-ACR-16 expression. (A) Sample traces represented as inward currents produced in response to 100 μ M ACh. (B) Bar chart (mean \pm SEM) showing (left to right) current (in nA) generated in response to 100 μ M ACh produced. Control (ctrl): *Asu*-*acr*-16 alone ($n = 21$). Black bar: *Asu*-*acr*-16 plus *Hco*-*ric*-3, *unc*-50 and *unc*-74 ($n = 15$). Vertical line fill: *Asu*-*acr*-16 plus *Asu* *ric*-3, *unc*-50 and *unc*-74 ($n = 15$). Horizontal line fill: *Asu*-*acr*-16 plus *Hco*-*ric*-3 ($n = 17$). Checkered fill: *Asu*-*acr*-16 plus *Xle*-*ric*-3 ($n = 20$). No fill: *Asu*-*acr*-16 plus *Asu*-*ric*-3 ($n = 23$). *Asu*-*acr*-16 on its own did not respond to ACh, and the largest current size was obtained when *Asu*-*acr*-16 was co-injected with *Asu*-*ric*-3. * $P < 0.05$; significantly different as indicated; Tukey's multiple comparison tests.

3.7.5 *Asu*-ACR-16 forms a nicotine-sensitive but levamisole-insensitive nAChR

reduced *acr-16*. All subsequent recordings were carried out on oocytes in which 25 ng *Asu-acr-16* was co-injected with 5 ng *Asu-ric-3*.

3.7.5 *Asu-ACR-16* forms a nicotine-sensitive but levamisole-insensitive nAChR

Figure 3.3 shows the rank order potency series for a selection of nine nicotinic agonists and eight cholinergic anthelmintic agonists tested on the expressed *Asu-ACR-16* nAChR. The nicotinic and anthelmintic agonists were tested at 100 μ M, except for

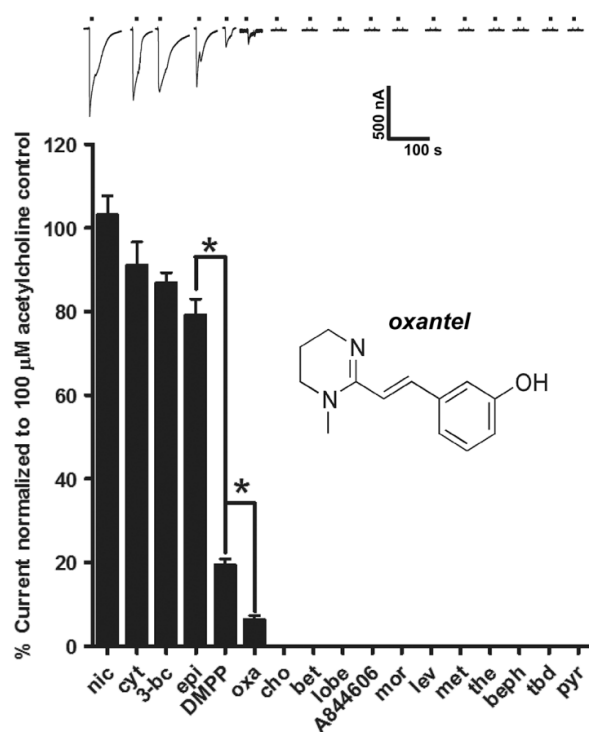


Figure 3.3 Effects of nAChR agonists and anthelmintics on *Asu-ACR-16*. Sample traces and bar chart (mean \pm SEM) showing rank order potency series for nAChR agonists: nicotine (nic), cytisine (cyt), 3-bromocytisine (3-bc), epibatidine (epi), DMPP, choline (cho), betaine (bet), lobeline (lobe) and A844606; and cholinergic anthelmintics: oxantel (oxa), morantel (mor), levamisole (lev), methyridine (met), thenium (the), bephenium (beph), tribendimidine (tbd) and pyrantel (pyr); on *Asu-ACR-16*. Overall, the rank order potency series for agonists and anthelmintics on *Asu-ACR-16* when normalized to the control 100 μ M ACh current was as follows: 100 μ M nic ($n = 21$) \sim 100 μ M cyt ($n = 21$) \sim 100 μ M 3-bc ($n = 15$) \sim 100 μ M epi ($n = 15$) $>$ 100 μ M DMPP ($n = 21$) $>$ 100 μ M oxa ($n = 36$) \gggg 100 μ M cho ($n = 15$) = 100 μ M bet ($n = 15$) = 100 μ M lobe ($n = 15$) = 100 μ M A844606 ($n = 15$) = mor ($n = 21$) = 100 μ M lev ($n = 21$) = 100 μ M met ($n = 15$) = 100 μ M the ($n = 15$) = 100 μ M beph ($n = 15$) = 30 μ M tbd ($n = 15$) = 100 μ M pyr ($n = 15$). * $P < 0.05$; significantly different as indicated; Tukey's multiple comparison tests.

tribendimidine, which was tested at a concentration of 30 μ M due to its limited solubility. Representative traces of inward currents induced by each nicotinic or anthelmintic agonist are shown along with their mean \pm SEM normalized values as bar charts. Nicotine, cytisine, 3-bromocytisine and epibatidine were the most potent (>80% of the control ACh current), whereas DMPP was least potent (<20% of the control ACh current). Choline, betaine, lobeline and A844606 were not active on the *Asu*-ACR-16 nAChR. With the exception of oxantel, which showed a very weak agonist effect (<10% of the control ACh current), the *Asu*-ACR-16 nAChR was not activated by any of the other anthelmintic drugs tested (morantel, levamisole, methyridine, thenium, bphenium, tribendimidine and pyrantel). The rank order potency series for agonists and anthelmintics on *Asu*-ACR-16 when normalized to the internal standard control 100 μ M ACh current was as follows: *nicotine* ~ *cytisine* ~ 3-*bromocytisine* ~ *epibatidine* > *DMPP* > *oxantel* >>> *choline* = *betaine* = *lobeline* = *A844606* = *morantel* = *levamisole* = *methyridine* = *thenium* = *bphenium* = *tribendimidine* = *pyrantel*. Nicotine was among the most potent agonists, while none of the cholinomimetic anthelmintics produced any effect, except for the small effect of oxantel. This agonist potency series shows that this nAChR is distinct from the levamisole receptors of nematodes.

3.7.6 *Asu*-ACR-16 desensitization

Desensitization was a feature of the *Asu*-ACR-16 receptor responses and was characterized by the peak and waning current responses observed during maintained (for 10 s) agonist applications. We observed receptor desensitization with all potent agonists. The time constants for desensitization observed with different agonists are shown in Figure 3.4: the mean time constants for desensitization rates ranged between 6.2 and 12.6 s, with the

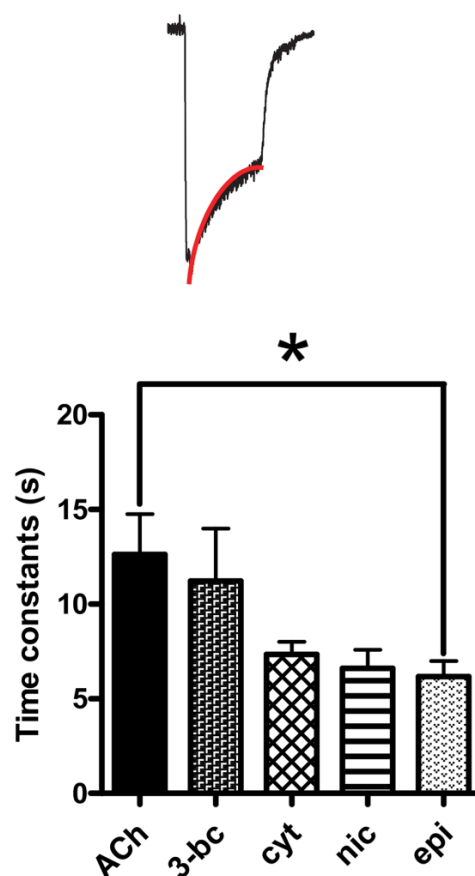


Figure 3.4 *Asu*-ACR-16 desensitization rate constant fit. Bar chart (mean \pm SEM) showing *Asu*-ACR-16 desensitization in response to ACh, 3-bromocytisine (3-bc), cytosine (cyt), nicotine (nic) and epibatidine (epi). The rank order for *Asu*-ACR-16 time constants of desensitization was as follows: 100 μ M ACh (12.6 ± 2.1 s, $n = 6$) \sim 100 μ M 3-bc (11.2 ± 2.8 s, $n = 6$) \sim 100 μ M cyt (7.3 ± 0.7 s, $n = 6$) \sim 100 μ M nic (6.6 ± 1.0 s, $n = 4$) \sim 100 μ M epi (6.2 ± 0.8 s, $n = 6$). *Insert*: Sample trace with red line signifying desensitization fit. * $P < 0.05$; significantly different as indicated; Tukey's multiple comparison tests.

time constant for desensitization depending on the agonist and significantly higher for ACh than for epibatidine. However, these time constants were markedly longer than the vertebrate $\alpha 7$ receptor, which has desensitization time constants in the 230–1300 ms range (McCormack *et al.*, 2010): the slower desensitization rates may be explained in part by the absence of the amino acids: V251, L254 and L255 in *Asu*-ACR-16.

3.7.7 Nicotine as a potent agonist

Figure 3.5 shows representative recordings and concentration–response relationships of inward currents induced by the application of different concentrations of ACh (Figure 3.5A), top trace, and nicotine (Figure 3.5A), lower trace. The first application of an agonist for each new recording was always 100 μM ACh, which was used as the internal standard for normalization. The EC_{50} for nicotine ($4.5 \pm 0.2 \mu\text{M}$, $n = 6$) was statistically significantly smaller than that for ACh (EC_{50} of $5.9 \pm 0.1 \mu\text{M}$, $n = 6$), which, on this basis, nicotine is more potent than ACh. Interestingly, there was no significant difference between the maximum response for nicotine (I_{max} of $82.5 \pm 3.4\%$, $n = 6$) and that for ACh (I_{max} of $82.7 \pm 2.4\%$, $n = 6$). There was also no significant difference between the Hill slopes, n_H , for

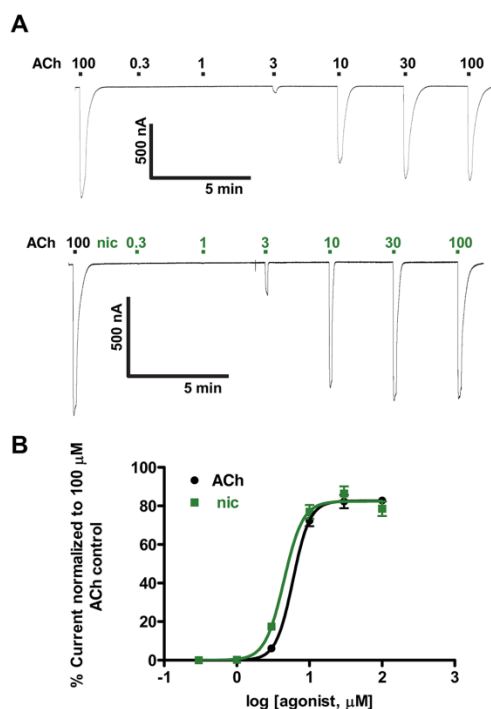


Figure 3.5 Nicotine (nic) and ACh concentration–response relationships for *Asu*-ACR-16 in the absence of antagonists. (A) Sample traces for ACh (top trace) and nicotine (lower trace) dose–response relationships for *Asu*-ACR-16. (B) ACh and nic dose–response curves for *Asu*-ACR-16. EC_{50} values (mean \pm SEM, μM) were 5.9 ± 0.1 for ACh, Hill slope (n_H) = 3.9 ± 0.3 , $n = 6$, and 4.5 ± 0.2 for nic, $n_H = 3.4 \pm 0.2$, $n = 6$.

both nicotine and ACh. However, both the nicotine and ACh concentration–response curves were very steep, with Hill slopes, N_H , of 3.4 ± 0.2 , $n = 6$, for nicotine and 3.9 ± 0.3 , $n = 6$, for ACh, showing strong cooperativity consistent with homomeric receptors containing multiple ligand binding sites.

3.7.8 Rank order antagonist potencies: *Asu*-ACR-16 is not sensitive to α -BTX

We tested 10 μ M concentrations of eight nAChR antagonists of mammalian or nematode receptors on the expressed *Asu*-ACR-16 nAChR. The antagonists were α -bungarotoxin (α -BTX), dihydro- β -erythroidine (DH β E), d-tubocurarine (dTC), hexamethonium, mecamylamine, methyllycaconitine (MLA), derquantel, and paraherquamide. The mean % inhibition of the control 100 μ M ACh current response was used to determine the rank order potency of the antagonists. α -BTX, an $\alpha 7$ receptor selective antagonist, had little effect on the *Asu*-ACR-16 receptor and was the least potent (inhibition, $5.5 \pm 0.8\%$ $n = 6$) antagonist in the rank order series. In this respect, the *Asu*-ACR-16 receptor was unlike the mammalian $\alpha 7$ nAChR. Mecamylamine, MLA and dTC were the most potent. The rank order of potency (Figure 3.6A) was *mecamylamine = MLA = dTC* > *paraherquamide ~ derquantel ~ hexamethonium ~ DH β E* > *α -BTX*.

3.7.9 Non-competitive derquantel antagonism and mixed antagonism of DH β E

We tested the effects of the nAChR antagonists, derquantel and DH β E on ACh (Figure 3.6B1). The concentration–response plots (Figure 3.6B2) show that derquantel acts as a non-competitive antagonist, with 1 μ M derquantel producing a statistically significant reduction in the maximum response, but no significant change in the EC_{50} . I_{max} and EC_{50} values were respectively $82.7 \pm 2.4\%$ and $5.9 \pm 0.1 \mu$ M, $n = 6$, for ACh and $63.8 \pm 2.8\%$ and

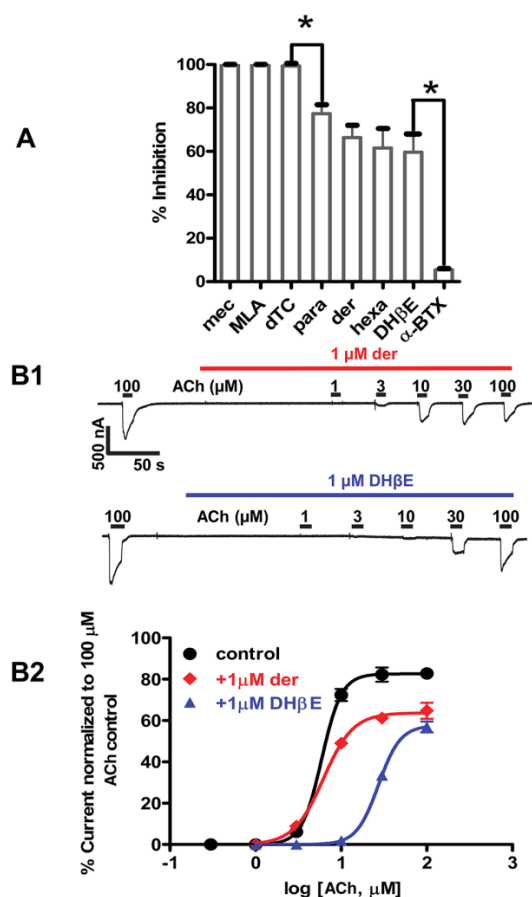


Figure 3.6 (A) Effects of selected nAChR antagonists on *Asu*-ACR-16-mediated ACh responses. Bar chart showing effects of selected nAChR antagonists on *Asu*-ACR-16. Results were expressed as mean (\pm SEM) % inhibition of currents elicited by 100 μ M ACh, $n = 6$, for all antagonists. dTC, mecamylamine (mec) and MLA completely blocked *Asu*-ACR-16-mediated ACh responses, while paraherquamide (para), derquandel (der), hexamethonium (hexa) and DH β E only produced a partial block of *Asu*-ACR-16-mediated ACh responses and α -BTX produced an almost insignificant block of *Asu*-ACR-16-mediated ACh responses. Rank order potency series for the nAChR antagonists each tested at a concentration of 10 μ M was as follows: mecamylamine ($n = 6$) = MLA ($n = 6$) \approx dTC ($n = 6$) > paraherquamide ($n = 6$) \sim derquandel ($n = 6$) \sim hexamethonium (hexa) ($n = 6$) \sim DH β E ($n = 6$) > α -BTX ($n = 6$). * $P < 0.05$; significantly different as indicated; Tukey's multiple comparison tests. We used ANOVA and Bartlett's test for variance inhomogeneity and found no significant difference and Tukey's multiple comparison tests. (B) Dose-response relationships for *Asu*-ACR-16 in the presence of antagonists. (B1) Sample traces for ACh concentration-response relationships for *Asu*-ACR-16 in the presence of 1 μ M derquandel and 1 μ M DH β E. (B2) ACh concentration-response plots for *Asu*-ACR-16 in the presence of 1 μ M derquandel and 1 μ M DH β E. Derquandel caused a reduction in the maximum response, but no change in EC₅₀, whereas DH β E caused both a reduction in the maximum response and a right shift in the EC₅₀.

$6.2 \pm 0.5 \mu\text{M}$, $n = 6$, for derquantel. DH β E produced mixed competitive and non-competitive antagonism (Figure 3.6B2) characterized by a significant right shift in the EC_{50} and a statistically significant reduction of the maximum response. EC_{50} and I_{max} values were respectively $5.9 \pm 0.1 \mu\text{M}$ and $82.7 \pm 2.4\%$, $n = 6$, for ACh and $29.0 \pm 1.0 \mu\text{M}$ and $58.0 \pm 3.1\%$, $n = 6$, for DH β E. These observations suggest that antagonists of this receptor act at more than one site that may include the agonist-binding site and/or a different allosteric site.

3.7.10 PAMS of human $\alpha 7$ nAChRs inhibit *Asu*-ACR-16 responses

Ion channel receptor opening may be increased (agonists) or decreased (competitive antagonists) by drugs binding to the ligand binding site, or the opening can be increased by PAMs or decreased by negative allosteric modulators binding to a site other than the ligand binding site (allosteric sites). Ivermectin and genistein are $\alpha 7$ receptor type 1 PAMs (Sattelle *et al.*, 2009), which increase the response to a fixed concentration of an agonist by increasing the amplitude of the current response; PNU120596 is an $\alpha 7$ receptor type 2 PAM (Kalappa and Uteshev, 2013) whose action is characterized by both an increased amplitude of response and the reduction of desensitization of the current response to a fixed concentration of agonist.

We were interested to see if ivermectin, genistein and PNU120596 were PAMs of the *Asu*-ACR-16. We tested the effects of ivermectin ($10 \mu\text{M}$), genistein ($3 \mu\text{M}$) and PNU120596 ($3 \mu\text{M}$) separately on responses to 10, 30 and $100 \mu\text{M}$ ACh (Supporting Information S3.3). We did not observe potentiation in any experiment, but we saw modest reductions in the amplitudes of the responses. Figure 3.7 shows bar charts of the mean \pm SEM [$n = 6$ (ivermectin), $n = 6$ (genistein), $n = 6$ (PNU120596)] currents of the control and test responses

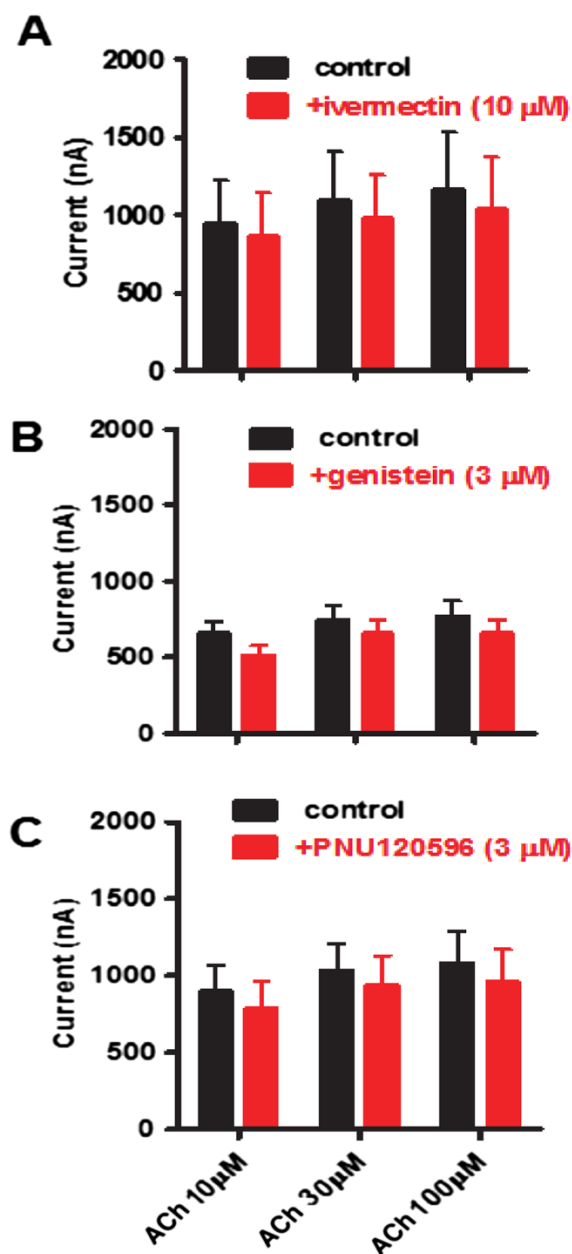


Figure 3.7 Effects of PAMs of human- $\alpha 7$ on *Asu*-ACR-16-mediated ACh responses. Bar charts showing blocking actions of human- $\alpha 7$ PAMs; (A) 10 μ M ivermectin ($n = 6$), (B) 3 μ M genistein ($n = 6$) and (C) 3 μ M PNU120596 ($n = 6$), on the responses of *Asu*-ACR-16 to ACh. The type 1 PAMs, ivermectin and genistein, as well as the type 2 PAM, PNU120596, caused a reduction in *Asu*-ACR-16 responses to 10, 30 and 100 μ M ACh, with the reduction being more pronounced at 10 than at 30 or 100 μ M ACh.

3.7.11 Calcium permeability of *Asu*-ACR-16

in the presence of the allosteric modulator. Two-way ANOVA showed that ivermectin, genistein and PNU120596 had a statistically significant inhibitory effect on *Asu*-ACR-16 ACh responses. This inhibitory effect of ivermectin, genistein and PNU120596 was opposite to the stimulatory effect on mammalian $\alpha 7$ receptors (Sattelle *et al.*, 2009).

3.7.11 Calcium permeability of *Asu*-ACR-16

The calcium permeability of nAChRs varies and relates to the channel pore region formed by the TM2 domain of the subunit (Corringer *et al.*, 1999a; Tapia *et al.*, 2007). We tested the calcium permeability of the *Asu*-ACR-16 receptor by determining the shift in the reversal potential of the current–voltage (I–V) plot following a change in the concentration of Ca^{2+} in the extracellular solution (Supporting Information S3.4). Increasing the concentration of Ca^{2+} from 1 to 10 mM produced an inward rectification of the current through the *Asu*-ACR-16 receptor and a small positive shift of the I–V plot of 2.4 ± 2.1 mV ($n = 6$). A shift of 2.4 mV indicates relative calcium permeability ($P_{\text{Ca}}/P_{\text{Na}}$) of 0.4 when calculated from the GHK equation. The $\alpha 7$ receptor is much more permeable to calcium than the *Asu*-ACR-16 receptor. The $P_{\text{Ca}}/P_{\text{Na}}$ reported for $\alpha 7$ nAChRs is 20, calculated from a 29 ± 3 mV shift under similar conditions (Séquéla *et al.*, 1993), which was significantly (two-tailed *t*-test) bigger than the 2.4 mV shift observed for *Asu*-ACR-16.

3.8 Discussion

This study reports for the first time the reconstitution in the *Xenopus* oocyte expression system of a fully functional homomeric nAChR, ACR-16, from a parasitic nematode. This finding is of significant importance in anthelmintic drug discovery in that it provides an efficient platform for screening anthelmintic compounds.

3.8.1 Comparison of pharmacology of *Asu*-ACR-16 with *Cel*-ACR-16

Previous work on the functional reconstitution in *Xenopus* oocytes and pharmacological characterization of ACR-16 has focused on the model nematode, *C. elegans* (Ballivet *et al.*, 1996). In agreement with Ballivet *et al.* (1996), *Asu*-ACR-16 was more sensitive to nicotine than ACh, but insensitive to levamisole and pyrantel. However, the Hill slopes for nicotine ($n_H = 3.4 \pm 0.2$, $n = 6$) and ACh ($n_H = 3.9 \pm 0.3$, $n = 6$) concentration–response curves for *Asu*-ACR-16 were slightly steeper than those reported for *Cel*-ACR-16 ($n_H = 2.2$ for nicotine and $n_H = 2.1$ for ACh). In any case, the Hill slopes for both *Asu*-ACR-16 and *Cel*-ACR-16 reveal strong cooperativity associated with homomeric receptors. The steeper Hill slopes for *Asu*-ACR-16 may account for its higher sensitivity (as shown by EC_{50} values) to nicotine and ACh when compared with those for *Cel*-ACR-16 (*Asu*-ACR-16's EC_{50} values were $4.5 \pm 0.2 \mu\text{M}$, $n = 6$, for nicotine and $5.9 \pm 0.1 \mu\text{M}$, $n = 6$, for ACh. On the other hand, for *Cel*-ACR-16, EC_{50} values were $12.6 \mu\text{M}$ for nicotine and $55.4 \mu\text{M}$ for ACh. Despite the high degree of sequence identity (74.75% identity) between *Asu*-ACR-16 and *Cel*-ACR-16 (Ce21), there exist significant differences in terms of the antagonist pharmacology of these two receptors. In accordance with Ballivet *et al.* (1996), *Asu*-ACR-16 was nearly insensitive to α -BTX, but highly sensitive to dTC. In contrast, *Asu*-ACR-16 was highly sensitive to MLA, but moderately sensitive to hexamethonium and DH β E.

3.8.2 Comparison of pharmacology of *Asu*-ACR-16 with $\alpha 7$ nAChRs

Alignment of *Asu*-ACR-16 with human $\alpha 7$ nAChRs shows similarities but important differences in amino acid residues, suggesting differences in their pharmacologies. We find similarities in agonist sensitivity to ACh, nicotine and epibatidine of *Asu*-ACR-16 and $\alpha 7$ receptors (Raymond *et al.*, 2000; Li *et al.*, 2011). However, *Asu*-ACR-16 was insensitive to

the $\alpha 7$ -selective agonist, A844606. *Asu*-ACR-16 was highly sensitive to MLA just like $\alpha 7$ (Briggs *et al.*, 1995), but in contrast to the sensitivity of $\alpha 7$ receptors to α -BTX (Zhao *et al.*, 2003), we observed *Asu*-ACR-16 to be quite insensitive to α -BTX. The PAMs of $\alpha 7$ (ivermectin, genistein and PNU120596) were inhibitory on *Asu*-ACR-16. Lastly, we found that the relative calcium permeability ratio of *Asu*-ACR-16 was about 50 \times smaller than that of the $\alpha 7$ receptor (Séquela *et al.*, 1993). The pharmacology of *Asu*-ACR-16 receptors is thus different to that of $\alpha 7$ nAChRs, indicating that the *Asu*-ACR-16 receptor has potential as a drug target site.

3.8.3 Comparison of pharmacology of *Asu*-ACR-16 with levamisole receptors

Asu-ACR-16 is different from the classical cholinergic levamisole receptor. The levamisole receptor subtypes are composed of different mixtures of heterologous subunits (UNC-29, UNC-38, ACR-8, LEV-1, ACR-13 and UNC-63) (Martin *et al.*, 2012b), whereas *Asu*-ACR-16 consists of only one subunit (ACR-16). Unlike the levamisole receptors, which are sensitive to levamisole but insensitive to nicotine, *Asu*-ACR-16 is sensitive to nicotine but insensitive to levamisole. All three ancillary proteins, RIC-3, UNC-50 and UNC-74, are required for robust expression of levamisole-sensitive receptors (Boulin *et al.*, 2008), while ACR-16 requires only RIC-3 for optimal expression in *Xenopus* oocytes (Sattelle *et al.*, 2009; Bennett *et al.*, 2012).

Another important difference between *Asu*-ACR-16 and the levamisole receptor can be seen in their antagonist pharmacologies. The levamisole receptor was only slightly inhibited by the nAChR antagonist, DH β E (Richmond and Jorgensen, 1999), whereas *Asu*-ACR-16 was strongly inhibited by DH β E. MLA and hexamethonium are also less potent on levamisole receptors. Because the pharmacology of ACR-16 is different from the levamisole

receptors, a selective anthelmintic directed at ACR-16 may have the appropriate properties to bypass resistance.

3.8.4 Differences in α -BTX potency, allosteric modulation and Ca^{2+} permeability

Site-directed mutagenesis of nAChR subunits has been exploited as one of the tools in understanding the pharmacological differences between nAChR types. In a bid to provide reasons for the differences between the pharmacology of $\alpha 7$ receptors and *Asu*-ACR-16, we reviewed and compared the amino acids known to affect receptor pharmacology. In $\alpha 7$ for instance, the amino acids critical for α -BTX binding are ERFYECCKEYPYPD in the C-loop (Balass *et al.*, 1997). The corresponding residues in *Asu*-ACR-16 are EKFYDCCPEYPYPD: the RK, ED and KP substitutions may explain why α -BTX is not as potent as an antagonist of the *Asu*-ACR-16 receptor.

There are seven residues in $\alpha 7$ nAChRs important for positive allosteric modulation by ivermectin (Figure 3.0A, dark green arrows). Remarkably, none of these amino acids are conserved in *Asu*-ACR-16, which may explain why a positive allosteric effect of ivermectin for *Asu*-ACR-16 was not detected. Mutations in four of these residues (A225D, Q272, T456Y and C459) caused a significant reduction in the potency of ivermectin as a PAM, while mutations in the other three (S222M, M253L and S276V) caused ivermectin to act as an antagonist (Collins and Millar, 2010). *Asu*-ACR-16 contains the M253L substitution consistent with the observed inhibitory effect of ivermectin. Furthermore, we found that PNU120596 was not an allosteric modulator of *Asu*-ACR-16, in contrast to its action at $\alpha 7$ receptors. The amino acid residues between TM2 and TM3 in $\alpha 7$ responsible for PNU120596 positive allosteric modulation (AEIMPATSDS) (Bertrand *et al.*, 2008) are replaced with SEISPPTSEA in *Asu*-ACR-16 (blue-edged box, Figure 3.0A). These differences may

account for the lack of positive allosteric modulation by PNU120596 in *Asu*-ACR-16. The amino acid differences in allosteric modulatory sites may allow for the design of selective drugs targeted at *Asu*-ACR-16.

Three residues, E237, L254 and L255, play key roles in the Ca^{2+} permeability of $\alpha 7$ nAChRs (grey and grey outline arrows, Figure 3.0A). In these receptors, mutations E237A, L254R/T and L255R/T/G cause a reduction in Ca^{2+} permeability (Bertrand *et al.*, 1993). When compared with *Asu*-ACR-16, only one (E237) of these three residues is conserved. Amino acid differences at one or more positions may account for the reduction in the Ca^{2+} permeability of the *Asu*-ACR-16 compared with the $\alpha 7$ receptor.

3.8.5 Ubiquitous distribution of *Asu*-ACR-16 receptor and its function

ACR-16 has been identified as one of the proteins required for the excitatory current at the neuromuscular junction of *C. elegans* (Richmond and Jorgensen, 1999; Francis *et al.*, 2005). In fact, *acr-16* null mutants show nearly normal motor behaviour. Severe locomotion deficits were, however, seen with *acr-16:unc-63* or *acr-16:unc-29* double mutants (Touroutine *et al.*, 2005; Li *et al.*, 2014), showing that, in combination with other subunits, its function was essential.

The ubiquitous distribution of the *Asu*-ACR-16 message in tissues like the intestine and reproductive tract suggests that this receptor has functions which are not limited to regulation of fast neuromuscular transmission. The presence of *Asu*-ACR-16 in non-excitabile tissues suggests that *Asu*-ACR-16 also has slower paracrine/autocrine and homeostatic or differentiation functions associated with digestion and reproduction (Kawashima and Fujii, 2008). A paracrine and endocrine intestinal function for ACh is also supported by the presence of an organized distribution of acetylcholinesterase just beneath and adjacent to the

intestinal epithelium (Lee, 1996). The wide tissue distribution of *Asu*-ACR-16 message suggests that a selective agonist may have advantages as an anthelmintic.

3.8.6 Consideration of *Asu*-ACR-16 as a drug target

Our findings show the *Asu*-ACR-16 receptor is pharmacologically different from previously characterized nAChRs and may serve as a potential target for therapeutic drug discovery. Given that *Asu*-ACR-16 shares some similarities with the mammalian $\alpha 7$ nAChR in terms of agonist pharmacology, it seems more likely that a drug directed at allosteric modulation sites may be more selective because the actions of $\alpha 7$ PAMs on the *Asu*-ACR-16 receptor were clearly different from those observed on the mammalian $\alpha 7$ receptor. This is particularly of interest because in recent years, PAMs have received considerable attention as nAChR-targeted therapeutic agents (Williams *et al.*, 2011). The $\alpha 7$ nAChR has been more exploited in this regard because of its implication in cognitive disorders such as Alzheimer's disease and schizophrenia, and drugs targeting $\alpha 7$ PAM sites have been suggested to have therapeutic potential for these disorders (Bertrand and Gopalakrishnan, 2007). Therefore, targeting the corresponding sites in *Asu*-ACR-16 may give rise to potential therapeutics which will not affect the mammalian host. It may therefore be possible to identify a suitable novel cholinergic anthelmintic which is 'resistance busting' if it were to activate a vital cholinergic receptor that was composed of different novel nAChR subunits.

3.9 Acknowledgements

We would like to express our gratitude to Debra J Woods, Zoetis Animal Health, Kalamazoo, MI, USA, for the generous supply of derquantel. We would also like to thank Professor Shu Hua Xiao, National Institute of Parasitic Diseases, Shanghai, Peoples' Republic of China, for the gift of tribendimidine. Research funding was by The Hatch Act,

State of Iowa; NIH grant R01 AI047194 National Institute of Allergy and Infectious Diseases to R.J.M.; NIH grant R21AI092185 National Institute of Allergy and Infectious Diseases to A.P.R.; and the Schlumberger “Faculty for the Future” programme to M.A. and A.P.R. The funding agencies had no role in the design, execution or publication of this study. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institute of Allergy and Infectious Diseases.

3.10 Author Contributions

M.A. conceived and designed the research study, performed the research, analysed the data, contributed reagents/materials/analysis tools and wrote the paper. S.K.B. performed the research. E.C. performed the research, analysed the data and contributed reagents/materials/analysis tools. C.L.C. wrote the paper. C.N. analysed the data, contributed reagents/materials/analysis tools and wrote the paper. C.J.M. performed the research. S.V. performed the research. A.P.R. conceived and designed the research study, analysed the data, contributed reagents/materials/analysis tools and wrote the paper. R.J.M. conceived and designed the research study, analysed the data, contributed reagents/materials/analysis tools and wrote the paper.

3.11 Conflict of interest

The authors declare no conflicts of interest.

3.12 Declaration of transparency and scientific rigour

This Declaration acknowledges that this paper adheres to the principles for transparent reporting and scientific rigour of preclinical research recommended by funding agencies, publishers and other organisations engaged with supporting research.

3.13 Supporting Information

	Signal peptide	
Asu-ACR-16	MSVQRALHYYLCSQLL---LHLIYAVEGSHERRLYEDLMRDYNNLERP VANHSQFVTVYL	57
Cel-ACR-16	-----MSVCTLLISCAILAAPTLGSLQERRLYEDLMRNYNLERP VANHSQFVTVHL	52
	:*	
	D A	
Asu-ACR-16	KVSLQQLIIDVDEKNQIVYVNAWLDYAWNDYKLRWDKEEYGNITDVRFPAGKIWKPDVLLY	117
Cel-ACR-16	KVALQQLIIDVDEKNQIVYVNAWLDYTWNDYNLVWDKAEYGNITDVRFPAGKIWKPDVLLY	112
	:*	
	E Cys loop B	
Asu-ACR-16	NSVDATLDSTYPTNMVVYNTGDISWIHPGIFKISKIDIKWFFPFDEQRCFFKFGSWTYDG	177
Cel-ACR-16	NSVDTNFDSTYQTNMIVYSTGLVHWVHPGIFKISKIDIQWPPPFDEQKCFKFGSWTYDG	172
	:*:	
	F C	
Asu-ACR-16	FKLLDLPKGGFDISEYMPSGEWALPMTTVSRTEKFYDCPEPYDLTFYLMRRRTLYY	237
Cel-ACR-16	YKLLDLPATGGFDISEYISNGEWALPLTTVERNEKFYDCPEPYDVHFYLMRRRTLYY	232
	:*:	
	TM1 TM2	
Asu-ACR-16	GFNLIMPCILTTMTLLGFTLPPDAGEKITLQITVLLSICFFLSIVSEISPTSEAVPLL	297
Cel-ACR-16	GFNLIMPCILTTMTLLGFTLPPDAGEKITLQITVLLSICFFLSIVSEMSPTSEAVPLL	292
	:*:	
	TM3	
Asu-ACR-16	GIFFCMIVVTASTVFTVYVNLHYRTPETHMGITTRTLLLYWFPYILRMRPGVYLT	357
Cel-ACR-16	GIFFTCCMIVVTASTVFTVYVNLHYRTPETHDMGPWRNLLYWIPIWILRMRPGHNLT	352
	:*:	
	WQTLPLPLFPCSKPKKHSESLIRNVKDVETGSSRSNSLDVERRVHQYMSGLTNGTGAPMCT	417
Cel-ACR-16	YASLPSLFS-TKPNRHSESLIRNIKDNEHSLSRANSFDADCRNLQYIMTQSVSNGLTSLG	411
	:*:	
	VLNGGPATVAGAPMDIGQQATLLVLRQRIYQELKTIITRRMIEADREGAQSNWKFAMVVD	477
Cel-ACR-16	SIPSTMISNGTTTQVATLLILHRIVHELKIVTKRMIEGDKKEEQACNNWKFAMVVD	471
	:*:	
	TM4	
Asu-ACR-16	RLCLYVFTFIVASSCGILLSAPYTIA 504	
Cel-ACR-16	RLCLYVFTFIIIVSTIGIFWSAPYLVA 498	
	:*:	

Supporting Figure S3.0 Amino acid sequence alignment of *Asu*-ACR-16 and *Cel*-ACR-16 nAChR subunits. The signal peptide (bright green box), ACh-binding loops A-F (pink boxes), cys-loop (yellow box) and transmembrane regions TM1 -TM4 (turquoise boxes) are indicated. The vicinal cysteines (blackboxed box) that characterize an α -subunit are present in the C-binding loop. The blue-edged box between TM2 and TM3 represents the region where PNU120596 acts on $\alpha 7$.

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Asu-ACR-16 : MSVQRAL-HYYL--CSQLL---HLYAVEGSEYERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 84
Tca-ACR-16 : MSLQRAFSNYCLI--SHLLI---HLCVAVHASEYERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 85
Llo-ACR-16 : --MLQSWINHSILVWCLHLILLFAFLQMITGSEYERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 88
Hco-ACR-16 : -----MWSLLIACSFVA----VAVVIAIYDERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 78
Ace-ACR-16 : -----MRSLLVCCSLLA-ICILRCTSASEYERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 81
Cel-acr-16 : -----MSVCTLLIISCALLA-----APTLGSLQERRLYEDLMRDVNNLERFVANHSCQVPTWYLVKVSLLQIIVDVERKNCIVVYVNAWLLYAW : 79

                                     Cys-loop
Asu-ACR-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 174
Tca-ACR-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 175
Llo-ACR-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 178
Hco-ACR-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 168
Ace-ACR-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 171
Cel-acr-16 : NDYKRERWKEEYGNITDVRFPAGRIWKPDVLLYNSVDFNFDSTVETNNVWVNTGDISIIPFGIFPKISCKIDRWFFPDECCCFKFFGSGWT : 169

                                     YxCC                                     TM1
Asu-ACR-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 264
Tca-ACR-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 265
Llo-ACR-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 268
Hco-ACR-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 258
Ace-ACR-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 261
Cel-acr-16 : MDGFKLDLQFGKGCFCISEYMPSEGEWALHMTTVSSTKFKFYCCPEPYDPLLFYLMRRTLYYGFNLI MPCILITMMTLLGFTLPPDAGE : 259

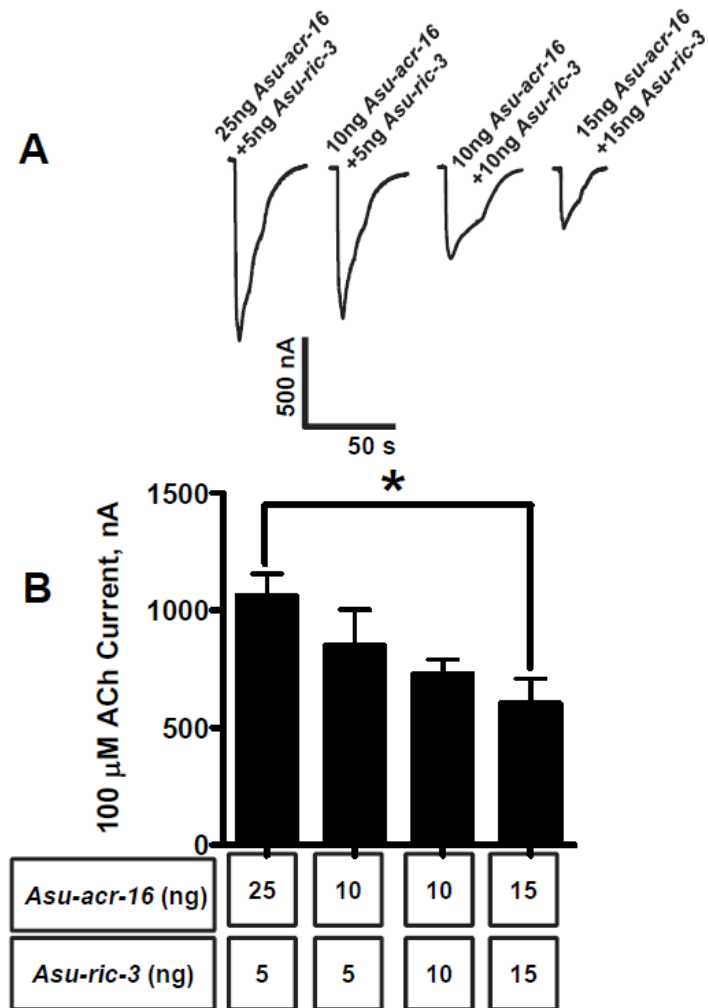
                                     TM2                                     TM3
Asu-ACR-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 354
Tca-ACR-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 355
Llo-ACR-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 358
Hco-ACR-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 348
Ace-ACR-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 351
Cel-acr-16 : KITLQITVLLSICFFLSIVSEMSPTSEAVPLLGIFFSCCMIVVTASTVFTVYVNLNLYRTEETHENGTITRRTLLYVYILRMERPGV : 349

Asu-ACR-16 : YETWQTLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDVERVHGM--SGLINCTGAPMCTVNLNGGPATVAGAFMIGQQATLLIVL : 441
Tca-ACR-16 : YETWQTLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDVERVHGM--SGLINCTGAPVCTVNLNGAPAAIGGAFLLIGQQATLLIVL : 443
Llo-ACR-16 : NISWHTLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDLADCVCCGM--SGLINCTGAPVCTVNLNGAPAAIGGAFLLIGQQATLLIVL : 444
Hco-ACR-16 : KITYATLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDLADCVCCGM--SGLINCTGAPVCTVNLNGAPAAIGGAFLLIGQQATLLIVL : 432
Ace-ACR-16 : KITYATLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDLADCVCCGM--SGLINCTGAPVCTVNLNGAPAAIGGAFLLIGQQATLLIVL : 436
Cel-acr-16 : NITYATLDFELDFCSYFKRHSESLIRNVDVDTGSSFSNSLDLADCVCCGM--SGLINCTGAPVCTVNLNGAPAAIGGAFLLIGQQATLLIVL : 436

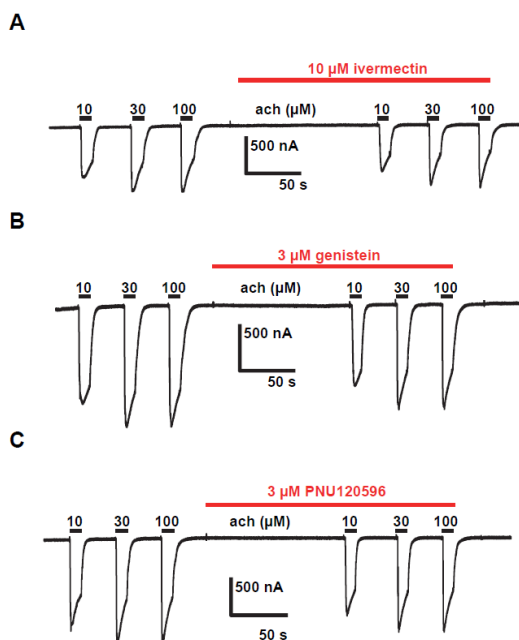
                                     TM4
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Tca-ACR-16 : QRIVCELTPIFRRMIEADREGTQSNNWKFAAMVVDRLCLYVFTVFIIVASSCGILLSAFYIIR- : 505
Llo-ACR-16 : QRIVCELTPIFRRMIEADREGAQSNNWKFAAMVVDRLCLYVFTVFIIVASSCGILLSAFYIIR- : 506
Hco-ACR-16 : QRIVCELTPIFRRMIEADREGAQSNNWKFAAMVVDRLCLYVFTVFIIVASSCGILLSAFYIIR- : 494
Ace-ACR-16 : QRIVCELTPIFRRMIEADREGAQSNNWKFAAMVVDRLCLYVFTVFIIVASSCGILLSAFYIIR- : 498
Cel-acr-16 : QRIVCELTPIFRRMIEADREGAQSNNWKFAAMVVDRLCLYVFTVFIIVASSCGILLSAFYIIR- : 498

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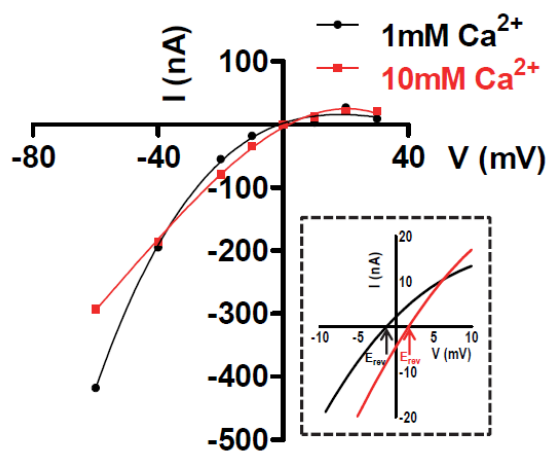
Supporting Figure S3.1 Alignment of ACR-16 sequences from *Asu*, *Toxocara canis*, *Loa loa*, *Hco*, *Ancylostoma ceylanicum* and *C. elegans*. Predicted signal peptide sequences are shaded in grey. Amino acids conserved between the different ACR-16 sequences are highlighted in blue. The Cys-loop, the four transmembrane regions (TM1-TM4) and the primary agonist binding site are noted above the sequence.



Supporting Figure S3.2 Effects of varied amounts of *Asu-acr-16* and *Asu-ric-3* on *Asu-ACR-16* expression. (A) Sample traces represented as inward currents produced in response to 100 μ M ACh. (B) Bar chart (mean \pm SEM) showing current sizes produced by 25 ng *Asu-acr-16* and 5 ng *Asu-ric-3* (1062 ± 94.1 , $n = 6$), 10 ng *Asu-acr-16* and 5 ng *Asu-ric-3* (848.8 ± 155.4 , $n = 6$), 10 ng *Asu-acr-16* and 10 ng *Asu-ric-3* (727.3 ± 63.1 , $n = 6$); 15 ng *Asu-acr-16* and 15 ng *Asu-ric-3* (602.8 ± 106.8 , $n = 6$) in response to 100 μ M ACh. * $P < 0.05$, Tukey's multiple comparison tests.



Supporting Figure S3.3 Sample traces showing the effects of PAMs of $\alpha 7$; (A) 10 μM ivermectin, (B) 3 μM genistein and (C) 3 μM PNU120596, on *Asu*-ACR-16-mediated ACh responses.



Supporting Figure S3.4 Calcium permeability of *Asu*-ACR-16 with 30 μM ACh currents: representative I-V plot for oocytes expressing *Asu*-ACR-16, showing current change with voltage in 1 mM (black line) and 10 mM (red line) Ca^{2+} recording solutions. I-V relationship was plotted using a cubic polynomial equation and interpolated to measure the E_{rev} . The mean \pm SEM for the positive shift of the I-V plot for six observations was $2.4 \pm 2.1\text{mV}$, and this corresponded to a relative calcium permeability ratio of 0.4. Insert: magnified view of the I-V fitted line from -10 to 10 mV, showing the E_{rev} in 1 and 10 mM Ca^{2+} .

**CHAPTER 4. FILARICIDAL ACTIVITIES OF *DANIELLIA OLIVERI* AND
*PSOROSPERMUM FEBRIFUGUM***

Manuscript in preparation for submission to *PLoS Neglected Tropical Diseases* (2017)

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4.1 Abstract

Currently approved drugs for treatment of onchocerciasis and lymphatic filariasis; ivermectin, diethylcarbamazine (DEC) and albendazole, are only effective against the microfilariae (mfs), with little or no effect on adult worms (macrofilariae). Effective control is therefore hindered by the lack of macrofilaricides, leaving the adult worms, which may live for over 15 years to continue to produce mfs and exacerbate the disease symptoms. Additionally, the repeated use of ivermectin, DEC and albendazole has generated concerns of resistance development. Clearly, there is the need for the development of new drugs that will be effective against the adult worms, while more effective microfilaricidal compounds are also desirable. To contribute to the search for new antifilarial drugs, we screened extracts and chromatographic fractions of the plants; *Daniellia oliveri* and *Psorospermum febrifugum* for activity against *O. ochengi* mfs and against both adult *O. ochengi* and *B. pahangi*. We found

crude extracts of *D. oliveri* to be effective in killing adult *O. ochengi* and *B. pahangi* based on the MTT/formazan assay and the Worminator system. Additionally, some extracts of *D. oliveri* and *P. febrifugum* were also active on *O. ochengi* microfilariae based on motility reduction. Results from our three assay systems identified *D. oliveri* hexane bark (DO_{BHEX}), dichloromethane stem bark (DO_{BDCM}) and dichloromethane leaf (DO_{LDCM}) as active in all three assay systems. The activity and lack of cytotoxicity for these extracts encouraged us to select them for bioassay-guided fractionation. Importantly, DO_{BHEX} IC₅₀ for adult *O. ochengi* was about 12x smaller than that for the mfs, which is desirable in cases of co-endemicity with *Loa loa* due to severe adverse reactions associated with *L. loa* mf death. Furthermore, *B. pahangi* activity was retained in some of the Sep-Pak and HPLC fractions, although our results also suggest the possibility of compounds acting in synergy which may be present in 2 or more HPLC fractions. We conclude therefore that *D. oliveri* has potential as a natural plant source for the discovery and development of suitable macrofilaricides and that there is some validity in its traditional use.

4.2 Author Summary

Human onchocerciasis and lymphatic filariasis are classified by the WHO as “Neglected Tropical Diseases” (NTDs), and have the highest disease burdens of the filarial infections, affecting over 150 million people worldwide and placing a billion people at risk. Current control of these infections is limited to the use of antifilarial drugs which are only microfilaricidal. Effective control is therefore hindered by the lack of adulticides (macrofilarides), the adult worms can live for over 15 years in humans continuing to exacerbate symptoms of the disease and reproduce. Clearly, macrofilarides are needed, while more efficacious and safer microfilaricides are also desirable. In this study, we used the

MTT/formazan assay and the Worminator system to screen plant extracts and chromatographic fractions for activity against *O. ochengi* microfilariae and adults, the best-known laboratory model for *O. volvulus*, and against adult *Brugia pahangi* as a model for human lymphatic filariasis-causing species.

4.3 Introduction

Subcutaneous filariasis, otherwise known as onchocerciasis or river blindness, and lymphatic filariasis (LF), commonly known as elephantiasis, are debilitating diseases of the poor. They are among the diseases currently classified by the World Health Organization as “Neglected Tropical Diseases” (NTDs) (Hotez *et al.*, 2007). Onchocerciasis is caused by the filarial nematode, *Onchocerca volvulus*, and transmitted by the bite of the blackfly, *Simulium damnosum* (Winthrop *et al.*, 2011). Approximately 37 million people globally suffer from onchocerciasis, the majority of which are in Africa where >100 million people are at high risk of infection (Gustavsen *et al.*, 2011). Onchocerciasis is the world’s second leading infectious cause of blindness, after trachoma. In Africa, hyper endemic villages can have significantly higher infection rates, where >10% of an entire village may be blind (Boatin & Richards, 2006). Additionally, onchocerciasis presents a spectrum of other debilitating pathologies which include grave and unbearable itching, disfiguring dermatitis, and depigmentation (Enk, 2006). LF is caused by the filarial nematode parasites *Brugia malayi*, *B. timori*, and *Wuchereria bancrofti*, and is transmitted by a variety of mosquitoes (*Anopheles spp*, *Culex spp*, *Aedes spp*, *Mansonia spp*) depending on the geographical area (de Souza *et al.*, 2012). Disease manifestations include painful and profound disfigurement of the skin (particularly of the lower portion of the body), lymphedema, elephantiasis and scrotal swelling which may eventually lead to permanent disability. LF is the second leading

cause of chronic disability worldwide, after mental illness. Over 1.2 billion people are threatened by LF, with ≥ 120 million people infected, and ~ 40 million people disfigured or incapacitated by the disease (Ottesen *et al.*, 1997). Hence, individuals infected with either onchocerciasis and/or LF not only suffer physical disability, but also suffer mental, social and economic losses, resulting in depression, stigma and poverty (Hotez *et al.*, 2006; Weiss, 2008).

Current control of onchocerciasis and LF relies on mass drug administration of ivermectin, DEC and albendazole (Gyapong *et al.*, 2005; Liang *et al.*, 2008; Richard-Lenoble *et al.*, 2003). However, these drugs are only effective against the juvenile worms (microfilariae) or larval stage of the parasites, with limited activity against the adults. This leaves the adult worms to continue to produce microfilariae and exacerbate the disease symptoms. Effective control of onchocerciasis and LF is therefore hindered by the lack of adulticides (macrofilaricides). There also exist other factors such as poor compliance, and poor safety, which limit the use of these drugs. Despite ≥ 15 years of mass treatment with ivermectin, in some parts of Africa (e.g North and West Regions of Cameroon) transmission of onchocerciasis has still not been interrupted (Katarbarwa *et al.*, 2013; Katarbarwa *et al.*, 2011). Additionally, the emergence of ivermectin resistance in parasites of veterinary importance has generated concern that resistance will eventually extend to *O. volvulus* (Felippelli *et al.*, 2014; Lustigman & McCarter, 2007). Current treatment also poses life-threatening side effects in onchocerciasis and LF patients who are co-infected with *Loa loa*. Co-infection with high levels of *L. loa* microfilariae present can cause serious adverse reactions including encephalopathy (brain damage), kidney failure, and even death (Awadzi, 2003; Boussinesq & Gardon, 1997; Boussinesq *et al.*, 2003; Gardon *et al.*, 1997). These

adverse reactions are attributed to the sudden killing of the very large microfilariae population. DEC is further contraindicated in onchocerciasis patients due to the likelihood of severe reactions involving the skin and eye (Molyneux *et al.*, 2003). Therefore, there is a pressing need for new and safer filaricidal compounds for more effective control or eradication of onchocerciasis and LF.

Historically, plants have been important sources of therapeutic compounds (Farnsworth, 1990; Farnsworth *et al.*, 1985). For instance, *Papaver somniferum* (the opium poppy) is the source of morphine (Vallejo *et al.*, 2011); *Cinchona officinalis* is the source for the antimalarial medication, quinine; artemisinin which is also used for treatment of malaria was isolated from *Artemisia annua* (sweet wormwood) (Willcox, 2009); and *Digitalis lanata* (foxglove) is the source for digoxin used in treatment of congestive heart failure (Hollman, 1996). Plants as traditional medicine have been identified to play an important role in the remedy of diseases (Martkoplshvili & Kvavadze, 2015). About 70-80% of the population in developing countries rely on traditional medicine for their health needs (Wachtel-Galor & Benzie, 2011). Nevertheless, use of traditional medicine has evolved over the years and is no longer limited to developing countries. Interest in natural therapy has greatly increased in developed countries like the United States, with an increased interest in some forms of traditional medicine like herbal, dietary or nutritional supplements (Harrison *et al.*, 2004; Qato *et al.*, 2008). Literature on the antifilarial activities of plant extracts and chromatographic fractions of medicinal plants implies plant natural products may serve as sources of lead compounds for the development of new and safe filaricides (Cho-Ngwa *et al.*, 2010; Ndjonka *et al.*, 2011; Samje *et al.*, 2014).

Daniellia oliveri (DO) and *Psorospermum febrifugum* (PF) are among the plants commonly used for the traditional treatment of onchocerciasis and LF in Bambui, North West Cameroon. Bambui is a village located in the highlands of the North West Region of Cameroon where the vegetation is predominantly of the forest savannah type. This area has many fast-flowing streams, providing a good breeding site for blackfly and mosquito species and thus transmission of arthropod-borne infections including onchocerciasis and LF.

D. oliveri (family Caesalpinaceae) is a deciduous, medium-sized flowery tree that can reach up to 25 – 35 m tall. The plant predominantly grows in the forest areas of West and Central Africa. The genus *Daniellia* comprises of 10 species, with only *D. oliveri* extending to Sudan and Uganda. *D. oliveri*, locally known as ‘kahi’ in Bambui, NW Cameroon is traditionally used for the treatment of all worm infections including onchocerciasis and lymphatic filariasis and is also used for treating stomach upset. It is administered as a decoction of the stem bark, prepared by boiling and drinking one cup twice daily.

P. febrifugum (family Hypericaceae) is a flowering shrub or tree that can reach 4 m tall. The plant is generally widespread in tropical Africa, predominantly in the savanna from Guinea to West Cameroon. *P. febrifugum* is locally known as ‘sawayki’ in Bambui, NW Cameroon where it is traditionally used to treat onchocerciasis and rashes of any sort. It is prepared and administered just like *D. oliveri* except that the decoction is also bathed with and the oily supernatant applied as body lotion.

Treatment of onchocerciasis and LF is greatly hampered by the lack of macrofilaricides, new and safer microfilaricides to replace or complement currently available filaricidal drugs are needed. Despite the claimed efficacy of *D. oliveri* and *P. febrifugum* in the traditional treatment of onchocerciasis and LF, no scientific evidence for this claim has

been demonstrated. The overall aim of our study was to screen extracts and chromatographic fractions of *D. oliveri* and *P. febrifugum* for activity against adult *Onchocerca sp* and *Brugia sp* as a way of contributing to the search for suitable macrofilaricides. We also screened plant extracts for microfilaricidal activity. For this study, we used *O. ochengi* as a model for the human equivalent, *O. volvulus* for screening for *Onchocerca* activity. *B. pahangi* was used for screening for LF activity because it is a suitable laboratory model organism for *B. malayi* (Bulman *et al.*, 2015).

4.4 Materials and Methods

4.4.1 Collection and identification of plants

Plants were collected from Bambui in Tubah Sub-Division, North West Cameroon based on ethnopharmacological information (Figure 4.0A: *Daniellia oliveri*; Figure 4.0B: *Psorospermum febrifugum*). Voucher specimens of all plants harvested were prepared and taken to the National Herbarium, Yaounde, Cameroon for expert identification. The plants and parts used for this study and other valuable information can be seen in Table 4.0.



Figure 4.0 Pictures of *Daniellia oliveri* (A) and *Psorospermum febrifugum* (B).

Table 4.0 Classification and traditional uses of plants screened.

Family	Scientific Name	Common Name	Traditional uses	Preparation and administration	Plant parts used	Code adopted
Caesalpinaceae	<i>Daniellia oliveri</i>	Kahi	Treatment of all worm infections including river blindness, lymphatic filariasis, as well as stomach upset	Bark boiled and decoction drunk one cup x2/day	Leaves (L) and stem bark (B)	DO
Hypericaceae	<i>Psorospermum febrifugum</i>	Sawayki	Treatment of onchocerciasis and rashes of any sort	Bark boiled and decoction drunk one cup x2/day. Decoction also bathed with. Oily supernatant applied as body lotion	Leaves (L) and stem bark (B)	PF

4.4.2 Preparation of plants extracts

The plant parts collected were air-dried in Bambui to eliminate moisture before transporting them to the University of Buea. They were further dried in an oven (40 °C) for 2 days, and ground to fine powder using an electric blender or a grinding mill. The resultant powders were weighed and put in labeled receptacles. Powders were then sequentially macerated with HPLC grade hexane (HEX), dichloromethane (DCM) and methanol (MeOH), with the plant material always fully submerged in solvent. For each solvent, the slurry was allowed to stand closed at room temperature for 48 hours to prevent the solvent from evaporating and then filtered using Whatmann No. 1 filter paper. Extracts were concentrated under reduced pressure on a rotary evaporator (BUCHI Rotavapor R-200, Switzerland). The concentrated extracts were transferred into labeled vials and residual solvent evaporated at

ambient temperature. Once all residual solvent had evaporated, the resultant crude extracts were weighed, and their respective percentage (%) yield determined as shown in Table 4.1.

The % yield for each plant extract was calculated using the formula:

$$\% \text{ yield} = (\text{Weight of crude extract} \div \text{Dry weight of plant part}) \times 100$$

The vials were then sealed and stored at $-20\text{ }^{\circ}\text{C}$ or $-80\text{ }^{\circ}\text{C}$.

Table 4.1 Percent (%) yield of plant extracts.

Plant	Dry weight (Wt) of plant part (g)	Hexane (HEX)		Dichloromethane (DCM)		Methanol (MeOH)	
		Wt (g)	% yield	Wt (g)	% yield	Wt (g)	% yield
<i>Daniella oliveri</i>	750.0 (leaves)	17	2.3	12	1.6	16.8	2.2
	500.0 (stem bark)	4.6	0.9	4.3	0.9	52.3	10.5
<i>Psorospermum febrifugum</i>	600.0 (leaves)	3.0	0.5	10.9	1.8	51.4	8.6
	300.0 (stem bark)	21.7	7.2	48.1	16.0	120.2	40.1

4.4.3 *Onchocerca ochengi* adult worm assay

Viable *O. ochengi* adult worm masses were extracted from cattle skin as previously described (Cho-Ngwa *et al.*, 2010). Fresh pieces of umbilical cattle skin containing palpable nodules were obtained from the slaughterhouse in Douala, Cameroon and immediately transported to the laboratory. The skin was thoroughly washed 2x with soap and distilled water, drained and transferred to a sterile laminar flow hood where it was entirely covered

with 70% ethanol and allowed to evaporate completely (Figure 4.1: *Left*). Adult worm masses, which are generally pale orange-yellow in appearance, were extracted from the nodules by careful dissection with a sterile blade (Figure 4.1: *Right*). Individual worm masses were immediately submerged in sterile 24-well culture plates containing 1 ml of complete culture medium (CCM) [RPMI-1640 supplemented with 25 mM HEPES, 2.0 g/L sodium bicarbonate, 20 mM L-glutamine, 10% new born calf serum (SIGMA, USA), 200 units/ml penicillin, 200 µg/ml streptomycin and 2.5 µg/ml amphotericin B (Sigma, USA)], pH 7.4] per well. Worm masses were incubated at 37 °C, 5% CO₂ supplemented humidified air (HERACell 150, Heraeus, Germany) overnight. Viability of the extracted adult worms was ascertained by microscopic examination using an inverted microscope (Euromex, Holland). Dead and damaged worms were discarded, and only viable worms were retained for our assays.

For the *O. ochengi* adult worm assay, a stock solution of 25 mg/ml of the plant extracts was prepared by dissolving 25 mg of the plant extract in 1 ml of ≥99.9% dimethyl sulfoxide (DMSO). The extracts were tested in triplicate at an initial single concentration of 500 µg/ml by adding 40 µl of extract stock in 1 ml of CCM to each well of a 24-well plate

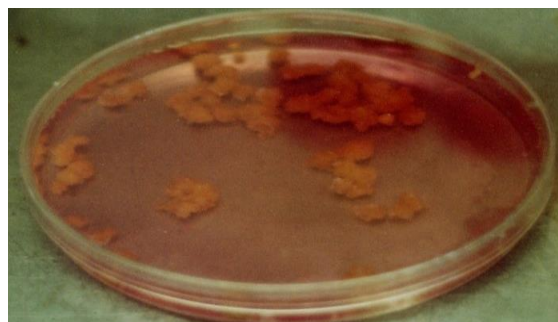


Figure 4.1 *Onchocerca ochengi* nodular masses. *Left*: Inner surface of infected cattle skin revealing nodules. *Right*: Extracted nodular worm masses.

already containing one worm in 1 ml CCM. Extracts that showed no activity at this concentration were not investigated further. 1% DMSO (the highest concentration of used in our assays) served as the negative control, while 10 μ M auranofin served as positive control. *Macrophilariae* cultures were incubated at 37 °C, 5% CO₂ in humidified air for 5 days (120 hours), without any change of CCM. After incubation, adult worm viability was assessed using the MTT/formazan assay (Comley *et al.*, 1989). Each nodular worm mass was placed in a well of a 48-well plate containing 500 μ l of 0.5 mg/ml MTT (Sigma-Aldrich) in incomplete culture medium (CCM without serum). The plates were then incubated in the dark at 37 °C for 30 mins, after which individual worms were blotted on tissue paper and transferred to a clean white sheet of paper (Figure 4.2). % inhibition of purple color formazan formation relative to the negative control was then visually estimated. Mean % inhibition of purple color formazan formation relative to the negative control worm masses correlates with

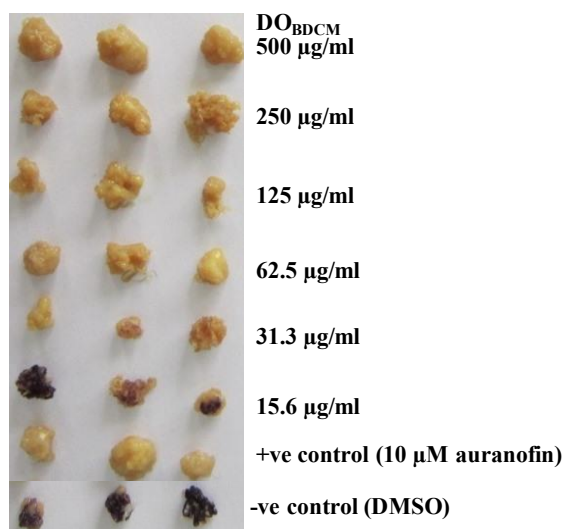


Figure 4.2 Illustration of the MTT/formazan assay for an active extract (*Daniellia oliveri* dichloromethane stem bark extract, DO_{BDCM}). Each extract concentration was tested in triplicate. DO_{BDCM} caused a 100% inhibition of purple formazan formation (which correlates with worm death) from 500 μ g/ml down to 31.3 μ g/ml.

worm death. Extracts that showed 100% inhibition of formazan were considered active and further tested at 6 concentrations from 500 µg/ml to 15.6 µg/ml to determine their IC₅₀ values.

4.4.4 *Onchocerca ochengi* microfilaria (mf) assay

Extraction of *O. ochengi* mfs followed the method of Cho-Ngwa *et al.* (2010) with slight modification. Infected cattle skin was obtained, cleaned and sterilized as described in section 4.4.3. Using autoclaved thumbtacks, the skin was tightly attached to a wooden board whose surface had been covered with 70% ethanol with the outer surface of the skin was facing up (Figure 4.3: *Left*). The outer surface was shaved with a sterile blade, and then rinsed twice with distilled water. Excess moisture from the skin was removed with a clean dry cloth. The entire skin was covered with 70% ethanol and then evaporated in a laminar flow hood. Skin snips approximately 0.5 – 1 mm apart were obtained. Individual skin snips were submerged in 20 ml of CCM and incubated at room temperature for 2 hours to allow for emergence of mfs. Emerged mfs were concentrated by centrifugation at 400 xg for 10 minutes. The supernatant was discarded and the pelleted mfs were resuspended in fresh CCM, and the highly motile mfs quantified with the aid of an inverted microscope (Euromex, Holland) (Figure 4.3: *Right*). Mfs were distributed into 96-well culture plate to obtain an average of 10-15 mfs per well (final volume 100 µl).

Fully confluent monkey kidney epithelial cells (LLC-MK2) obtained from American Type Culture Collection (ATCC, Virginia, USA) served as a feeder layer for the mf assays. The cultures were maintained under the same conditions as described for the adult worm assay. Extracts were tested in duplicate at 8 different serially diluted concentrations from 250

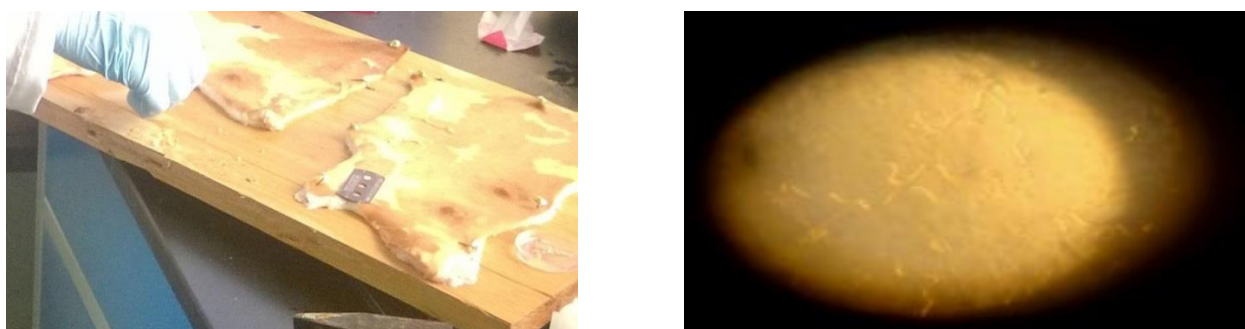


Figure 4.3 *Onchocerca ochengi* microfilariae. *Left*: Outer surface of infected cattle skin for extraction of skin snips. *Right*: Extracted microfilariae observed under the microscope.

$\mu\text{g/ml}$ to $1.95 \mu\text{g/ml}$. $100 \mu\text{l}$ of 2x the concentration of each serial dilution was added to corresponding wells of plates already containing $100 \mu\text{l}$ of mfs to give a total volume of $200 \mu\text{l}$, and a final 1x concentration. 1% DMSO was used as negative control while $10 \mu\text{g/ml}$ ivermectin served as positive control. Mf viability was assessed by microscopic examination for mean motility scoring (relative to the positive control) every 24 hours post addition of drug for 120 hours. The scale used for motility scoring ranged from 0 – 100% (100% for complete inhibition, 75% for only head or tail moving, 50% for entire worm moving sluggishly, 25% for little change in motility, 0% for no inhibition). $10 \mu\text{g/ml}$ ivermectin produced 100% inhibition of mf motility by day 5. An extract was considered active if it produced 100% inhibition of mf motility $\leq 250 \mu\text{g/ml}$. The serial dilutions also allowed for the determination of the IC_{50} values of the active extracts.

4.4.5 *Brugia pahangi* adult worm assay

The *B. pahangi* assays were carried out using the Worminator motility tracking system described by Marcellino *et al.* (2012). Adult female *B. pahangi* were shipped from University of Missouri-Columbia (UMC, Columbia, MO) or the NIAID/NIH Filariasis Research Reagent Resource Center (FR3) (Athens, GA) in 24-well plates or 50 ml falcon

tubes containing media (RPMI-1640 with 25 mM HEPES, 2.0 g/L NaHCO₃, 5% heat inactivated FBS, and 1X Antibiotic/Antimycotic solution), with 1 worm per well or 80 worms per falcon tube. Individual worms were carefully transferred into fresh 24-well plates containing 500 µl/well fresh media. Worms were observed under an inverted microscope to ascertain viability. Damaged or sluggish worms were discarded, and only highly motile worms were retained for assays. A stock extract or chromatographic fraction concentration of 30 mg/ml in DMSO was prepared and tested in quadruplicate at an initial working concentration of 300 µg/ml. The negative control wells had 1% DMSO and positive control wells had 10 µM auranofin. Worms were cultured in a 5% CO₂ incubator at 37 °C for 72 hours (3 days) post drug addition.

The Worminator was used to record videos of each worm plate for approximately 60 seconds, and mean motility units (MMUs) (number of pixels displayed per second) determined for each worm (Marcellino *et al.*, 2012). Videos were recorded at time 0, 4, 24, 48 & 72 hours post drug exposure. % inhibition of motility was calculated by dividing MMUs of test worms by the average MMUs of the controls, multiplying the value by 100, and subtracting from 100. Extracts which showed $\geq 95\%$ inhibition of motility or chromatographic fractions which showed $\geq 75\%$ inhibition of motility were considered active and further screened under the same conditions at 6 concentrations (300, 100, 30, 10, 3 and 1 µg/ml) to determine IC₅₀ values.

4.4.6 Bioassay-guided fractionation of plant extracts

Bioassay-guided fractionation was done on the most active plant extracts based on IC₅₀ values using Sep-Pak cartridges (Waters corporation, MA, USA), followed by semi-preparative High Performance Liquid Chromatography (HPLC).

Sep-Pak Silica Plus cartridges were used for non-polar (hexane) extracts. Elution was achieved with a step gradient of hexane and isopropanol mixture (100:0, 100:0, 90:10, 50:50, 10:90), and a final elution with 100% chloroform (CHCl_3) or dichloromethane (DCM). For dichloromethane extracts whose polarity is midway that of hexane and methanol, we carried out an additional fractionation using Sep-Pak C-18 Plus cartridges. Here, elution was achieved with a step gradient of methanol and water mixture (20:80, 20:80, 40:60, 80:20, 100:0) For both cartridges, the ratio of extracts to solvent system was always 2:1, which was achieved by re-suspending 10 mg of extract in 5 ml of the appropriate solvent system. The resulting Sep-Pak fractions generated were separately concentrated using in-house air at a maximum temperature of 40 °C.

Active Sep-Pak fractions were selected for further fractionation using a Hewlett Packard 1050 Series HPLC System coupled with a Hewlett Packard/Agilent 1050 Diode Array Detector (DAD)/Multiple Wavelength UV Detector (MWD) and silica (straight phase) semi-preparative column (SUPELCOSIL LC-SI SEMI-PREP, 25 cm x 10 mm, 5 μm ; Catalog No. 58365). Elution was performed with a 100 – 0% gradient of 99.6% hexane in 0.4% isopropanol (solvent A) and a 0 – 100% gradient of 50% hexane in 50% isopropanol (solvent B) during 30 mins, with an additional 5 mins collection of the eluent, at a flow rate of 4 ml/min to produce 7 subfractions (F1 – F7), collected over 5 min intervals. Detection was accomplished in a Hewlett Packard 1050 Series HPLC System coupled with a Hewlett Packard/Agilent 1050 Diode Array Detector (DAD)/Multiple Wavelength UV Detector (MWD) at 220, 264 and 320 nm.

4.4.7 Cytotoxicity on N27 cells using the MTS assay

Cytotoxicity of active extracts on N27 cells, an immortalized rat mesencephalic neuronal cell line was assessed using the MTS [3-(4,5-dimethylthiazol-2-yl)-5-(3-carboxymethoxyphenyl)-2-(4-sulfophenyl)-2H-tetrazolium, inner salt] assay (Cory *et al.*, 1991). The MTS assay is a colorimetric method for assessing the viability of cells in proliferation or cytotoxicity assays, and is based on the ability of the mitochondria of viable cells to biologically reduce the pale-yellow MTS compound to a purple formazan product. The resulting formazan product formed is quantified by colorimetry, and the quantity of formazan formed is directly proportional to the amount of viable cells in culture.

For our cytotoxicity studies, N27 cells were seeded in 96-well culture plates 5,000 cells/100 μ l of RPMI growth media (RPMI-1640 medium containing 10% fetal bovine serum, 2 mM L-glutamine, 50 units penicillin, and 50 μ g/ml streptomycin). Treatment with active extracts followed once the cells had achieved 40 – 50% confluence. All treatments were performed in sextuplicate. 30 μ M H₂O₂ served as positive control, while the negative control had cells and growth media containing 1% DMSO. After plating, cells were incubated at 37 °C, 5% CO₂ in humidified air (Forma Scientific CO₂ water jacketed incubator) for 24 hours. At the end of the incubation, 10 μ l of MTS reagent (CellTiter 96® Aqueous One Solution Reagent, Promega G3580) was added to each well and mixed. The plates were then covered with aluminium foil and incubated at 37 °C, 5% CO₂ in humidified air (Forma Scientific CO₂ water jacketed incubator) for 90 mins. The plates were then read at 490 nm and 670 nm using a SpectraMax M2^e reader (Molecular Devices, USA). Cell viability was assessed as (Abs_{490-670nm}) for the extracts and H₂O₂ treated cells relative to the

untreated controls. SI values were then calculated by mean IC₅₀ N27 cell/mean IC₅₀ parasite. Extracts with SI values >1 are more selective for parasites than N27 cells.

4.4.8 Data analysis

Results obtained for biological activity and cytotoxicity assays were analyzed using GraphPad Prism 5.0 or 6.0 software (Molecular Devices, USA), and expressed as mean \pm S.E.M. Statistical analysis for the cytotoxicity assay was done using unpaired student t-test. A *p*-value < 0.05 was considered significant.

4.4.9 Phytochemical screening

Concentrated crude extract residues were used to detect the presence of the secondary plant metabolites; alkaloids, steroids, flavonoids, saponins, tannins, coumarins and cardiac glycosides using standard methods with some modifications (Schiff, 1980).

4.4.9.1 Test for saponins (Frothing test). Briefly, saponins were tested by dissolving 0.5 g of the crude extract in a test tube containing 3 ml of distilled hot water, followed by vigorous shaking for 1 minute. The observation of persistent foaming indicated the presence of saponins.

4.4.9.2 Test for flavonoids (Cyanidin test). 0.5 g of crude extract was dissolved in ~3 ml methanol plus 2 ml of concentrated hydrochloric acid. ~0.1 g of magnesium turnings was then added to the mixture. A brick red coloration with effervescence indicated the presence of flavonoids.

4.4.9.3 Test for steroids (Liebermann-Burchard test). 0.5 g of crude extract was dissolved in 5 ml dichloromethane, then 0.5 ml of acetic anhydride was added, followed by three drops of concentrated sulphuric acid. Observation of a blue-green coloration indicated the presence of steroids.

4.4.9.4 Test for tannins (Ferric chloride test). 0.5 g of crude extract was dissolved in a boiling tube containing 20 ml distilled water and boiled for an hour. 3 – 4 drops of ferric chloride were added and allowed to stand for ~15 minutes. A blue-black coloration indicated a positive test for tannins.

4.4.9.5 Test for Alkaloids (Dragendorff's test). The sample (~0.5 g) was dissolved in about 3 ml of dichloromethane and then spotted on a thin layer chromatographic plate which was developed in 20% hexane in ethylacetate. The presence of alkaloids in the developed chromatogram was detected by spraying with freshly prepared Dragendorff's reagent in a fume chamber. A positive reaction on the chromatogram was indicated by an orange or darker colored spot against a yellow background, confirming the presence of alkaloids.

4.4.9.6 Test for coumarins. To 2 ml of the crude extract was added 1 ml of ammonium hydroxide. One drop was spotted on filter paper and observed under a UV lamp for the presence of blue or green fluorescence, indicating the presence of coumarins.

4.4.9.7 Test for cardiac glycosides. Approximately 1 ml of aqueous extract of the plants was added to 2 ml of glacial acetic acid plus one drop of ferric chloride. 1 ml of concentrated sulfuric acid was then added. The appearance of violet and brownish rings below the interface, followed by the formation of a greenish ring in the acetic acid layer confirmed the presence of cardiac glycosides.

4.5 Results

4.5.1 Activity of *D. oliveri* and *P. febrifugum* extracts on *O. ochengi* adult worms and mfs

A total of 12 extracts were generated from the leaves and stem bark of the 2 plants (6 extracts per plant) using solvents of different polarities (hexane, dichloromethane and methanol). A summary of the activity of the plant extracts is provided in Table 4.2.

Table 4.2 IC₅₀ values (mean ± S.E.M) of extracts with macro- and/or microfilaricidal activity against *O. ochengi*.

Extracts	<i>Onchocerca ochengi</i>	
	IC ₅₀ mf (µg/ml)	IC ₅₀ adult worm (µg/ml)
DO _{LHEX}	Inactive	Inactive
DO _{LDCM}	16.2 ± 0.0, n = 2	43.3 ± 9.2, n = 3
DO _{LMeOH}	Inactive	Inactive
DO _{BHEX}	185.2 ± 0.0, n = 2	13.9 ± 1.7, n = 3
DO _{BDCM}	9.7 ± 0.0, n = 2	22.5 ± 0.0, n = 3
DO _{BMeOH}	Inactive	Inactive
PF _{LHEX}	Inactive	Inactive
PF _{LDCM}	132.4 ± 0.0, n = 2	Inactive
PF _{LMeOH}	8.8 ± 0.0, n = 2	Inactive
PF _{BHEX}	4.0 ± 0.0, n = 2	Inactive
PF _{BDCM}	7.2 ± 0.0, n = 2	Inactive
PF _{BMeOH}	6.6 ± 0.0, n = 2	Inactive

Of the 12 extracts screened, 3 were active against adult *O. ochengi* (Figure 4.4). These were the hexane extract of the stem bark, and the dichloromethane extracts of the leaves and stem bark of *D. oliveri* (DO_{BHEX}, DO_{LDCM} and DO_{BDCM}). Of these 3, DO_{BHEX} recorded the lowest IC₅₀ of $13.9 \pm 1.7 \mu\text{g/ml}$ (n = 3) for *O. ochengi* microfilaricidal activity. Remarkably, DO_{BHEX} also recorded the lowest IC₁₀₀ of $31.3 \mu\text{g/ml}$ (n = 3).

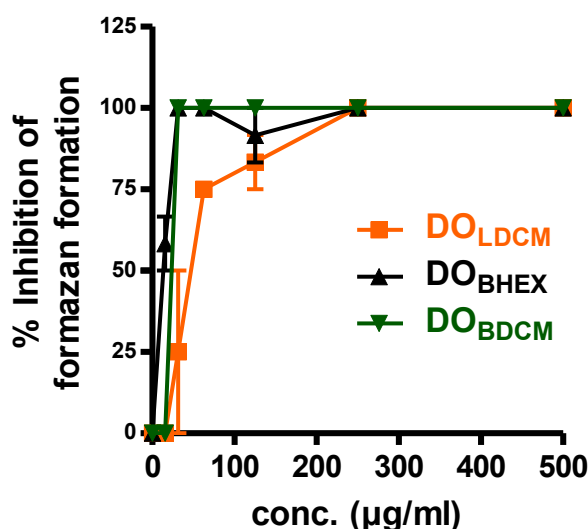


Figure 4.4 Dose-dependent inhibition of formazan formation (decrease in worm viability) after 120 hours of incubation with extracts of *Daniellia oliveri*. Results are plotted as mean \pm S.E.M. The order of potency was DO_{BHEX} (IC₅₀ $13.9 \pm 1.7 \mu\text{g/ml}$, n = 3) > DO_{BDCM} (IC₅₀ $22.5 \pm 0.0 \mu\text{g/ml}$, n = 3) > DO_{LDCM} (IC₅₀ $43.3 \pm 9.2 \mu\text{g/ml}$, n = 3).

For the *O. ochengi* mf assay, 8 of the 12 extracts screened showed a dose-dependent microfilaricidal activity (Figure 4.5). These were DO_{BHEX}, DO_{LDCM}, DO_{BDCM}, dichloromethane leaf extract of *P. febrifugum* (PF_{LDCM}), methanol leaf extract of *P. febrifugum* (PF_{LMeOH}), hexane stem bark extract of *P. febrifugum* (PF_{BHEX}), dichloromethane stem bark extract of *P. febrifugum* (PF_{BDCM}), and methanol stem bark extract of *P. febrifugum* (PF_{BMeOH}). The effects of these extracts were also time-dependent. Note, of the

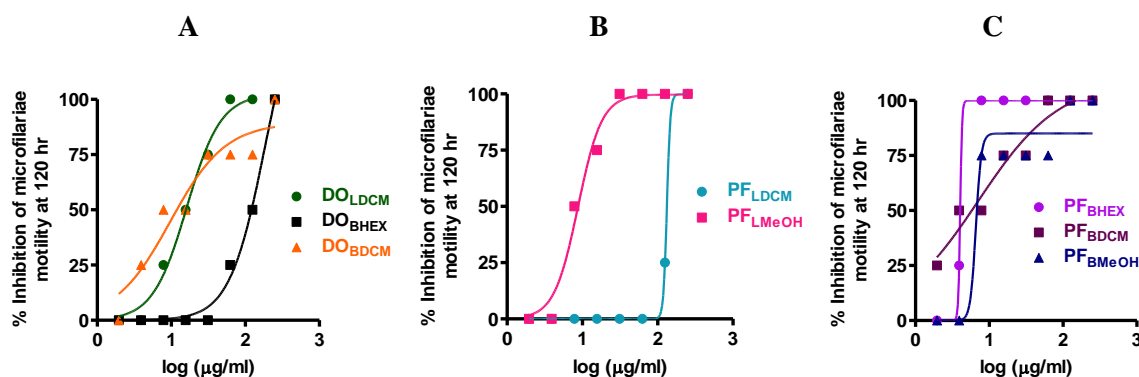


Figure 4.5 Dose-dependent inhibition of microfilariae motility after 120 hours of incubation with extracts of *Daniellia oliveri* (A) and *Psorospermum febrifugum* (B & C). Results are plotted as mean \pm S.E.M (n = 2). Note that the *D. oliveri* microfilaricidal extracts (DO_{BHEX}, DO_{LDCM}, DO_{BDCM}) were also active against adult worms.

extracts that showed both *O. ochengi* adult worm and mf activity (DO_{BHEX}, DO_{LDCM} and DO_{BDCM}), DO_{BHEX} was more active on adult *O. ochengi* (IC₅₀ 13.9 \pm 1.7 μ g/ml, n = 3) compared to the mfs (IC₅₀ 185.2 \pm 0.0 μ g/ml, n = 2). PF_{BHEX} recorded the lowest IC₅₀ of 4.0 \pm 0.0 μ g/ml (n = 2) for *O. ochengi* microfilaricidal activity, and the lowest IC₁₀₀ of 7.8 μ g/ml. PF_{LMeOH} had an IC₅₀ and IC₁₀₀ of respectively 8.8 \pm 0.0 μ g/ml and 31.3 μ g/ml (n = 2) for *O. ochengi* microfilaricidal activity.

4.5.2 Activity of extracts and chromatographic fractions of *D. oliveri* and *P. febrifugum* on adult *B. pahangi*

Adult *B. pahangi* were more sensitive to the extracts than *O. ochengi*. Of the 12 extracts initially screened for activity against adult *B. pahangi* at 300 μ g/ml, 11 (DO_{LHEX}, DO_{LDCM}, DO_{LMeOH}, DO_{BHEX}, DO_{BDCM}, DO_{BMeOH}, PF_{LHEX}, PF_{LDCM}, PF_{BHEX}, PF_{BDCM} and PF_{BMeOH}) were active, while only PF_{LMeOH} was inactive (Figure 4.6). The effects were also time-dependent, with DO_{LDCM} and DO_{BDCM} causing close to 100% inhibition of motility after only 4 and 24 hours of incubation.

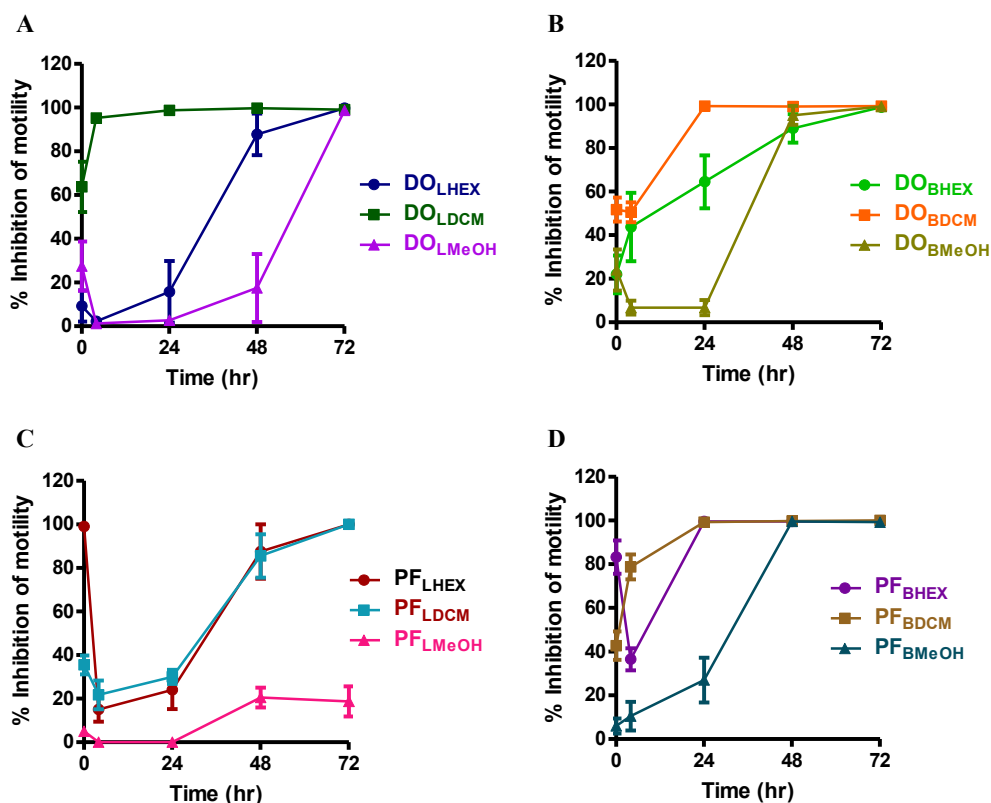


Figure 4.6 Time-dependent inhibition of adult *Brugia pahangi* motility following incubation with extracts of *Daniellia oliveri* and *Psorospermum febrifugum*. Results are plotted as mean \pm S.E.M (n = 4). All 12 extracts tested (except PF_{LMeOH}) caused a 100% inhibition of motility after 72 hours of incubation. Remarkably, DO_{LDCM} and DO_{BDCM} caused close to 100% inhibition of motility after only 4 and 24 hours of incubation.

Of these 11 active extracts, 3 (DO_{BHEX}, DO_{LDCM} and DO_{BDCM}) were selected for further screening for IC₅₀ determination as they were also active on both adult *O. ochengi* and mfs (Figure 4.7). DO_{LDCM} and DO_{BDCM} were equally potent on adult *B. pahangi* with IC₅₀ values of $6.1 \pm$ and $6.3 \pm$ μ g/ml respectively (n = 4). These IC₅₀ values were lower than the 59.0 ± 1.2 μ g/ml (n = 4) recorded for DO_{BHEX} (Table 4.3).

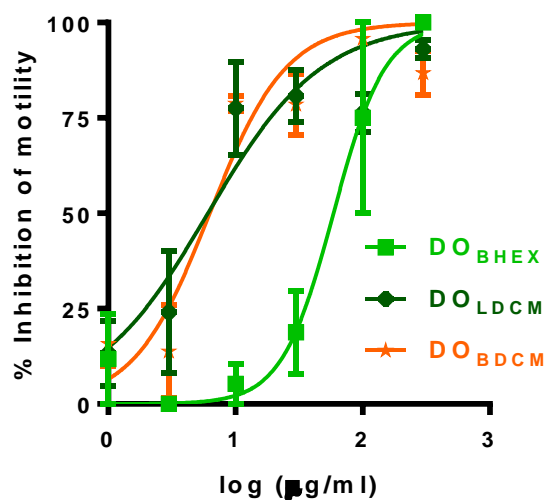


Figure 4.7 Dose-dependent inhibition of adult *Brugia pahangi* motility after 72 hours of incubation with extracts of *Daniellia oliveri*. Results are plotted as mean \pm S.E.M (n = 4). The order of potency was DO_{LDCM} (IC_{50} 6.1 ± 1.3 μ g/ml, n = 4) \sim DO_{BDCM} (IC_{50} 6.3 ± 1.2 μ g/ml, n = 4) $>$ DO_{BHEX} were (IC_{50} 59.0 ± 1.2 μ g/ml, n = 4).

Table 4.3 IC_{50} values (mean \pm S.E.M) for all active extracts.

Extracts	<i>Onchocerca ochengi</i>		<i>Brugia pahangi</i>
	IC_{50} mf (μ g/ml)	IC_{50} adult worm (μ g/ml)	IC_{50} adult worm (μ g/ml)
DO_{LHEX}	Inactive	Inactive	< 300
DO_{LDCM}	16.2 ± 0.0 , n = 2	43.3 ± 9.2 , n = 3	6.1 ± 1.3 , n = 4
DO_{LMeOH}	Inactive	Inactive	< 300
DO_{BHEX}	185.2 ± 0.0 , n = 2	13.9 ± 1.7 , n = 3	59.0 ± 1.2 , n = 4
DO_{BDCM}	9.7 ± 0.0 , n = 2	22.5 ± 0.0 , n = 3	6.3 ± 1.2 , n = 4
DO_{BMeOH}	Inactive	Inactive	< 300
PF_{LHEX}	Inactive	Inactive	< 300
PF_{LDCM}	132.4 ± 0.0 , n = 2	Inactive	< 300
PF_{LMeOH}	8.8 ± 0.0 , n = 2	Inactive	Inactive
PF_{BHEX}	4.0 ± 0.0 , n = 2	Inactive	< 300
PF_{BDCM}	7.2 ± 0.0 , n = 2	Inactive	< 300
PF_{BMeOH}	6.6 ± 0.0 , n = 2	Inactive	< 300

Following IC₅₀ determination, DO_{BHEX}, DO_{LDCM} and DO_{BDCM} were subjected to solid-phase extraction using Sep-Pak Plus cartridges. 18 Sep-Pak fractions were generated from DO_{BHEX}, DO_{LDCM} and DO_{BDCM} (6 fractions per extract), and tested for adult *B. pahangi* activity in quadruplicate at 300 µg/ml for 72 hours (Figure 4.8).

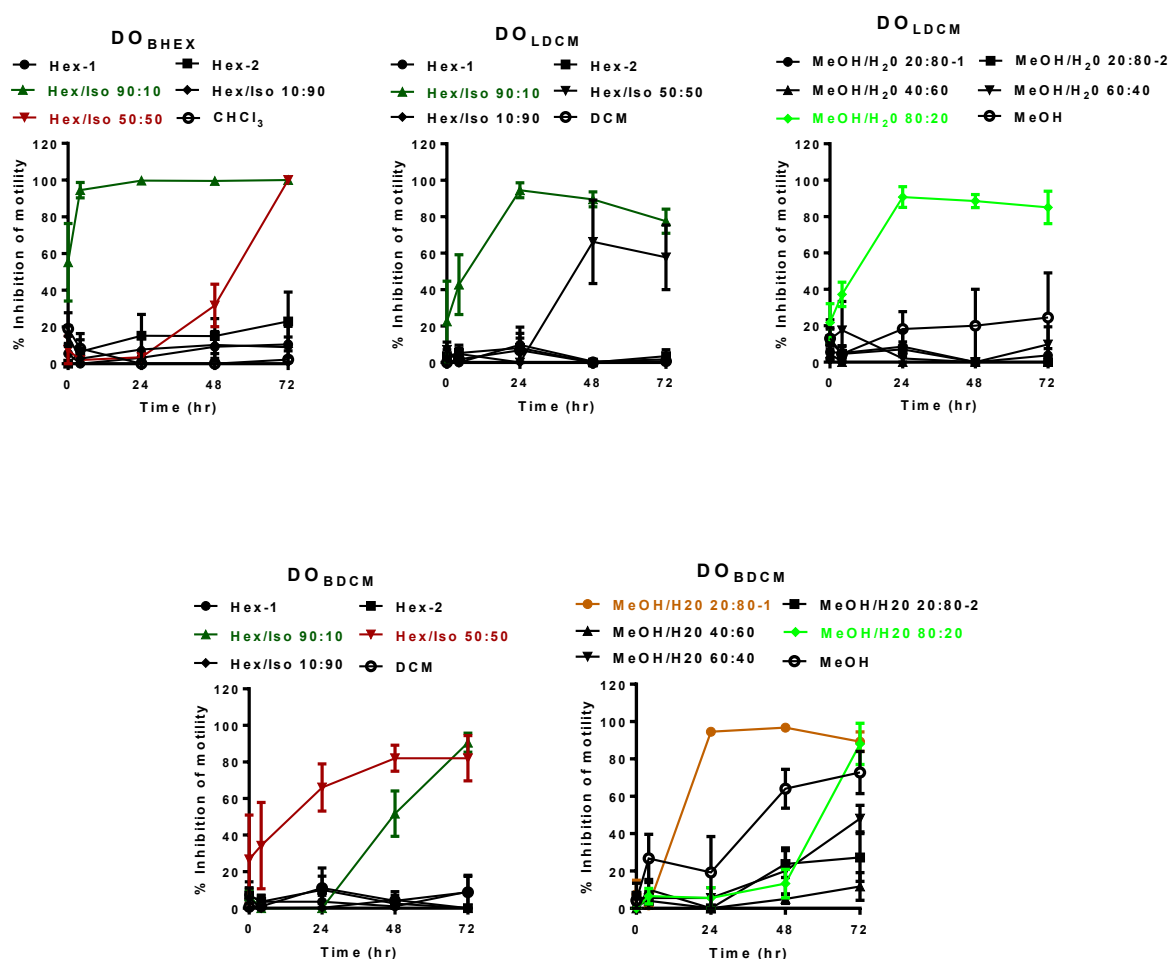


Figure 4.8 Time-dependent inhibition of adult *Brugia pahangi* motility following treatment with *Daniellia oliveri* Sep-Pak fractions. Results are plotted as mean \pm S.E.M (n = 4). Active fractions from Sep-Pak Silica Plus cartridges are colored green and red, green for Hex/Iso 90:10 and red for Hex/Iso 50:50 fractions. Active fractions from Sep-Pak C-18 Plus cartridges are colored light green (MeOH/H₂O 80:20) and brown (MeOH/H₂O 20:80-1).

Sep-Pak fractions that showed activity after 72 hours of incubation were selected for IC_{50} determination (Figure 4.9). These were DO_{BHEX} eluted with 90% hexane in 10% isopropanol (DO_{BHEX} Hex/Iso 90:10), DO_{BHEX} eluted with 50% hexane in 50% isopropanol (DO_{BHEX} Hex/Iso 50:50), DO_{LDCM} eluted with 90% hexane in 10% isopropanol (DO_{LDCM} Hex/Iso 90:10) and DO_{LDCM} eluted with 80% methanol in 20% water (DO_{LDCM} MeOH/H₂O 80:20). Of the 2 active DO_{BHEX} Sep-Pak fractions (DO_{BHEX} Hex/Iso 90:10 and DO_{BHEX} Hex/Iso 50:50, Figure 4.9A), DO_{BHEX} Hex/Iso 90:10 was selected for HPLC because based on IC_{50} , it was more potent (IC_{50} 27.3 ± 1.2 μ g/ml, $n = 4$) than DO_{BHEX} Hex/Iso 50:50 (IC_{50} 122.2 ± 1.3 μ g/ml, $n = 4$). Likewise, DO_{LDCM} Hex/Iso 90:10 was selected for HPLC as it was more potent (IC_{50} 15.2 ± 1.3 μ g/ml, $n = 4$) than DO_{LDCM} MeOH/H₂O 80:20 (IC_{50} 33.3 ± 1.3 μ g/ml, $n = 4$), Figure 4.9B.

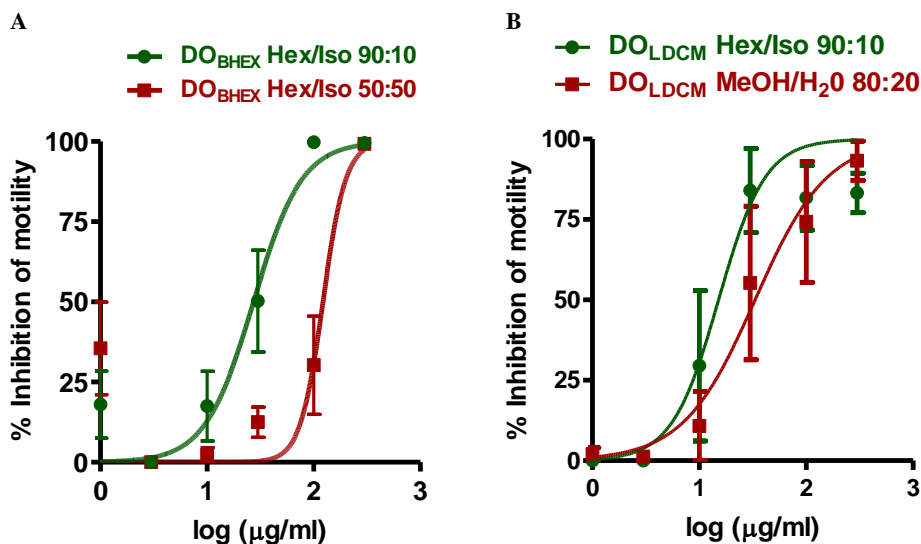


Figure 4.9 Dose-dependent inhibition of adult *B. pahangi* motility after 120 hrs of incubation with Sep-Pak fractions from *D. oliveri* stem bark hexane extract (A) and leaf dichloromethane extract (B). Results are plotted as mean \pm S.E.M ($n = 4$). DO_{BHEX} Hex/Iso 90:10 (IC_{50} 27.3 ± 1.2 μ g/ml, $n = 4$) was more potent than DO_{BHEX} Hex/Iso 50:50 (IC_{50} 122.2 ± 1.3 μ g/ml, $n = 4$). DO_{LDCM} Hex/Iso 90:10 (IC_{50} 15.2 ± 1.3 μ g/ml, $n = 4$) was more potent than DO_{LDCM} MeOH/H₂O 80:20 (IC_{50} 33.3 ± 1.3 μ g/ml, $n = 4$).

Seven HPLC subfractions (F1 – F7) from each of the selected Sep-Pak fractions were generated and again tested for adult *B. pahangi* activity at 300 $\mu\text{g/ml}$ (Figures 4.10). Only active fractions were selected for IC_{50} determination and further purification. These were $\text{DO}_{\text{BHEX Hex/Iso 90:10}}$ F4 (IC_{50} 50.7 \pm 1.0 $\mu\text{g/ml}$, n = 4) and $\text{DO}_{\text{LDCM Hex/Iso 90:10}}$ F3 (IC_{50} 141.5 \pm 1.1 $\mu\text{g/ml}$, n = 4) (Figures 4.11A & 4.11B).

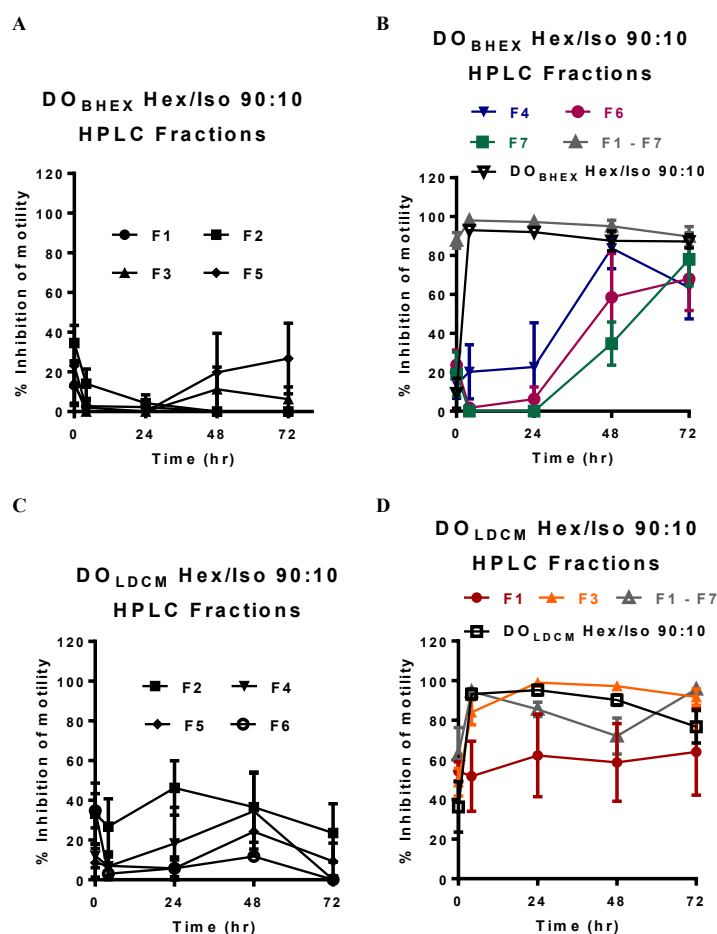


Figure 4.10 Time-dependent inhibition of adult *Brugia pahangi* motility following treatment with HPLC fractions from the hexane stem bark Sep-Pak fraction eluted with 90% hexane in 10% isopropanol ($\text{DO}_{\text{BHEX Hex/Iso 90:10}}$) (A & B) and the dichloromethane leaf Sep-Pak fraction eluted with 90% hexane in 10% isopropanol ($\text{DO}_{\text{LDCM Hex/Iso 90:10}}$) (C & D). Results are plotted as mean \pm S.E.M (n = 4). Active HPLC fractions were: F4, F6 & F7 from the Sep-Pak fraction $\text{DO}_{\text{BHEX Hex/Iso 90:10}}$, and F3 from Sep-Pak fraction $\text{DO}_{\text{LDCM Hex/Iso 90:10}}$.

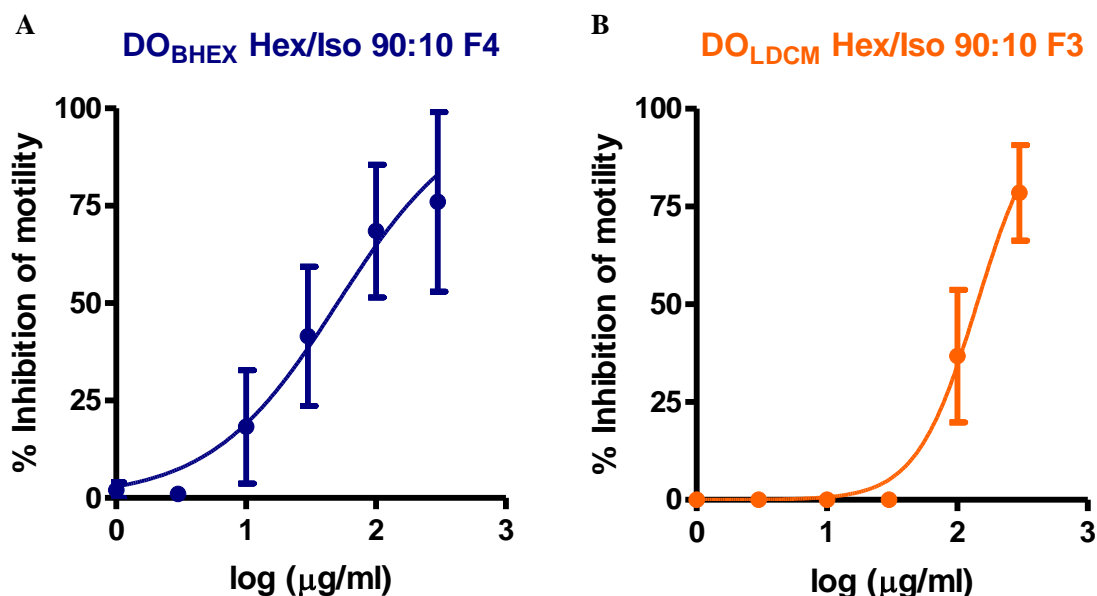


Figure 4.11 Dose-dependent inhibition of adult *Brugia pahangi* motility after 72 hours of incubation with HPLC fractions; F4 from the hexane stem bark Sep-Pak fraction eluted with 90% hexane in 10% isopropanol (A) and F3 from the dichloromethane leaf Sep-Pak fraction eluted with 90% hexane in 10% isopropanol (B). Results are plotted as mean \pm S.E.M (n = 4). DO_{BHEX} Hex/Iso 90:10 F4 (IC₅₀ 50.7 \pm 1.0 μ g/ml, n = 4) was more potent than DO_{LDCM} Hex/Iso 90:10 F3 (IC₅₀ 141.5 \pm 1.1 μ g/ml, n = 4).

4.5.3 Cytotoxicity of active extracts

N27 cytotoxicity was established for the active extracts using the MTS assay. The N27 IC₅₀ values were compared to the IC₅₀ values for the parasites to determine the Selectivity Index (SI). Of all 12 active extracts evaluated at an initial single high concentration of 250 μ g/ml for toxicity to N27 cells, DO_{BHEX} and PF_{BDCM} showed no cytotoxicity when compared to the untreated controls (Figure 4.12A). On the other hand, all the other extracts tested showed a significant reduction ($p < 0.001$) in cell viability compared to the untreated control. These extracts were further tested at 8 serially diluted concentrations from 500 to 3.91 μ g/ml to determine their IC₅₀ values (Figures 4.12B–D).

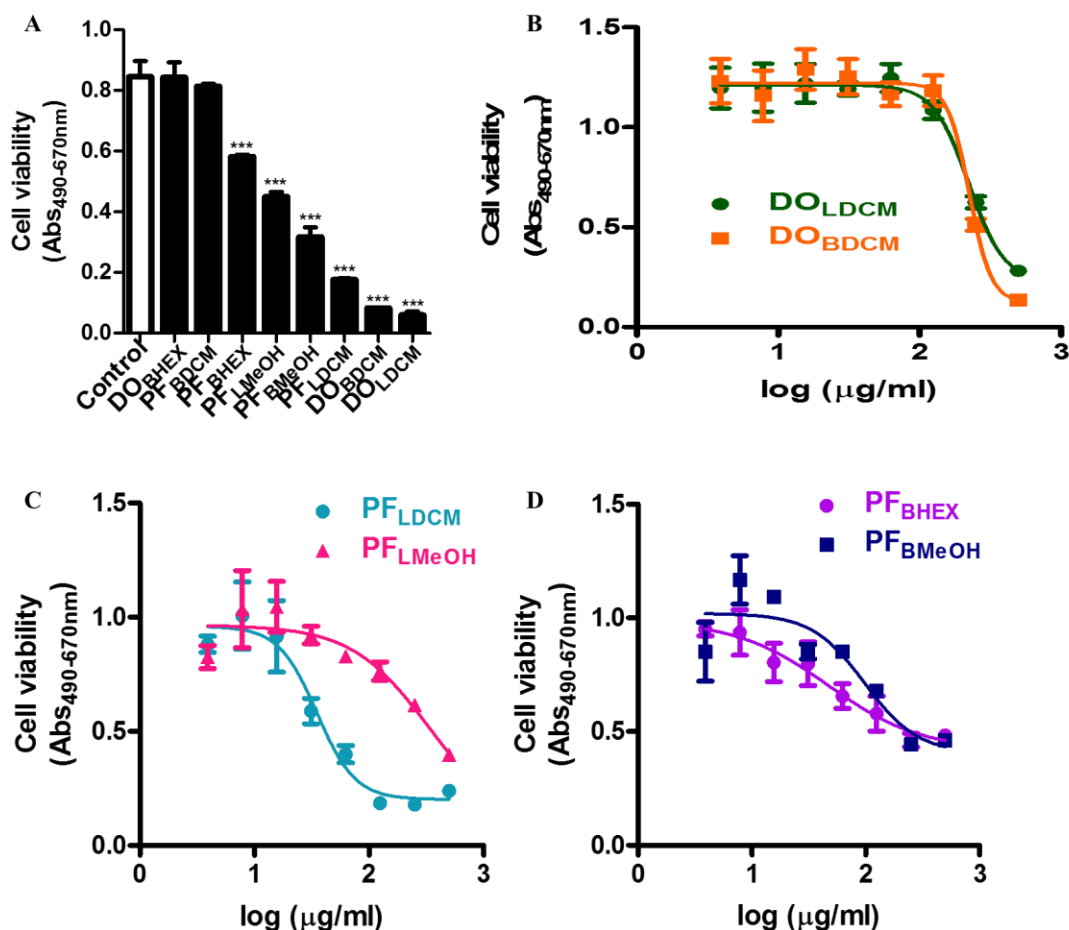


Figure 4.12 Effects of extracts of *Daniellia oliveri* and *Psorospermum febrifugum* on N27 cell viability after 24 hours of incubation with 250 µg/ml (n = 6) (A) and 500 down to 3.91 µg/ml (B – D) of the extracts. Results are plotted as mean ± S.E.M. Mean IC₅₀ ranged from 35 to >250 µg/ml (n = 4). ***p < 0.001 (unpaired student t-test).

IC₅₀ (mean ± S.E.M) values for the extracts on N27 cells are shown in Table 4.4.

Comparing the IC₅₀ values for N27 cells with that for parasites revealed only PF_{LDCM} to be more toxic to N27 cells than to parasites (Table 4.5). All other extracts were more selective for parasites than for N27 cells with an SI of >1. The higher the SI value, the more toxic the extract is to parasites than cells. Therefore, the higher the SI value, the better or ‘safer’ the extract and the more potentially useful for therapeutic drug development.

Table 4.4 IC₅₀ (mean ± S.E.M) for extracts of *Daniellia oliveri* and *Psorospermum febrifugum* on N27 cells.

Extract	IC ₅₀ (Mean ± S.E.M, µg/ml)
DO _{LDCM}	222.8 ± 1.1, n = 4
DO _{BDCM}	224.6 ± 1.1, n = 4
PF _{LDCM}	35.1 ± 1.2, n = 4
PF _{LM_eOH}	331.1 ± 6.9, n = 4
PF _{BHEX}	47.0 ± 1.8, n = 4
PF _{BMeOH}	98.2 ± 1.4, n = 4

4.5.4 Phytochemical analysis of active extracts

The active extracts were screened for the presence of phytochemicals as described in the Materials and Methods section. The presence (+) and absence (-) of the different phytochemicals screened are shown in Table 4.6. In general, steroids and saponins were found to be present in all active extracts, while coumarins were absent. The 3 promising extracts (DO_{BHEX}, DO_{LDCM} and DO_{BDCM}) with activity against both *O. ochengi* and *B. pahangi* tested positive for one or more of the following phytochemicals: alkaloids, flavonoids and cardiac glycosides, but negative for tannins.

Table 4.5 Selectivity index (SI) values (Mean IC₅₀ cell/Mean IC₅₀ parasite) for extracts of *Daniellia oliveri* and *Psorospermum febrifugum*.

Extracts	Mean IC ₅₀ N27 cells (µg/ml)	<i>Onchocerca ochengi</i>				<i>Brugia pahangi</i>	
		Mf		Adult		Adult	
		Mean IC ₅₀ (µg/ml)	SI	Mean IC ₅₀ (µg/ml)	SI	Mean IC ₅₀ (µg/ml)	SI
DO _{LHEX}	tbd	Inactive	/	Inactive	tbd	89.8	/
DO _{LDCM}	222.8	16.2	13.8	43.3	5.1	6.1	36.5
DO _{LMeOH}	tbd	Inactive	/	Inactive	/	81.9	/
DO _{BHEX}	> 250	185.2	> 1.3	13.9	> 18.0	59.0	> 4.2
DO _{BDCM}	224.6	9.7	23.2	22.5	10.0	6.3	35.7
DO _{BMeOH}	/	Inactive	/	Inactive	/	44.0	/
PF _{LHEX}	/	Inactive	/	Inactive	/	153.7	/
PF _{LDCM}	35.1	132.4	0.3	Inactive	/	< 300	/
PF _{LMeOH}	331.1	8.8	37.6	Inactive	/	Inactive	/
PF _{BHEX}	47.0	4	11.8	Inactive	/	< 300	/
PF _{BDCM}	> 250	7.2	> 34.7	Inactive	/	< 300	/
PF _{BMeOH}	98.2	6.6	14.9	Inactive	/	< 300	/

Table 4.6 Phytochemical analysis of all active extracts.

Class of compound	<i>Daniellia oliveri</i> extracts			<i>Psorospermum febrifugum</i> extracts				
	DO _{LDCM}	DO _{BHEX}	DO _{BDCM}	PF _{LDCM}	PF _{LMeOH}	PF _{BHEX}	PF _{BDCM}	PF _{BMeOH}
Alkaloids	-	+	-	+	+	+	+	+
Steroids	+	+	+	+	+	+	+	+
Flavonoids	+	-	+	+	+	+	+	+
Saponins	+	+	+	+	+	+	+	+
Tannins	-	-	-	+	+	-	-	+
Cuomarins	-	-	-	-	-	-	-	-
Cardiac glycosides	+	-	+	-	+	+	-	-

Key: (+) = present, (-) = absent

4.6 Discussion

Onchocerciasis and LF are two major NTDs whose control is hindered by the lack of suitable drugs that will kill adult worms. The aim of this project was to screen medicinal plants for activity against the parasites that cause onchocerciasis and LF in a bid to identify new compounds that could serve as leads for macrofilaricidal drug development. Based on ethnopharmacological information, *D. oliveri* and *P. febrifugum* are plants commonly used by the traditional healers of Bambui, NW Cameroon to treat onchocerciasis and LF. However, there is no documented scientific evidence to support the claimed efficacy of *D. oliveri* and *P. febrifugum* in treating onchocerciasis and LF. Our study is the first report of scientific evidence for *in vitro* filaricidal activity of *D. oliveri* and *P. febrifugum*. Of 12 crude extracts prepared from *D. oliveri* and *P. febrifugum* using solvents of different polarities

(hexane, dichloromethane and methanol), all 12 extracts showed a time- and dose-dependent activity against *O. ochengi* mfs, adult *O. ochengi* or adult *B. pahangi*. Interestingly, 3 (DO_{BHEX} , DO_{LDCM} and DO_{BDCM}) of the 12 extracts were active against all life cycle stages of *O. ochengi* and *B. pahangi* used in this study. Thus, DO_{BHEX} , DO_{LDCM} and DO_{BDCM} have potential as sources of lead compounds for broad spectrum filaricidal activity. The low IC_{50} values (6 – 185 $\mu\text{g/ml}$) recorded by DO_{BHEX} , DO_{LDCM} and DO_{BDCM} and their lack of cytotoxicity encouraged us to select these extracts for further purification (Table 4.5).

Sep-Pak fractions of DO_{BHEX} , DO_{LDCM} and DO_{BDCM} which showed activity against *B. pahangi* were further fractionated using semi-preparative HPLC. Seven HPLC fractions collected at different time points were generated for each active Sep-Pak fraction. These fractions were tested for activity against *B. pahangi* and IC_{50} 's determined from dose-response curves. After analysis of the HPLC fractions, we propose that DO_{BHEX} Hex/Iso 90:10 F4 (IC_{50} 50.7 ± 1.0 $\mu\text{g/ml}$, $n = 4$) and DO_{LDCM} Hex/Iso 90:10 F3 (IC_{50} 141.5 ± 1.1 $\mu\text{g/ml}$, $n = 4$) are further purified to identify the active compounds.

The potency of extracts varied during the course of the fractionation process. For example, crude extract DO_{BHEX} recorded an IC_{50} adult *B. pahangi* of 59.0 ± 1.2 $\mu\text{g/ml}$, the most potent resulting Sep-Pak fraction was DO_{BHEX} Hex/Iso 90:10 IC_{50} 27.3 ± 1.2 $\mu\text{g/ml}$, while HPLC fraction DO_{BHEX} Hex/Iso 90:10 F4 IC_{50} 50.7 ± 1.0 $\mu\text{g/ml}$ was the most potent. However, when we combined all seven HPLC fractions of extract DO_{BHEX} Hex/Iso 90:10, the activity was similar to that of the parent Sep-Pak fraction (Figure 4.10B). This led us to conclude that active compounds are present in two or more HPLC fractions acting additively or in synergy.

Our results show that the HPLC fractions DO_{BHEX} Hex/Iso 90:10 F4 and DO_{LDCM} Hex/Iso 90:10 F3 have potential as sources of macrofilaricides. Additionally, we recommend that various combinations of the HPLC fractions be tested as this may yield combinations with enhanced activity. Knowing that phytochemicals have a wide range of pharmacological activities, the phytochemicals present in our promising extracts which we report in Table 4.6 suggest that the bioactive compounds in the extracts may be from these groups of plant chemicals (alkaloids, steroids, flavonoids, saponins and cardiac glycosides). The presence of one or more of these phytochemicals have been reported in the following plants with demonstrated activity against *O. ochengi*: *Margaritaria discoidea*, *Homalium africanum*, *Craterispermum laurinum*, *Morinda lucida*, *Tragia benthami*, *Piper umbellatum* and *Annona senegalensis* (Cho-Ngwa *et al.*, 2010; Cho-Ngwa *et al.*, 2016; Ndjonka *et al.*, 2011). Also, the anthelmintic activity for some of these phytochemicals like alkaloids, flavonoids and saponins has been published elsewhere (Ayers *et al.*, 2007; Wang *et al.*, 2010a; Wang *et al.*, 2010b). Overall, our results justify the traditional use of *D. oiveri*. However, more studies focusing on identifying the active compounds are necessary, as well as determining their mode of action.

4.7 Acknowledgements

We would like to express our gratitude to the indigenes and traditional healers of Bambui, North West Cameroon for providing us with valuable information on the medicinal plants used in this study.

This work was funded by Schlumberger Foundation Faculty for the Future Grant to MA & APR; NIH R01 AI047194–12 to RJM; and R21AI092185–01 to APR. We would like to acknowledge the Burroughs Wellcome Fund Collaborative Research Travel Award to MA.

We are grateful to the Biotechnology Unit members of the University of Buea Department of Biochemistry and Molecular Biology; Organic Chemistry Lab members of the University of Buea Department of Chemistry; team members of the UC San Francisco Small Molecule Discovery Center; Dr Goff lab members at ISU; Adhithiya Charli and Dr Vellareddy Anantharam of ISU.

4.8 Author Contributions

Conceived and designed the experiments: MA, FCN, GAA, RJM & APR. Performed the experiments: MA, MS, SBB, CB, NK, SV. Analyzed the data: MA, NK, RJM & APR. Contributed reagents/materials/analysis tools: MA, FCN, GAA, JS, RJM & APR. Wrote the manuscript: MA, RJM & APR.

**CHAPTER 5. CURIUSER AND CURIUSER: THE MACROCYCLIC LACTONE,
ABAMECTIN, IS ALSO A POTENT INHIBITOR OF
PYRANTEL/TRIBENDIMIDINE NICOTINIC ACETYLCHOLINE RECEPTORS OF
GASTRO-INTESTINAL WORMS**

A paper published in *PLoS One* (2016)¹

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5.1 Abstract

Nematode parasites may be controlled with drugs, but their regular application has given rise to concerns about the development of resistance. Drug combinations may be more effective than single drugs and delay the onset of resistance. A combination of the nicotinic antagonist, derquantel, and the macrocyclic lactone, abamectin, has been found to have synergistic anthelmintic effects against gastro-intestinal nematode parasites. We have observed in previous contraction and electrophysiological experiments that derquantel is a potent selective antagonist of nematode parasite muscle nicotinic receptors; and that abamectin is an inhibitor of the same nicotinic receptors. To explore these inhibitory effects further, we expressed muscle nicotinic receptors of the nodular worm, *Oesophagostomum dentatum* (Ode-UNC-29:Ode-UNC-63:Ode-UNC-38), in *Xenopus* oocytes under voltage-clamp and tested effects of abamectin on pyrantel and acetylcholine responses. The receptors were antagonized by 0.03 μ M abamectin in a non-competitive manner (reduced R_{max} , no

change in EC_{50}). This antagonism increased when abamectin was increased to 0.1 μM . However, when we increased the concentration of abamectin further to 0.3 μM , 1 μM or 10 μM , we found that the antagonism decreased and was less than with 0.1 μM abamectin. The bi-phasic effects of abamectin suggest that abamectin acts at two allosteric sites: c We also tested the effects of 0.1 μM derquantel alone and in combination with 0.3 μM abamectin. We found that derquantel on these receptors, like abamectin, acted as a non-competitive antagonist, and that the combination of derquantel and abamectin produced greater inhibition. These observations confirm the antagonistic effects of abamectin on nematode nicotinic receptors in addition to GluCl effects, and illustrate more complex effects of macrocyclic lactones that may be exploited in combinations with other anthelmintics.

5.2 Introduction

Gastro-intestinal nematode parasite infections of both humans and animals are a global public health problem. These infections cause livestock production losses, morbidity, and if left uncontrolled, may result in death (Pullan *et al.*, 2014). In the absence of effective sanitation and vaccines, control of nematode parasite infections is achieved by the use of anthelmintic drugs, many of which act on ligand-gated ion channels (LGICs) (Beech & Neveu, 2015; Greenberg, 2014; Wolstenholme, 2011). The nicotinic acetylcholine receptor (nAChR) is a prototypic pentameric LGIC. Different subunit combinations or different stoichiometry of the same nAChR subunits can give rise to multiple receptor subtypes with different pharmacological properties (Buxton *et al.*, 2014; Williamson *et al.*, 2009). There are a limited number of anthelmintics which are currently approved for use (Wolstenholme, 2011). Those that act on nAChRs include: imidazothiazoles (levamisole) (Martin & Robertson, 2007), tetrahydropyrimidine derivatives (pyrantel, oxantel, morantel) (Rayes *et*

al., 2001), spiroindoles (derquantel) (Lee *et al.*, 2002), and tribendimidine (Robertson *et al.*, 2015). The macrocyclic lactones (ivermectin, abamectin, moxidectin) act on glutamate-gated chloride channels (GluCl_s) (Wolstenholme & Rogers, 2005); the benzimidazoles (albendazole, mebendazole) act on β -tubulin (Lacey, 1990); and piperazine acts on GABA receptors (Martin, 1997). Other more recent drugs include the amino-acetonitrile derivatives (monepantel) which act on LGICs receptors comprised of DEG-3/DES-2 nAChR subunits (Rufener *et al.*, 2010); and the cyclooctadepsipeptide (emodepside) whose mode of action is understood to be on SLO-1 potassium channels (Guest *et al.*, 2007; Martin *et al.*, 2012a) and latrophilin receptors (Saeger *et al.*, 2001).

The increased use of anthelmintics has led to the development of resistance in both animal and human nematode parasites (Wolstenholme & Martin, 2014). Resistance to anthelmintics presents a serious drawback in the control of nematode parasite infections and is an increasing medical concern (Kotze *et al.*, 2014). Combination therapy involving anthelmintic drugs of different classes is an important approach that may slow the development of anthelmintic drug resistance. The simultaneous development of resistance to two drugs is less likely than the development of resistance to one drug alone; hence combinations are predicted to slow the development of resistance (Leathwick, 2012). Startect[®] (derquantel and abamectin combination, Figure 5.0) is a more recently introduced anthelmintic combination that is marketed for use in sheep, but it has been shown to have effects on nematode parasites of other host species such as *Ascaris suum* of pigs (Puttachary *et al.*, 2013). In this study, we investigated the effects of derquantel alone, abamectin alone, and a combination of derquantel and abamectin on a nAChR subtype from the nematode parasite *Oesophagostomum dentatum*. This subtype is comprised of *Ode-UNC-29:Ode-UNC-*

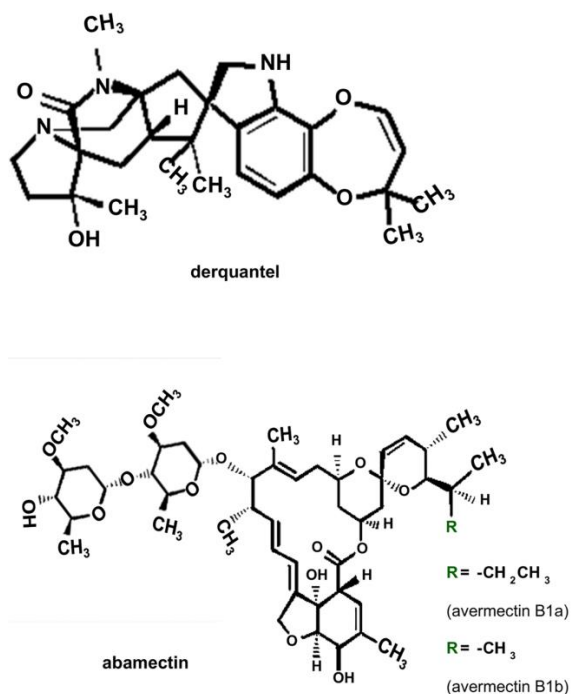


Figure 5.0 Structures of derquantel and abamectin. **A:** Structure of derquantel. **B:** Structure of abamectin. Abamectin is a mixture of avermectin B1a and avermectin B1b. Avermectin B1a differs from avermectin B1b by a functional group at the 'R' position, and makes up more than 80% of abamectin, while avermectin B1b makes up less than 20% of abamectin.

63:*Ode*-UNC-38 (29-63-38) nAChR subunits. Other pharmacologically characterized nAChR subtypes of *O. dentatum* are *Ode*-UNC-29:*Ode*-UNC-63 (pyrantel-sensitive nAChR), *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-ACR-8 (acetylcholine-sensitive nAChR), and *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38:*Ode*-ACR-8 (levamisole-sensitive nAChR) (Buxton *et al.*, 2014). We chose *O. dentatum* parasite for further investigation because the worm is easily maintained and passaged, and it is a Clade V nematode, just like the model free-living nematode, *Caenorhabditis elegans* (Blaxter *et al.*, 1998). *O. dentatum* is a common nodule worm in pigs, very similar to other *Oesophagostomum* species which infect humans, most notably in northern Togo and Ghana (Polderman *et al.*, 1991). The *O. dentatum* nAChR subtype, *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38 used in this study is

preferentially activated by pyrantel and tribendimidine, and it is antagonized in a non-competitive manner by derquantel (Buxton *et al.*, 2014). We show here that abamectin is a potent antagonist of these nAChRs, and that a combination of derquantel and abamectin has greater effects than derquantel or abamectin used alone. These additive effects support the continued use of the derquantel and abamectin combination for the control of nematode parasites.

5.3 Materials and Methods

Experiments described in this study have been conducted according to US national and international welfare guidelines. The Office for Responsible Research at Iowa State University, IACUC Log #3-2-5134-s specifically approved this study and granted permission for the culture of the *Oesophagostomum* parasites. There was no animal suffering or surgery required.

5.3.1 Cloning of nAChR subunits from *O. dentatum* and ancillary factors from *Haemonchus contortus*

O. dentatum nAChR subunits and *H. contortus* ancillary factors used in this research study have been previously cloned and reported (Buxton *et al.*, 2014).

5.3.2 Expression of *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* in *Xenopus laevis* oocytes

Defolliculated *X. laevis* oocytes were purchased from Ecocyte Bioscience (Austin, TX, USA). Oocyte microinjection was done using a Drummond nanoject II microinjector (Drummond Scientific, PA, and USA). 1.8 ng of each subunit cRNA (*Ode-unc-29*, *Ode-unc-63* and *Ode-unc-38*) and ancillary factor cRNA (*Hco-ric-3*, *Hco-unc-50* and *Hco-unc-74*) in a total volume of 36 nL in RNase-free water were microinjected into the animal pole of the

oocytes. Once micro-injected, the oocytes were transferred to a sterile 96-well culture plate (one oocyte/well) containing 200 μ L incubation solution (100 mM NaCl, 2 mM KCl, 1.8 mM $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 1 mM $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$, and 5 mM HEPES, 2.5 mM Na pyruvate, 100 U/mL penicillin and 100 μ g/mL streptomycin, pH 7.5) in each well. The oocytes were incubated at 19°C for 2–5 days, with a daily change of incubation solution.

5.3.3 Two-microelectrode voltage-clamp (TEVC) electrophysiology

We followed methods we have described in detail before (Buxton *et al.*, 2014). Briefly, 100 μ M BAPTA-AM was added to the oocytes in incubation media approximately 3 hours prior to electrophysiological recordings from the oocytes. TEVC recordings were carried out by impaling the oocytes with two microelectrodes; a voltage sensing electrode, V_m , and a current injecting electrode, I_m , were used to inject the current required to hold the membrane at the set voltage. The microelectrodes were pulled with a Flaming/Brown horizontal electrode puller (Model P-97, Sutter Instruments), filled with 3 M potassium chloride and the microelectrode tips carefully broken with a piece of tissue paper to achieve a low resistance of 2–5 M Ω in recording solution (100 mM NaCl, 2.5 mM KCl, 1 mM $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$ and 5 mM HEPES, pH 7.3). Current/voltage signals were amplified by an AxoClamp 2B amplifier (Molecular Devices, CA, USA). The amplified signals were converted from analog to digital format by a Digidata 1322A digitizer (Molecular Devices, CA, USA) and finally acquired on a desktop computer with the Clampex 9.2 data acquisition software (Molecular Devices, CA, USA).

5.3.4 Drugs

Acetylcholine (ach) and pyrantel (pyr) were purchased from Sigma-Aldrich (St Louis, MO, USA), while derquantel (der) and abamectin (aba) were gifts from Zoetis (Kalamazoo,

MI). Acetylcholine and pyrantel were dissolved in recording solution. Derquantel and abamectin were dissolved in DMSO and added to recording solution at a final concentration of $\leq 0.01\%$ DMSO.

5.3.5 Drug applications

Acetylcholine which is a natural agonist of many nAChRs served for normalization and as a control in our experiments. Each agonist concentration was applied for 10 s, with sufficient time allowed for wash off between drug applications. For every oocyte recording, 100 μM acetylcholine was applied initially and this current response was measured, subsequent responses were measured and normalized to this acetylcholine current. To generate control agonist concentration-response plots, acetylcholine was applied at different concentrations between 0.1–100 μM or pyrantel was applied at different concentrations between 0.03–10 μM . Higher concentrations of pyrantel were not tested because pyrantel acts as an open channel blocker at high concentrations (Robertson *et al.*, 1994). For the antagonist experiments, a control 100 μM acetylcholine was also first applied for 10s, and then followed by a 2 min or 10 min challenge with the antagonist (derquantel and/or abamectin), and a final application of the agonist (pyrantel) in the continued presence of the antagonist.

5.3.6 Data analysis

We used Clampfit 9.2 (Molecular Devices, CA, and USA) to measure peak current responses and normalized them to the first 100 μM acetylcholine responses. GraphPad Prism 5.0 software (GraphPad Software Inc., USA) was used to analyze the data, and results were expressed as mean \pm S.E.M. Concentration-response data points were fitted with the Hill equation as previously described: where R_{max} is the maximum response % relative to the

control 100 μM ach response; the EC_{50} is the concentration producing the half-maximum response and n_H is the slope factor or Hill coefficient (Boulin *et al.*, 2008). We used the unpaired two-tailed Student's t-test to test for statistical significance and a p value < 0.05 was considered significant.

The Bliss additive effect dose-response relationship for pyrantel current responses was calculated as previously described (Greco *et al.*, 1996) to predict the linear additive effects of derquantel and abamectin on the *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* nAChR. To do so, we determined: the normalized mean current responses to each control pyrantel concentration ($CR[pyr]$); the mean current responses to each concentration of pyrantel in the presence of derquantel (derquantel effect) and; the mean current responses to each concentration of pyrantel in the presence of abamectin (abamectin effect). We then used the fractional inhibition (mean reduction in response/ $CR[pyr]$) produced by derquantel alone, F_d , and abamectin alone, F_a , at each pyrantel concentration to determine the additive effect. We used $F_a(1-F_d)$ to denote the fractional inhibition produced by abamectin when derquantel is already present, and $F_d+F_a(1-F_d)$ to denote the fractional inhibition produced by the combination of derquantel and abamectin. Lastly, the normalized additive response was calculated as:

$$CR[pyr] - CR[pyr]\{F_d + F_a(1 - F_d)\}$$

The difference between the observed and calculated additive effects for the combination of derquantel and abamectin were tested for statistical significance using the paired two-tailed Student's t-test, taking $p < 0.05$ as significant.

5.4 Results

5.4.1 *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38 forms a pyrantel-sensitive nAChR

Representative traces (inward currents from oocytes expressing *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38) produced in response to different concentrations of acetylcholine and pyrantel are shown in Figure 5.1A and Figure 5.1B respectively. Figure 5.1C shows acetylcholine and pyrantel concentration-response relationships for *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38. The EC_{50} and maximum response (R_{max}) values for acetylcholine were $13.0 \pm 1.6 \mu\text{M}$ and $114.3 \pm 4.3\%$, $n = 4$. The EC_{50} and R_{max} values for pyrantel were $0.4 \pm 0.0 \mu\text{M}$ and $135.5 \pm 7.9\%$, $n = 6$ (S5.0 Table). Our results showed the EC_{50} for pyrantel to be significantly smaller ($p < 0.001$) than the EC_{50} for acetylcholine, but showed no significant difference ($p > 0.05$) in R_{max} between acetylcholine and pyrantel. Based on these EC_{50} values, pyrantel is 32.5 times more potent than acetylcholine on the *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38 nAChR. Also there was a slightly steeper Hill slope (nH) for pyrantel than acetylcholine ($nH = 1.2 \pm 0.1$, $n = 6$ for pyrantel; $nH = 1.0 \pm 0.1$, $n = 4$ for acetylcholine; $p < 0.05$). We used pyrantel rather than acetylcholine for most subsequent experiments because of its potency and because it is a more selective agonist than acetylcholine for this nAChR subtype (Buxton *et al.*, 2014).

5.4.2 Effects of abamectin on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38

We investigated pyrantel concentration-response relationships on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38 in the presence of $0.03 \mu\text{M}$ and $0.1 \mu\text{M}$ abamectin. A representative trace is shown in Figure 5.2A. The concentration-response plots, Figure 5.2B, show abamectin to be an antagonist of *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38. The EC_{50} and R_{max} values were: $0.4 \pm 0.0 \mu\text{M}$ and $135.5 \pm 7.9\%$, $n = 6$ for pyrantel in the absence of

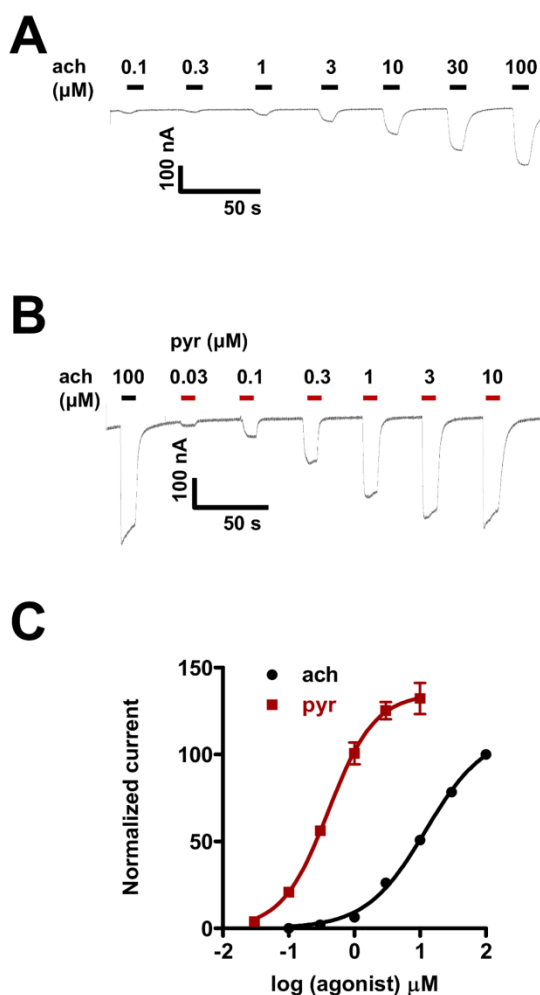


Figure 5.1 Acetylcholine and pyrantel concentration-response relationships for the *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* receptor. **A**: Representative trace (inward currents, holding potential -60mV , from oocytes expressing *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*) following 10 seconds applications of different acetylcholine concentrations, from $0.1 \mu\text{M}$ to $100 \mu\text{M}$. **B**: Representative trace (inward currents, holding potential -60mV , from oocytes expressing *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*) of the 10 seconds application of different pyrantel concentrations, from $0.03 \mu\text{M}$ to $10 \mu\text{M}$. An initial 10 seconds application of $100 \mu\text{M}$ acetylcholine served as the control. **C**: Concentration-response plots for acetylcholine ($n = 4$, black) and pyrantel ($n = 6$, red). Results were normalized to $100 \mu\text{M}$ acetylcholine current responses and expressed as mean \pm S.E.M.

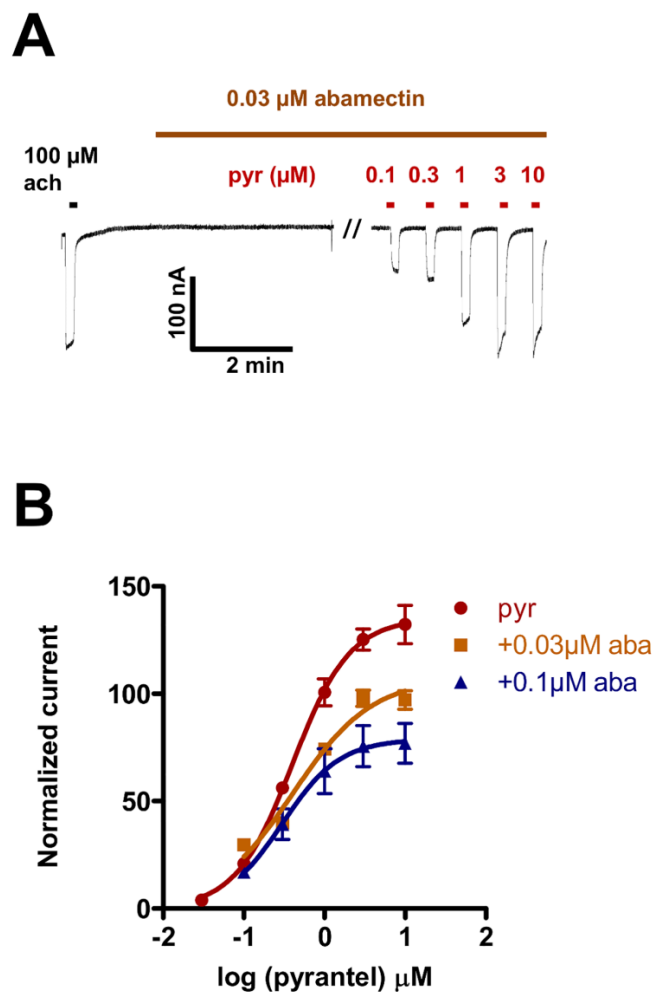


Figure 5.2 Pyrantel concentration-response relationships in the presence of 0.03 μM and 0.1 μM abamectin. **A**: Representative trace (inward currents, holding potential -60mV , from oocytes expressing *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*) of the 10 seconds application of the control 100 μM acetylcholine, followed by a 10 minutes application of abamectin (0.03 μM) and finally, a 10 seconds application of different pyrantel concentrations in the continued presence of abamectin. **B**: Concentration-response plots for pyrantel in the absence ($n = 6$, red) and presence of 0.03 μM abamectin ($n = 5$, orange) and 0.1 μM abamectin ($n = 6$, dark blue). Results were normalized to 100 μM acetylcholine current responses and expressed as mean \pm S.E.M. Notice 0.03 μM abamectin caused an inhibition of current responses to pyrantel, and this inhibition was greater with 0.1 μM abamectin.

abamectin; $0.4 \pm 0.0 \mu\text{M}$ and $107.3 \pm 4.7\%$, $n = 5$ for pyrantel in the presence of $0.03 \mu\text{M}$ abamectin; and $0.3 \pm 0.0 \mu\text{M}$ and $80.6 \pm 8.4\%$, $n = 6$ for pyrantel in the presence of $0.1 \mu\text{M}$ abamectin. There was no significant difference ($p > 0.05$) in the EC_{50} s between pyrantel in the absence and presence of $0.03 \mu\text{M}$ or $0.1 \mu\text{M}$ abamectin. But, there was a significant difference ($p < 0.05$) in R_{max} for pyrantel in the absence and presence of $0.03 \mu\text{M}$ abamectin, and this difference was greater ($p < 0.001$) in the presence of $0.1 \mu\text{M}$ abamectin. Hence, abamectin did not cause a significant change in EC_{50} , but did cause a significant reduction in R_{max} , showing that abamectin acts as a non-competitive antagonist of the *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38 nAChR.

When we increased the concentration of abamectin from $0.1 \mu\text{M}$ to $0.3 \mu\text{M}$, Figure 5.3A, we noticed that the EC_{50} for pyrantel in the presence of $0.3 \mu\text{M}$ abamectin remained unchanged: $0.3 \pm 0.1 \mu\text{M}$, $n = 5$ ($p > 0.05$). Although not statistically significant ($p > 0.05$), the mean value for the R_{max} for pyrantel in the presence of $0.1 \mu\text{M}$ abamectin (80.6 ± 8.4 , $n = 6$) appeared smaller than R_{max} in the presence of $0.3 \mu\text{M}$ abamectin (98.4 ± 6.5 , $n = 5$). This suggested that the inhibitory effects of lower concentrations of abamectin can be greater than those of higher concentrations. This reversed inhibitory effect was tested and confirmed when we increased the concentration of abamectin from $0.3 \mu\text{M}$ to $1 \mu\text{M}$ and $10 \mu\text{M}$. While the EC_{50} values did not change ($0.3 \pm 0.1 \mu\text{M}$, $n = 6$ in the presence of $1 \mu\text{M}$ abamectin, and $0.4 \pm 0.1 \mu\text{M}$, $n = 5$ in the presence of $10 \mu\text{M}$ abamectin), the R_{max} values increased to $108.0 \pm 3.5\%$, $n = 6$ in the presence of $1 \mu\text{M}$ abamectin, and $106.0 \pm 9.4\%$, $n = 5$ in the presence of $10 \mu\text{M}$ abamectin. We point out that the effects of abamectin were reversible on washing, although the current responses did not return to control responses even after a 10 mins wash.

S5.1 Table summarizes the EC_{50} , R_{max} , n_H and n numbers for these experiments.

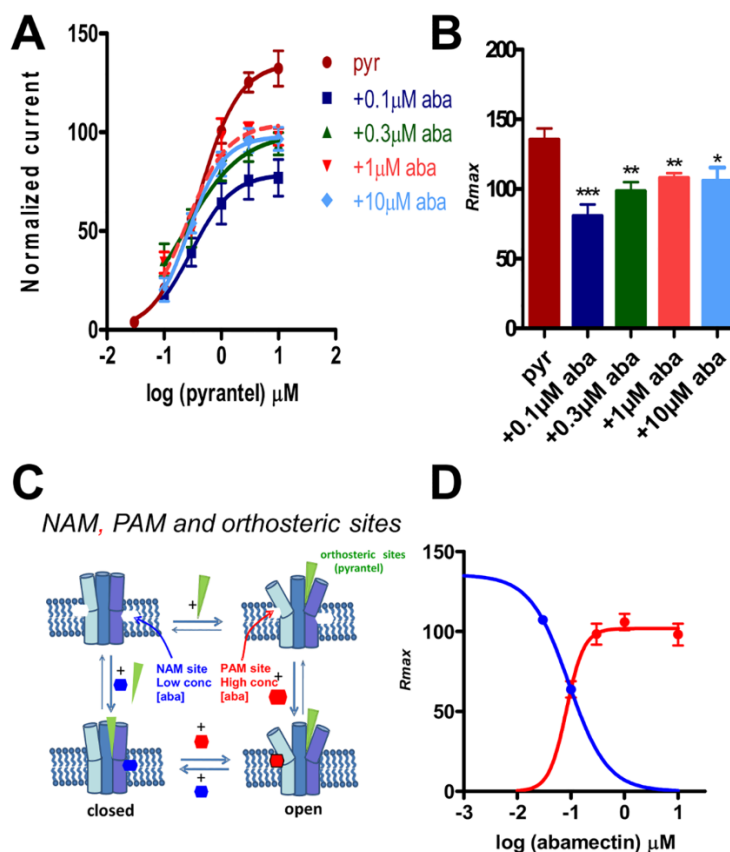


Figure 5.3. Effects of increasing concentrations of abamectin (above 0.1 μM) on the pyrantel concentration-response plots. **A**: Concentration-response plots for pyrantel in the absence ($n = 6$, red) and presence of 0.1 μM abamectin ($n = 6$, dark blue); 0.3 μM abamectin ($n = 5$, dark green); 1 μM abamectin ($n = 6$, pink); 10 μM abamectin ($n = 5$, light blue). Results were normalized to 100 μM acetylcholine current responses and expressed as mean \pm S.E.M. Increasing the concentration of abamectin from 0.1 μM to 0.3, 1 and 10 μM rather caused a reduction in the inhibition instead of a potentiation. **B**: Bar chart showing the mean \pm S.E.M of the maximum current responses (R_{max}) for pyrantel and the different abamectin concentrations. R_{max} for 0.1 μM abamectin ($n = 6$, dark blue), 0.3 μM abamectin ($n = 5$, dark green), 1 μM abamectin ($n = 6$, pink) and 10 μM abamectin ($n = 5$, light blue) were significantly lower than R_{max} for pyrantel alone ($n = 6$, red). * $p < 0.05$, ** $p < 0.01$ and *** $p < 0.001$, unpaired two-tailed student t-test. **C**: Model of ligand sites of action. Pyrantel binds to the orthosteric sites opening the channel. Low concentrations of abamectin (0.03 and 0.1 μM) bind to a negative allosteric site (NAM) in the lipid phase of the channel, inhibiting opening. Higher concentrations of abamectin (0.3, 1 and 10 μM) bind to a positive allosteric site (PAM) increasing opening. **D**: Abamectin R_{max} inhibition (blue curve) and inhibition reduction (red curve) dose response plots. The data points for inhibition used data from 0.03 μM and 0.1 μM abamectin from Figure 5.2. The data points for inhibition reduction used data from Figure 5.3B.

Interestingly, when the EC_{50} s for pyrantel alone are compared with that for pyrantel in the presence of 0.1 μ M, 0.3 μ M, 1 μ M or 10 μ M abamectin, there were no significant differences in the EC_{50} values. In contrast however, the R_{max} values for pyrantel in the presence of 0.1 μ M, 0.3 μ M, 1 μ M and 10 μ M abamectin were significantly less than the R_{max} for pyrantel alone, Figure 5.3B. We emphasize again that the R_{max} for pyrantel in the presence of abamectin concentrations ≥ 0.3 μ M were greater than the R_{max} for pyrantel in the presence of 0.1 μ M abamectin, with the difference being statistically significant ($p < 0.05$) for 1 μ M. These observations show that abamectin has a bi-phasic effect, suggesting two allosteric sites of action: a high affinity site causing antagonism, and a lower affinity site causing a reduction in the antagonism, Figures 5.3C and 5.3D.

5.4.3 Effects of derquantel and abamectin combination on *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*

For this set of experiments, we tested the combination of 0.3 μ M abamectin and 0.1 μ M derquantel. We selected 0.3 μ M abamectin because it is the reported concentration in *H. contortus* following the administration of abamectin at its therapeutic dose of 0.2 μ M at 12 hours (Lloberas *et al.*, 2013). 0.1 μ M derquantel was selected because the reported concentration is 13 μ M at 12 hours in the intestine (Jin, 2010) with an uncertain but lower concentration being present within the worm. Figures 5.4A and 5.4B show representative traces for *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* responses to pyrantel in the presence of 0.3 μ M abamectin alone, and the 0.1 μ M derquantel plus 0.3 μ M abamectin combination respectively. Concentration-response plots for pyrantel in the absence and presence of 0.1 μ M derquantel alone, 0.3 μ M abamectin alone, and the 0.1 μ M derquantel and 0.3 μ M abamectin combination are shown in Figure 5.4C. The calculated additive effect of the

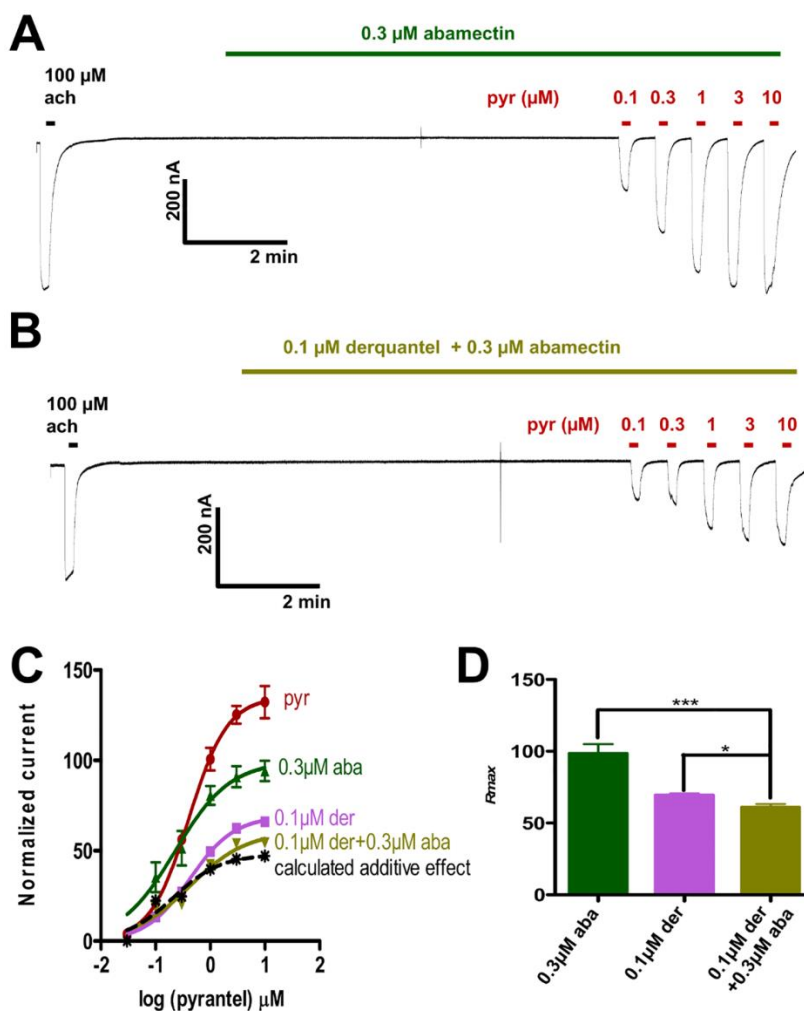


Figure 5.4 Effects of 0.1 μM derquantel alone, 0.3 μM abamectin alone, and derquantel and abamectin combination (0.1 μM derquantel + 0.3 μM abamectin) on the pyrantel concentration-response plots. **A**: Representative trace (inward currents from oocytes expressing *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*) of the 10 seconds application of the control 100 μM acetylcholine, followed by a 10 minutes application of 0.3 μM abamectin and finally, a 10 seconds application of different pyrantel concentrations in the continued presence of abamectin. **B**: Representative trace (inward currents from oocytes expressing *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*) of the 10 seconds application of the control 100 μM acetylcholine, followed by a 10 minutes application of derquantel and abamectin combination and finally, a 10 seconds application of different pyrantel concentrations in the continued presence of the derquantel and abamectin combination. **C**: Concentration-response plots for pyrantel in the absence ($n = 6$, red) and presence of 0.1 μM derquantel ($n = 4$, light purple); 0.3 μM abamectin ($n = 5$, dark green); 0.1 μM derquantel + 0.3 μM abamectin combination ($n = 6$, olive green). Results were normalized to 100 μM acetylcholine current responses and expressed as mean \pm S.E.M. Inhibition with 0.1 μM derquantel + 0.3 μM abamectin combination was greater than that with 0.1 μM derquantel alone and 0.3 μM abamectin alone. The calculated additive effect for the combination of derquantel and

abamectin (broken black) was not statistically different ($p > 0.05$, paired two-tailed student t-test) from the observed additive effect for the combination of derquantel and abamectin (olive green). **D:** Bar chart showing the mean \pm S.E.M of the maximum current responses (R_{max}) for 0.1 μ M derquantel ($n = 4$, light purple); 0.3 μ M abamectin ($n = 5$, dark green); 0.1 μ M derquantel + 0.3 μ M abamectin combination ($n = 6$, olive green). R_{max} for the combination of 0.1 μ M derquantel + 0.3 μ M abamectin was significantly smaller than R_{max} for 0.1 μ M derquantel alone and for 0.3 μ M abamectin alone. * $p < 0.05$ and *** $p < 0.001$, unpaired two-tailed student t-test.

combination of derquantel and abamectin is also shown in Figure 5.4C. The observed effect was not greater than the calculated additive effect ($p > 0.05$) so this combination does not show synergism. S5.2 Table shows the EC_{50} and R_{max} values for these experiments. There was no significant difference ($p > 0.05$) between EC_{50} values for pyrantel in the absence and presence of derquantel alone, abamectin alone or the derquantel and abamectin combination. However, as before the R_{max} values for pyrantel in the presence of 0.1 μ M derquantel alone, 0.3 μ M abamectin alone, and 0.1 μ M derquantel and 0.3 μ M abamectin combination were significantly smaller ($p < 0.001$) than the R_{max} for pyrantel in the absence of derquantel and/or abamectin. Thus both derquantel and abamectin show non-competitive antagonism on the *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* receptor. Figure 5.4D also shows that R_{max} values for pyrantel in the presence of 0.1 μ M derquantel alone and 0.3 μ M abamectin alone were significantly greater ($p < 0.05$ and $p < 0.001$) than R_{max} in the presence of 0.1 μ M derquantel and 0.3 μ M abamectin combination. Thus the combination of abamectin and derquantel together increases the antagonism but their combination was not significantly greater than the calculated additive effect.

We used pyrantel as the preferred agonist to study the effects of abamectin and derquantel on the *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* receptor because it is more selective than acetylcholine for this receptor (Buxton *et al.*, 2014). However, we also tested

the effects of abamectin and derquantel with acetylcholine as the agonist instead of pyrantel. We found, as with pyrantel, that a lower concentration of 0.1 μM abamectin was a more potent non-competitive acetylcholine antagonist than 0.3 μM or 1 μM abamectin, S5.0 Figure. We also found that 0.3 μM derquantel acts as a non-competitive antagonist of acetylcholine and that the combination of derquantel and abamectin shows additive inhibitory effects without demonstrating synergism, S5.1 Figure.

5.5 Discussion

5.5.1 Abamectin as a non-competitive antagonist of *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*

Abamectin, a mixture of avermectins B1a and B1b (Figure 5.0), belongs to the macrocyclic lactone class of anthelmintics which have been shown to act on GluCl_s (Wolstenholme & Rogers, 2005). In addition to the effect of abamectin on GluCl_s, Puttachary et al (Puttachary *et al.*, 2013) showed, using muscle contraction and current-clamp electrophysiological techniques, that abamectin acts as a non-competitive antagonist of *Ascaris suum* (Clade III nematode) somatic muscle nAChRs. In this paper we were interested to see if abamectin had similar effects on the expressed *O. dentatum* (Clade V nematode) receptor, *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*. Interestingly, we found that abamectin was also a potent non-competitive antagonist of this receptor (Figure 5.2B).

5.5.2 Bi-phasic effects of abamectin on *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*

The inverse dose-dependent bi-phasic effects of abamectin on *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38* suggest that abamectin has two allosteric sites of action on this receptor: one, a higher affinity negative allosteric modulator (NAM) site causing antagonism; and the other, with lower affinity, a positive allosteric modulator (PAM) site, causing a

reduction in the antagonism (Figure 5.3D). The NAM and PAM sites of action of abamectin on the receptors may be in the outer lipid phase of the membrane (Martin & Kusel, 1992) between the TM1 transmembrane domain of one receptor subunit and the TM3 domain of the adjacent receptor subunit (Hibbs & Gouaux, 2011). Since the receptor channel is composed of heterogeneous subunits, binding between one pair of subunits may stabilize closing (negative allosteric modulator) while binding between another pair of subunits may stabilize opening (positive allosteric modulator).

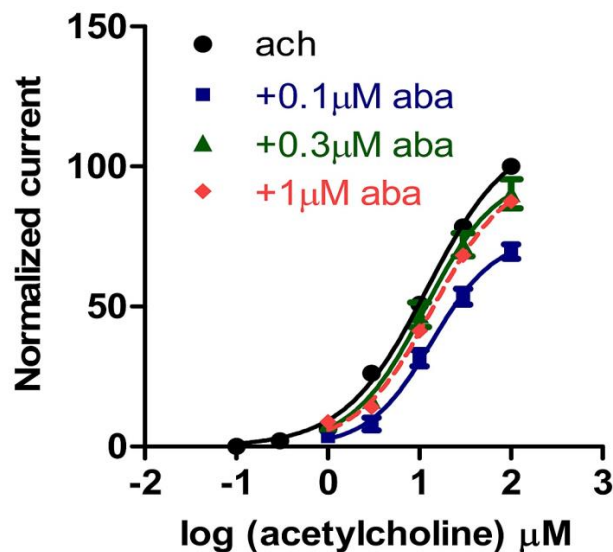
5.5.3 Derquantel and abamectin combination produces greater effects than either derquantel or abamectin used alone

The effects of a combination of derquantel and abamectin on a mixture of *in situ A. suum* somatic nAChR subtypes have been described by Puttachary et al (Puttachary *et al.*, 2013): when derquantel was used alone, *A. suum* somatic nAChRs were antagonized in a competitive manner (right-shift in EC_{50} , but no change in R_{max}); when abamectin was used alone, *A. suum* somatic nAChRs were antagonized in a non-competitive manner (reduction in R_{max} , but no change in EC_{50}); when derquantel and abamectin were used in combination, abamectin potentiated the antagonism of derquantel. In our experiments with *Ode-UNC-29:Ode-UNC-63:Ode-UNC-38*, derquantel showed non-competitive (Figure 5.4C) rather than competitive antagonism. With the combination of derquantel and abamectin together, the R_{max} was significantly smaller than for derquantel alone and abamectin alone (Figure 5.4D). Additionally, the effects of the combination were greater than those of 0.1 μM derquantel at pyrantel concentrations $\geq 0.3 \mu\text{M}$ suggesting that the use of abamectin and derquantel in combination is likely to be more effective than either one of the two drugs administered alone.

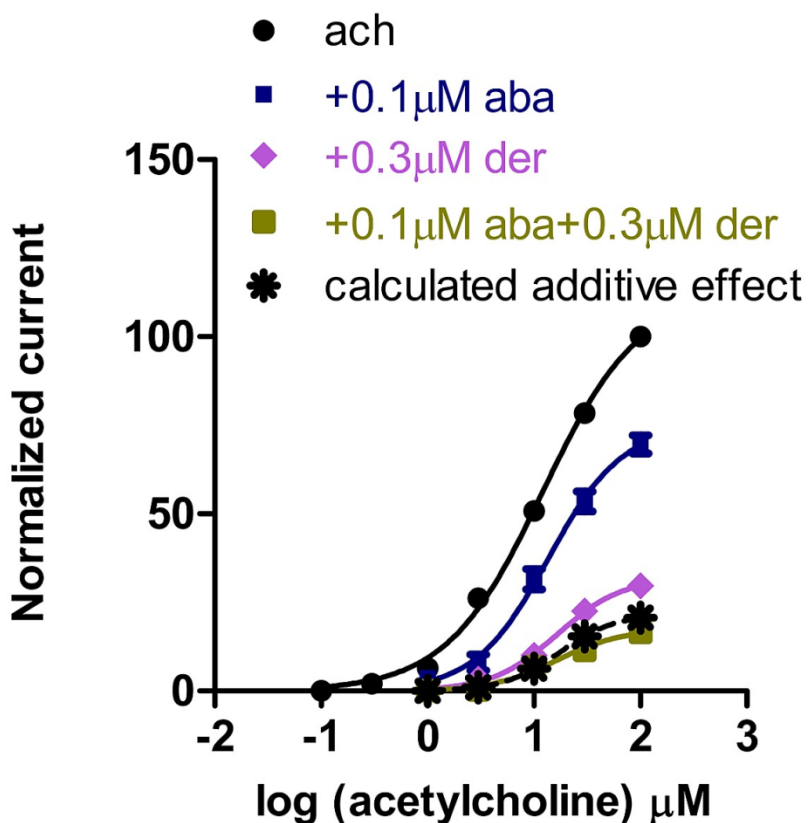
5.6 Conclusion

Our observations reveal that abamectin, in addition to its recognized effects on GluCl channels also has effects on an UNC-29: UNC-63: UNC-38 subtype of nematode nAChR and that the antagonism is non-competitive with a bi-phasic inverse dose-dependent effect characteristic of two sites of action. The higher affinity site, a negative allosteric site, produces more closing of the nAChR in contrast to the other lower affinity site, a positive allosteric site that produces more opening. The significant observation is that lower concentrations of abamectin produced greater inhibition of the nAChR than higher concentrations. The combination of derquantel and abamectin as Startect^R can produce inhibition of nematode worm movement and feeding. Derquantel and abamectin inhibits the nAChRs; and in addition, abamectin inhibits movement and feeding by activating GluCls. The double action of the combination of derquantel and abamectin has the potential to slow resistance development in nematode parasites by acting at a number of different sites of action. The emergence of resistance in numerous nematode parasite species makes the control of helminth infections with the currently available anthelmintics more difficult but the recent introduction and careful use of appropriate anthelmintic combinations may be used to reduce the rate of development of anthelmintic resistance. It should also be noted that effects of abamectin does not involve a simple mode of action and that there are effects on more than one LGIC in addition to the GluCls.

5.7 Supporting Information



S5.0 Figure Concentration-response plots for acetylcholine in the absence ($n = 4$, black) and presence of 0.1 μM abamectin ($n = 4$, dark blue), 0.3 μM abamectin ($n = 4$, dark green) and 1 μM abamectin ($n = 3$, pink). Results were normalized to 100 μM acetylcholine current responses and expressed as mean \pm S.E.M. The standard errors are smaller than the symbols and some are not visible. Notice 0.1 μM abamectin caused an inhibition of current responses to acetylcholine, and this inhibition was reduced with 0.3 and 1 μM abamectin.



S5.1 Figure. Concentration-response plots for acetylcholine in the absence ($n = 4$, black) and presence of 0.3 μM derquantel ($n = 4$, light purple); 0.1 μM abamectin ($n = 4$, dark blue); 0.3 μM derquantel + 0.1 μM abamectin combination ($n = 4$, olive green). Results were normalized to 100 μM acetylcholine current responses and were expressed as mean \pm S.E.M. The standard errors are smaller than the symbols and some are not visible. Inhibition with 0.3 μM derquantel + 0.1 μM abamectin combination was greater than that with 0.3 μM derquantel alone and 0.1 μM abamectin alone. The calculated additive effect (*) is also plotted.

S5.0 Table. EC_{50} , R_{max} , n_H and n numbers for acetylcholine and pyrantel on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38.

Drug	EC_{50} (mean \pm S.E.M, μ M)	R_{max} (mean \pm S.E.M, % 100 μ M acetylcholine response)	n_H	n
Acetylcholine	13.0 \pm 1.6	114.3 \pm 4.3	1.0 \pm 0.1	4
Pyrantel	0.4 \pm 0.0	135.5 \pm 7.9	1.2 \pm 0.1	6

S5.1 Table. EC_{50} , R_{max} , n_H and n numbers for pyrantel in the absence and presence of abamectin on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38.

Drug	EC_{50} (mean \pm S.E.M, μ M)	R_{max} (mean \pm S.E.M, % 100 μ M acetylcholine response)	n_H	n
Pyrantel	0.4 \pm 0.0	135.5 \pm 7.9	1.2 \pm 0.1	6
Pyrantel + 0.03 μ M abamectin	0.4 \pm 0.0	107.3 \pm 4.7	0.9 \pm 0.1	5
Pyrantel + 0.1 μ M abamectin	0.3 \pm 0.0	80.6 \pm 8.4	1.2 \pm 0.2	6
Pyrantel + 0.3 μ M abamectin	0.3 \pm 0.1	98.4 \pm 6.5	1.0 \pm 0.1	5
Pyrantel + 1 μ M abamectin	0.3 \pm 0.1	108.0 \pm 3.5	1.2 \pm 0.1	6
Pyrantel + 10 μ M abamectin	0.4 \pm 0.1	106.0 \pm 9.4	1.5 \pm 0.4	5

S5.2 Table. EC_{50} , R_{max} , n_H and n numbers for pyrantel in the absence and presence of derquantel, abamectin, and a combination of derquantel and abamectin on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38.

Drug	EC_{50} (mean \pm S.E.M, μM)	R_{max} (mean \pm S.E.M, % 100 μM acetylcholine response)	n_H	n
Pyrantel	0.4 \pm 0.0	135.5 \pm 7.9	1.2 \pm 0.1	6
Pyrantel + 0.1 μM derquantel	0.4 \pm 0.0	69.4 \pm 1.1	1.1 \pm 0.1	4
Pyrantel + 0.3 μM abamectin	0.3 \pm 0.1	98.4 \pm 6.5	1.0 \pm 0.1	5
Pyrantel + 0.1 μM derquantel + 0.3 μM abamectin	0.3 \pm 0.1	60.9 \pm 2.3	0.9 \pm 0.1	6

S5.3 Table. EC_{50} , R_{max} , n_H and n numbers for acetylcholine in the absence and presence of 0.1 μ M, 0.3 μ M and 10 μ M abamectin on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38.

Drug	EC_{50} (mean \pm S.E.M, μM)	R_{max} (mean \pm S.E.M, % 100 μM acetylcholine response)	n_H	n
Acetylcholine	13.0 \pm 1.6	114.3 \pm 4.3	1.0 \pm 0.1	4
Acetylcholine + 0.1 μM abamectin	14.0 \pm 1.1	75.1 \pm 2.0	1.3 \pm 0.1	4
Acetylcholine + 0.3 μM abamectin	11.6 \pm 1.0	98.5 \pm 4.7	1.1 \pm 0.0	4
Acetylcholine + 1 μM abamectin	14.4 \pm 1.0	99.6 \pm 1.6	1.1 \pm 0.1	3

S5.4 Table. EC_{50} , R_{max} , n_H and n numbers for acetylcholine in the absence and presence of derquantel, abamectin, and a combination of derquantel and abamectin on *Ode*-UNC-29:*Ode*-UNC-63:*Ode*-UNC-38.

Drug	EC_{50} (mean \pm S.E.M, μ M)	R_{max} (mean \pm S.E.M, % 100 μ M acetylcholine response)	n_H	n
Acetylcholine	13.0 \pm 1.6	114.3 \pm 4.3	1.0 \pm 0.1	4
Acetylcholine + 0.3 μ M derquantel	16.6 \pm 1.1	32.1 \pm 1.9	1.4 \pm 0.1	4
Acetylcholine + 0.1 μ M abamectin	14.0 \pm 1.1	75.1 \pm 2.0	1.3 \pm 0.1	4
Acetylcholine + 0.3 μ M derquantel + 0.1 μ M abamectin	15.8 \pm 1.6	17.2 \pm 1.6	1.5 \pm 0.2	4

5.8 Acknowledgements

We will like to thank Debra Woods of Zoetis (Kalamazoo, MI) for providing us with derquantel and abamectin.

5.9 Funding

Research reported in this publication was supported by the National Institute of Allergy and Infectious Diseases of the National Institutes of Health under Award Number R01AI047194 to RJM, R21AI092185-01A1 to APR and the Schlumberger Foundation to MA. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institutes of Health.

5.10 Author Contributions

Conceived and designed the experiments: MA APR RJM. Performed the experiments: MA SKB. Analyzed the data: MA APR RJM. Contributed reagents/materials/analysis tools: MA SKB APR RJM. Wrote the paper: MA APR RJM.

CHAPTER 6. GENERAL DISCUSSION

Many of the currently available anthelmintics used to control parasitic nematode infections act on nematode ion channels. However, there are a limited number of these anthelmintics and their repeated use has led to increasing worldwide reports of anthelmintic resistance development. Thus, the increased need for the development of alternative strategies to slow down or overcome the resistance problem. This PhD research has addressed three strategies by which resistance can be slowed or overcome. These include: (i) the identification of a new drug target ACR-16, (ii) identifying new therapeutic compounds from plant natural sources, and (iii) understanding interactions of drugs used in combination therapy.

ACR-16 is an $\alpha 7$ -like nAChR that forms homomeric receptors in nematodes. Earlier studies have focused on the cloning and expression of ACR-16 from the free-living model nematode, *C. elegans*. We have showed for the first time the cloning and expression of ACR-16 from a parasitic nematode, *A. suum*. We have demonstrated that although *A. suum* ACR-16 shares a high degree of similarity with *C. elegans* ACR-16, these two receptors have significant differences in antagonist pharmacology. We have shown that *A. suum* ACR-16 is different from the carefully studied levamisole receptors. *A. suum* ACR-16 is insensitive to levamisole (and other cholinomimetic anthelmintics) but very sensitive to nicotine. Based on these differences with levamisole receptors, developing drugs that target *A. suum* ACR-16 may circumvent resistance. Importantly, *A. suum* ACR-16 though closely related to vertebrate $\alpha 7$ receptors showed striking differences in sensitivity to α -BTX, allosteric modulation and calcium permeability which could be related to differences in key amino acid residues known to affect $\alpha 7$ receptor pharmacology. Therefore, targeting sites in *A. suum*

ACR-16 that are distinct from vertebrate $\alpha 7$ receptors are unlikely to affect the vertebrate host.

We have demonstrated that plant natural products have potential as sources of lead compounds for the development of macrofilaricidal drugs. We have showed that there is some validity for the traditional uses of *D. oliveri* and *P. febrifugum* in the treatment of filarial infections and that extracts from the medicinal plants *D. oliveri* and *P. febrifugum* are useful to medical practice. Our work focused on *D. oliveri* because extracts of this plant showed good activity against adult *O. ochengi* and *B. pahangi*, in addition to activity against *O. ochengi* microfilariae. This is interesting because a desirable anthelmintic drug is one that has a broad spectrum of action against various parasite species. Therefore, our study has shed more light on the discovery of novel therapeutic drugs from traditionally used plants. We have also demonstrated that *D. oliveri* has potential as a natural source for isolating macrofilaricidal compounds that would contribute to more effective control or elimination of filarial infections.

Finally, we have identified at least one mechanism in which a combination therapy is more effective than single drug approach. We showed that abamectin not only acts on GluCl_s but also has potent effects on pyrantel/tribendimidine nAChRs in *O. dentatum*. The inhibitory effect of abamectin on nAChRs increases the inhibition caused by derquantel (the other component of the combination therapy).

Future Directions

We would recommend more experiments be done in order to further validate ACR-16 as a potential drug target for anthelmintic development. First, we would recommend the expression of ACR-16 in a mammalian cell line which will provide a platform for high

throughput screening. Once this is done, various compounds known to be specific for the closely related human $\alpha 7$ receptors should be tested on ACR-16. Doing so will confirm our observations in electrophysiology studies that ACR-16's pharmacology is different from that of human $\alpha 7$, thus, confirming ACR-16 is a potential anthelmintic drug target. Since we have demonstrated that ACR-16, unlike levamisole receptors desensitizes quickly, we would not recommend the use of specific agonists as anthelmintic compounds. An agonist effect would not produce long term inhibition of ACR-16 mediated behaviors. Additionally, the observation that *acr-16* null *C. elegans* have a close to wild-type phenotype implies that antagonists are also unlikely to be effective. We propose that research should focus on the discovery of positive allosteric modulators of ACR-16 as the most attractive potential drugs.

For the filaricidal plant extracts, we intend to pursue the following: (i) active HPLC fractions will be further purified to allow for isolation of the compounds that are responsible for biological activity, (ii) structure-activity relationship studies will be exploited to increase the potency of the identified compounds if necessary, (iii) the mode of action of lead compounds will be determined, (iv) various combinations of bioactive compounds will be tested for synergistic effects as potential combination therapies, and (v) the efficacy and safety of identified compounds will be evaluated in both *in vitro* and *in vivo* systems.

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**APPENDIX A. INVESTIGATION OF ACETYLCHOLINE RECEPTOR DIVERSITY
IN A NEMATODE PARASITE LEADS TO CHARACTERIZATION OF
TRIBENDIMIDINE- AND DERQUANTEL-SENSITIVE nAChRs**

A paper published in *PLoS Pathogens* (2014)¹

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A1.0 Abstract

Nicotinic acetylcholine receptors (nAChRs) of parasitic nematodes are required for body movement and are targets of important “classical” anthelmintics like levamisole and pyrantel, as well as “novel” anthelmintics like tribendimidine and derquantel. Four biophysical subtypes of nAChR have been observed electrophysiologically in body muscle of the nematode parasite *Oesophagostomum dentatum*, but their molecular basis was not understood. Additionally, loss of one of these subtypes (G 35 pS) was found to be associated with levamisole resistance. In the present study, we identified and expressed in *Xenopus* oocytes, four *O. dentatum* nAChR subunit genes, *Ode-unc-38*, *Ode-unc-63*, *Ode-unc-29* and *Ode-acr-8*, to explore the origin of the receptor diversity. When different combinations of subunits were injected in *Xenopus* oocytes, we reconstituted and characterized four

pharmacologically different types of nAChRs with different sensitivities to the cholinergic anthelmintics. Moreover, we demonstrate that the receptor diversity may be affected by the stoichiometric arrangement of the subunits. We show, for the first time, different combinations of subunits from a parasitic nematode that make up receptors sensitive to tribendimidine and derquantel. In addition, we report that the recombinant levamisole-sensitive receptor made up of Ode-UNC-29, Ode-UNC-63, Ode-UNC-38 and Ode-ACR-8 subunits has the same single-channel conductance, 35 pS and 2.4 ms mean open-time properties, as the levamisole-AChR (G35) subtype previously identified *in vivo*. These data highlight the flexible arrangements of the receptor subunits and their effects on sensitivity and resistance to the cholinergic anthelmintics; pyrantel, tribendimidine and/or derquantel may still be effective on levamisole-resistant worms.

A2.0 Author Summary

Parasitic nematode infections of humans and animals are world-wide. In humans, they cause disease and perpetuate a cycle of poverty. In animals, the parasites cause welfare problems and production loss. In developing countries, the debilitating effect of nematode parasites in school children limits their education, and in adults reduces productivity. These two factors, along with the production loss associated with nematode infections of animals that affects human nutrition, sustain poverty. Treatment and prophylaxis of these parasites requires the use of anthelmintic drugs. Here, we employ the *Xenopus* oocyte expression system to investigate the diversity of anthelmintic receptors in the parasitic nematode *Oesophagostomum dentatum*. We demonstrate effects of the ‘novel’ anthelmintics tribendimidine and derquantel on these reconstituted receptors, revealing, for the first time, the subunits that make up a tribendimidine- and derquantel-sensitive receptor from a parasitic

nematode. We show that the receptor structure and pharmacology can be plastic, and depends on subunit composition and stoichiometry. The factors that affect the diversity of the receptor may contribute to anthelmintic resistance. Our results demonstrate the presence of acetylcholine receptor subtypes that may serve as anthelmintic targets and suggest that pyrantel, tribendimidine and/or derquantel may still be effective on levamisole-resistant worms.

A3.0 Introduction

Human nematode parasite infections are of public health concern in many developing countries where over a billion people are infected [1], [2]. Also very important for human nutrition are infections of livestock which cause significant production loss [3]. Treatment and prophylaxis for these nematode infections requires the use of anthelmintic drugs because sanitation is limited and vaccines are not available. Disturbingly, the regular use of anthelmintics has now been associated with treatment failures and gives rise to concerns about the development of resistance. Resistance has been seen, for example, against levamisole and pyrantel in animals [4]. These two ‘classic’ anthelmintics work by selectively opening ligand-gated nicotinic acetylcholine (nAChR) ion-channels of nematode muscle to produce depolarization, entry of calcium, contraction and spastic paralysis [5]. The nAChR is composed of 5 transmembrane subunits which surround the cation permeable channel pore. The importance of nAChRs has increased recently because of the introduction of novel cholinergic anthelmintics including: the agonist tribendimidine, which has been approved for human use in China [6]; the allosteric modulator monepantel [7], [8]; and the antagonist derquantel [9]. Tribendimidine is a symmetrical diamidine derivative of amidantel effective against *Ascaris*, hookworms, *Strongyloides stercoralis*, trematodes and tapeworms [10].

Molecular experiments using the free-living model nematode *C. elegans* suggest that tribendimidine acts as a cholinergic agonist like levamisole and pyrantel [11]. Derquantel is a 2-desoxo derivative of paraherquamide in the spiroindole drug class effective against various species of parasitic nematodes, particularly the trichostrongylid nematodes [12]. Derquantel is a selective competitive antagonist of nematode muscle nAChRs especially on the *B*-subtype nAChR from *Ascaris suum* [13]. In contrast to levamisole and pyrantel sensitive-nAChRs [14], [15], [16], the molecular basis for the action of tribendimidine and derquantel in parasitic nematodes are still not known. The chemical structures of the cholinergic anthelmintics are different and resistance to one of the cholinergic anthelmintics sometimes does not give rise to cross-resistance to other cholinergic anthelmintics [17]. These observations imply that the nAChR subtypes in nematode parasites may represent distinct pharmacological targets sensitive to different cholinergic anthelmintics. Therefore, in the present work, we have investigated mechanistic explanations for the variability and diversity of the cholinergic receptors of parasitic nematodes and their therapeutic significance.

The model nematode, *C. elegans*, possesses two muscle nAChR types: one sensitive to levamisole and one sensitive to nicotine [18]. The levamisole AChR type is composed of the five subunits, Cel-UNC-29, Cel-UNC-38, Cel-UNC-63, Cel-LEV-1 and Cel-LEV-8 [18], [19], [20], [21], [22]. The nicotine-AChR type is a homopentamer composed of Cel-ACR-16 subunits [23]. In *Ascaris suum*, there are three pharmacologically separate nAChR types on the body muscle: the *N*-type that is preferentially activated by nicotine; the *L*-type that is preferentially activated by levamisole and; the *B*-type that is preferentially activated by buphenium [13]. In *Oesophagostomum dentatum* there are four muscle nAChRs which are defined by their single-channel conductances: G 25 pS, G 35 pS, G 40 pS and G 45 pS. The

G 35 pS receptor type of *O. dentatum* is reduced in a levamisole-resistant isolate [24] but not in a pyrantel-resistant isolate [25]. Interestingly, the G 35 pS type of *O. dentatum* has a similar channel conductance to the *L*-type from the distantly related species, *A. suum* [13].

However, the precise molecular mechanisms of levamisole and pyrantel resistance occurring in *O. dentatum* isolates are still unknown because the *O. dentatum* genes encoding muscle nAChR subunits have not yet been identified. In order to determine a mechanistic explanation for the variability and pharmacological diversity of the muscle nAChR types in parasitic nematodes like *Oesophagostomum dentatum*, we took advantage of the *Xenopus* oocyte expression system [14], [26], [27].

In this study our first objective was to clone the four putative subunit genes *Ode-unc-38*, *Ode-unc-29*, *Ode-unc-63* and *Ode-acr-8*, which are homologues of the *C. elegans* levamisole muscle receptor genes [15], [16] and express them in *Xenopus laevis* oocytes to recapitulate the levamisole-sensitive AChRs of *O. dentatum*. In a previous study on *H. contortus* which is closely related to *O. dentatum*, we have reported that co-expression of four AChR subunits (Hco-UNC-38, Hco-UNC-63, Hco-UNC-29 and Hco-ACR-8) in *Xenopus* oocytes resulted in the robust expression of a levamisole sensitive nAChR [16]. In the present work we have identified and cloned the homologs of the corresponding genes in *O. dentatum* (*Ode-unc-38*, *Ode-unc-63*, *Ode-unc-29* and *Ode-acr8*) and express them in *Xenopus* oocytes. Of particular note is the evidence that these receptor subtypes are pharmacological targets of the new anthelmintic tribendimidine. Moreover, we demonstrate that the nAChR reconstituted with all four subunits is more sensitive to levamisole than pyrantel and has a single channel conductance of 35 pS, corresponding to the *L*-type previously observed *in vivo* in *O. dentatum* and *A. suum*. Another receptor type, made of 3

subunits, was more sensitive to pyrantel and the new anthelmintic derquantel had a selective effect against receptors activated by pyrantel rather than levamisole, providing the first insight of its molecular target composition in any parasitic nematode. These results provide a basis for understanding the greater diversity of the nAChR repertoire from parasitic nematodes and for deciphering the physiological role of nAChR subtypes targeted by distinct cholinergic anthelmintics. This study will facilitate more rational use of cholinergic agonists/antagonists for the sustainable control of parasitic nematodes impacting both human and animal health.

A4.0 Results

A4.1 Identification of *unc-29*, *acr-8*, *unc-38* and *unc-63* homologues from *O. dentatum* and phylogenetic comparison to related nematode species

Taking advantage of the phylogenetic closeness of *O. dentatum*, *C. elegans* and *H. contortus* in clade V of the nematode phylum, we used a candidate gene approach to identify full-length subunit cDNAs from *O. dentatum* of *unc-63*, *unc-29* and *acr-8* homologues. The previously available *O. dentatum* *unc-38*-like full-length cDNA sequence (Accession number GU256648) allowed the rapid cloning of the *Ode-unc-38* subunit cDNA. The UNC-38 and UNC-63 subunits being closely related in the UNC-38 “core” group [28], multi-alignment of *unc-63* and *unc-38* cDNA sequences from different nematode species allowed the design of degenerate primers that were able to specifically amplify the *unc-63* homologue from *O. dentatum*. To identify the *unc-29* homologue from *O. dentatum*, degenerate primers from the *H. contortus* and *C. elegans* *unc-29* sequences were used to amplify a partial 288 bp cDNA sequence, providing specific information to get the full-length cDNA by RACE-PCR standard procedures. To identify the *acr-8* homologue from *O. dentatum*, a partial cDNA of

861 bp was cloned using primers from *H. contortus* *acr-8*, allowing subsequent identification of the full-length cDNA encoding Ode-ACR-8 subunit. The four *O. dentatum* subunit transcripts were trans-spliced at their 5' end with the splice leader 1 (SL1). The predicted nAChR proteins displayed typical features of LGIC subunits including a secretion signal peptide, a cys-loop domain consisting of 2 cysteines separated by 13 amino acid residues and four transmembrane domains (TM1-4) (supplemental figure S1A–D). The Ode-UNC-38, Ode-UNC-63 and Ode-ACR-8 subunits contained in their N-terminal part the Yx(x)CC motif characteristic of the α -type subunits whereas the Ode-UNC-29 subunit sequence lacked these vicinal di-cysteines. The different nAChR subunit sequences, accession numbers, characteristics and closest levamisole subunit homologues of *C. elegans* and *H. contortus* are presented in Table 1. Alignment of the deduced amino acid sequences of the four *O. dentatum* nAChR subunits revealed 66 to 92% identity with their respective homologues from *C. elegans* and *H. contortus* (Table 1 and supplemental Fig. S1A–D), indicating that even in closely related species some interspecies polymorphisms could impact the nAChR subunit composition and pharmacological properties. The phylogenies shown in Fig. 1 (maximum likelihood tree) and supplemental Fig. S2 (distance tree) identify a single ortholog each for the *unc-38*, *unc-63*, *acr-8*, and *unc-29* subunits in *O. dentatum*. The branching topology is consistent, in each case, with a taxonomic position of *O. dentatum* with strongylida and outside the trichstrongyloidea [29]. Interestingly, this topology places the speciation of *O. dentatum* significantly before the previously identified trichostrongylid specific *unc-29* diversification event [15]. As such, these duplications cannot be shared with *O. dentatum*, although it is not possible to rule out other independent *unc-29* duplication events in *O. dentatum*. Clearly, further studies that include analysis of *unc-29* homolog

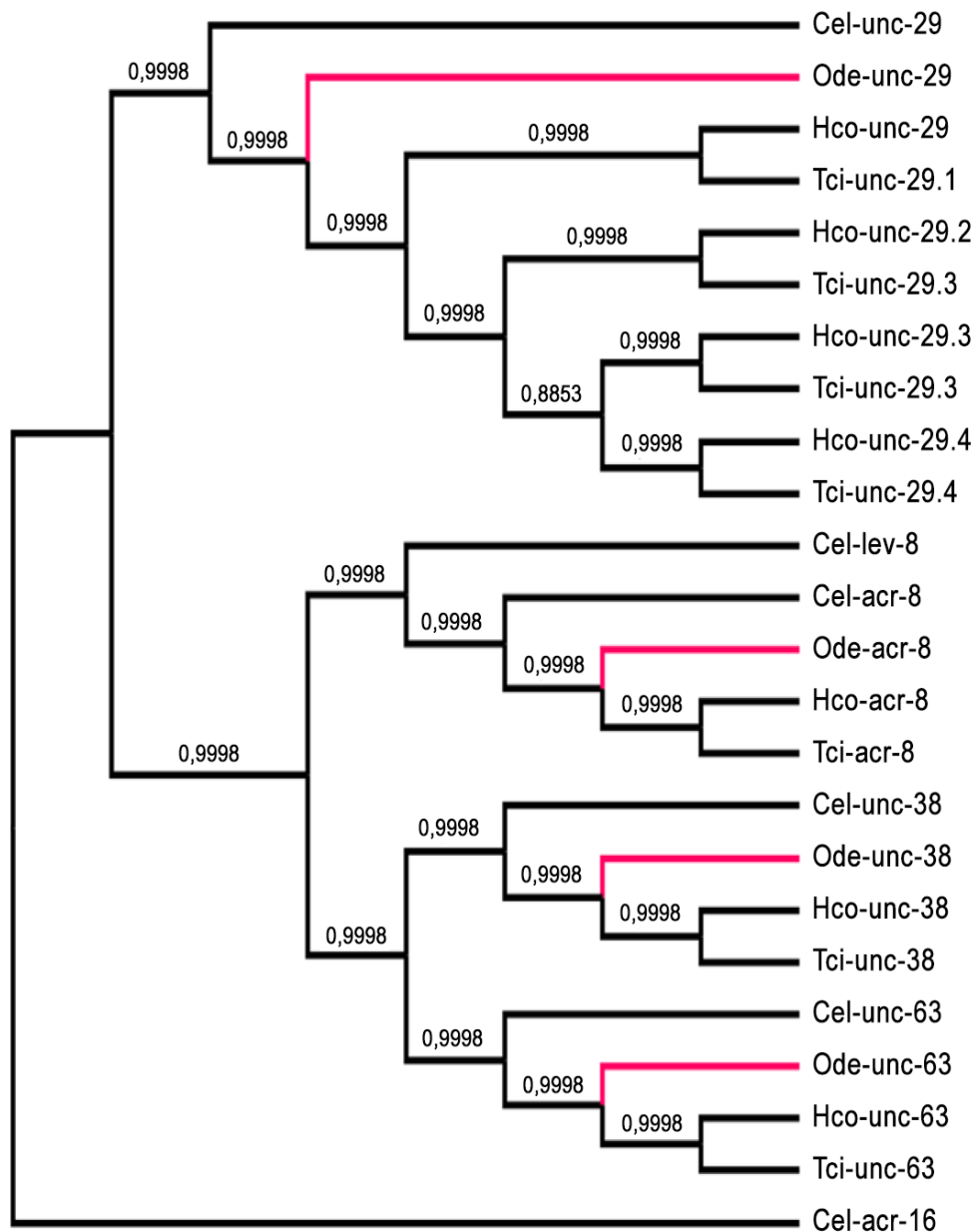


Figure 1. Maximum likelihood tree showing relationships of acetylcholine receptor (nAChR) subunit cDNA sequences in *Oesophagostomum dentatum* (Ode, highlighted in red), *Caenorhabditis elegans* (Cel), *Haemonchus contortus* (Hco) and *Teladorsagia circumcincta* (Tci). The *C. elegans* *acr-16* nAChR subunit sequence was used as an outgroup. Branch support was evaluated using the chi2 option of PhyML and values more than 0.9 were considered reliable.

Table 1. Comparison of *O. dentatum* AChR subunits with the homologs of *C. elegans* and *H. contortus*.

Gene name	Accession number	Full-length cDNA size (bp)	Deduced protein seq. length	% nucleotide identity		% amino acid identity/similarity	
				<i>C. elegans</i>	<i>H. contortus</i>	<i>C. elegans</i>	<i>H. contortus</i>
<i>Ode-unc-29</i>	JX429919	1637	497	66	73	78/87	85/90
<i>Ode-unc-38^a</i>	JX429920	1681	507	66	70	72/77	83/87
<i>Ode-unc-63</i>	HQ162136	2265	507	67	80	77/84	92/95
<i>Ode-acr-8</i>	JX429921	1851	538	62	77	66/93	80/97

^aSimilar to complete cDNA sequence GU256648.
doi:10.1371/journal.ppat.1003870.t001

sequences in a wide range of nematode species are required to understand the evolutionary impact of such duplication events.

A4.2 Expression of *Ode(29-63)*, the *Pyr-nAChR* and stoichiometry effect on pharmacological properties

Our investigation of *O. dentatum* receptor expression determined the minimum number of subunits that is required to reconstitute a functional muscle nAChR. Previous expression studies of *C. elegans* and *H. contortus* functional nAChRs in *Xenopus* oocytes required the use of ancillary proteins [16], [26]. Hence, the *H. contortus* ancillary factors *Hco-ric-3*, *Hco-unc-50* and *Hco-unc-74* were also injected to facilitate the expression of *O. dentatum* functional receptors in *Xenopus* oocytes. In control experiments we observed that oocytes injected with ancillary protein cRNAs did not produce current responses to 100 μ M acetylcholine or other cholinergic anthelmintics. We then injected different combinations of pairs of cRNAs (1:1) of: *Ode-unc-29*, *Ode-unc-38*, *Ode-unc-63* and *Ode-acr-8*.

Only those oocytes injected with 1:1 *Ode-unc29:Ode-unc-63* cRNA, regularly produced currents of >50 nA in response to 100 μ M acetylcholine or cholinergic anthelmintics, indicating that the two subunits could form functional receptors (Fig. 2). We

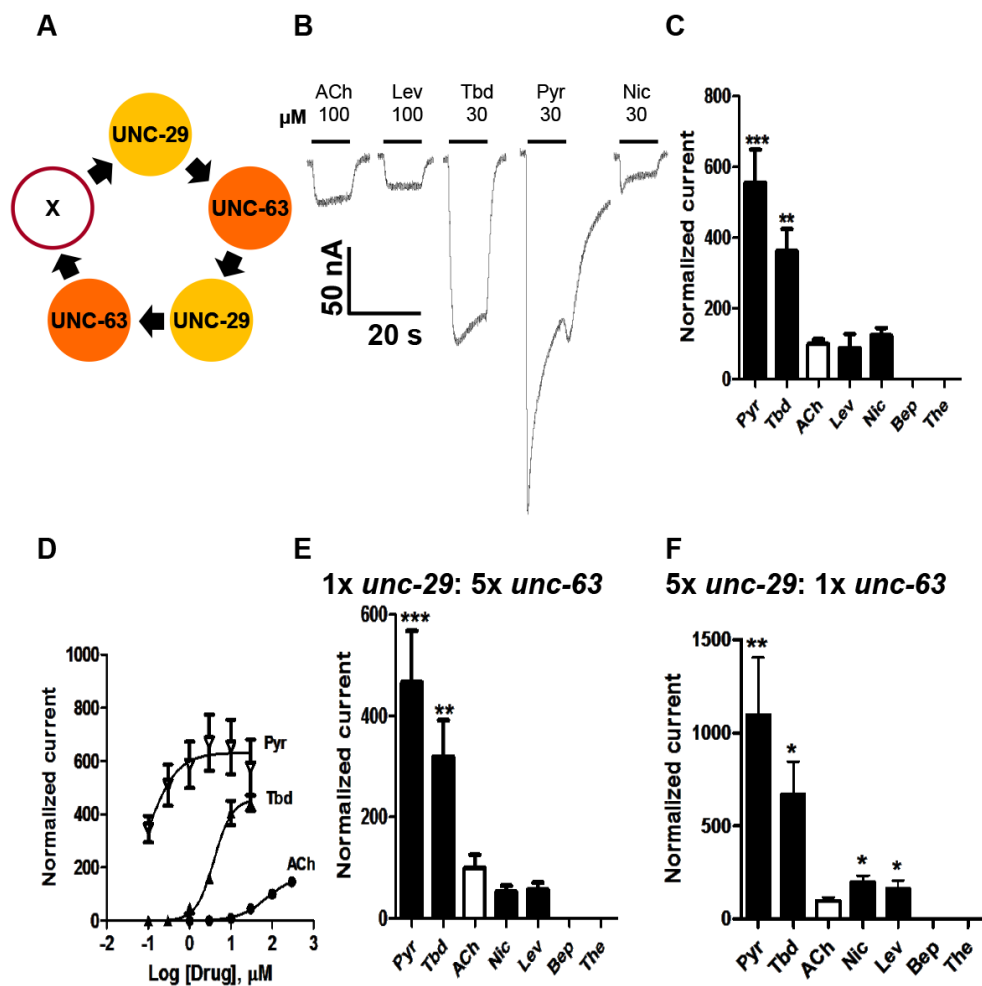


Figure 2. Voltage-clamp of oocytes injected with *O. dentatum* *Ode-unc-29* and *Ode-unc-63* nAChR subunits. (A) Diagram of possible subunit arrangements of *Ode-unc-29* and *Ode-unc-63*. X represents either UNC-63 or UNC-29 subunit. PyR, pyrantel; Tbd, tribendimidine, ACh, acetylcholine; Nic, nicotine; Bep, buprenorphine; The, thenium. (B) Representative traces showing the inward currents in oocytes injected with 1:1 *Ode-unc-29* and *Ode-unc-63*. (C) Bar chart (mean \pm se) of agonists-elicited currents in the *Ode-(29-63)* Pyr-nAChR, (paired *t*-test, ** $p < 0.01$, *** $p < 0.001$). All agonist responses have been normalized to the average 100 μ M ACh currents. (D) Dose-response relationships for Pyr (inverted Δ , $n=6$), Tbd (\blacktriangle , $n=5$) and ACh (\bullet , $n=6$) in the *Ode-(29-63)* Pyr-nAChR, (n =number of oocytes). (E) Bar chart (mean \pm se) of normalized currents elicited by different agonists in 1:5 *Ode-unc-29:Ode-unc-63* injected oocytes. Currents have been normalized to and compared with 100 μ M ACh currents (paired *t*-test, ** $p < 0.01$, *** $p < 0.001$). (F) Bar chart (mean \pm se) of normalized currents elicited by different agonists in oocytes injected with 5:1 *Ode-unc-29:Ode-unc-63*. Currents normalized to and compared with 100 μ M ACh currents (paired *t*-test, * $p < 0.05$, ** $p < 0.01$).

found that no other paired combination produced currents. Without both subunits in any of our subsequent injected mixes, no functional receptor could be reconstituted, demonstrating that Ode-UNC-29 and Ode-UNC-63 are essential *O. dentatum* levamisole receptor subunits. Injection of each of these subunits alone did not form receptors that responded to the agonists we tested, demonstrating that these subunits do not form homopentamers.

More than 75% of injected oocytes responded to acetylcholine. For our standard test concentrations, except for 100 μM acetylcholine and 100 μM levamisole, we used 30 μM drug concentrations of different important anthelmintics to limit effects of open-channel block. Interestingly, the novel anthelmintic tribendimidine elicited currents when perfused on oocytes expressing Ode-UNC-29 and Ode-UNC-63. The potency series of the agonists (anthelmintics) based on the normalized currents, Fig. 2C, was: 30 μM pyrantel >30 μM tribendimidine >30 μM nicotine \approx 100 μM levamisole \approx 100 μM acetylcholine. Neither 30 μM buphenium, nor 30 μM thenium, were active. Even at 30 μM , pyrantel produced currents bigger than 100 μM acetylcholine (Fig. 2C). We refer to this receptor type as: *Ode(29–63)*, or the *Pyr-nAChR*.

We determined the concentration current-response plot for pyrantel, tribendimidine and acetylcholine, Fig. 2D for *Ode(29–63)*. The EC_{50} values for pyrantel and tribendimidine were less than the EC_{50} for acetylcholine but the I_{max} values were larger for pyrantel and tribendimidine (Table 2). Thus the anthelmintics pyrantel and tribendimidine were much more potent and produced a greater maximum response than the natural ligand, acetylcholine and levamisole on this type of receptor. To date, this result represents the first characterization of a nematode tribendimidine-sensitive nAChR.

Table 2. Properties of the four main receptor subtypes obtained from dose-response relationships.

		<i>Ode(29-63)</i>	<i>Ode(29-63-38)</i>	<i>Ode(29-63-8)</i>	<i>Ode(29-63-8-38)</i>
Acetylcholine	EC_{50}	72.4±13.3	13.2±0.8	3.5±0.2	4.2±0.2
	I_{max}	100.0	100.0	100.0	100.0
	nH	1.28±0.31	1.10±0.044	1.18±0.055	0.77±0.06
Levamisole	EC_{50}	*	*	2.2±0.2	3.1±2.2
	I_{max}	*	*	73.0±2.4	119.0±3.7
	nH	*	*	1.36±0.18	0.87±0.10
Pyrantel	EC_{50}	0.09±0.005	0.4±0.1	ND	ND
	I_{max}	632.0±55.8	172.0±10.4	ND	ND
	nH	1.20±0.95	0.88±0.18	ND	ND
Tribendimidine	EC_{50}	3.9±0.8	2.2±0.5	0.8±0.1	0.3±0.6
	I_{max}	458.0±28.8	155.0±8.8	75.0±6.2	69.0±5.0
	nH	1.98±0.46	1.17±0.18	0.94±0.22	0.50±0.09

ND: Not determined.

*Dose-response measurements not possible due to the small size of currents elicited by the agonists on these receptor subtypes.

doi:10.1371/journal.ppat.1003870.t002

We were interested to see if there was evidence of pharmacological changes associated with variation in stoichiometry of the *Ode(29-63)* receptor. When we injected a 1:5 ratio of *Ode-unc-29:Ode-unc-63* cRNA with the same 1:1:1 ratio of ancillary proteins, the mean amplitudes of the pyrantel and tribendimidine currents were significantly increased (pyrantel: 6-fold increase from a mean of 104 nA to 653 nA, $p<0.01$; tribendimidine: 7-fold increase from a mean of 68 nA to a mean of 447 nA, $p<0.01$). The large increase in the size of the currents with increased *Ode-unc-63* cRNA suggests that increased UNC-63 favors expression of receptors with a stoichiometry of (UNC-63)₃: (UNC-29)₂ [14]. Also, when we injected 5:1 *Ode-29:Ode-63* cRNA, the normalized currents of 30 μ M nicotine and 100 μ M levamisole became significantly bigger than 100 μ M acetylcholine (Fig. 2C, E & F) suggesting increased expression of (UNC-63)₂: (UNC-29)₃. The increase in currents with the 1:5 and 5:1 *Ode-29:Ode-63* cRNA was not due to variability in currents with different

batches of oocytes because we observed the same effects when we injected 1:1, 1:5 and 5:1 *Ode-29:Ode-63* cRNA in the same batch of oocytes.

A4.3 Expression of *Ode(29-63-38)*, the *Pyr/Tbd-nAChR*

We subsequently added *unc-38* and injected *Ode-unc-29:Ode-unc-63:Ode-unc-38* cRNAs in the ratio 1:1:1, along with the three *H. contortus* ancillary factors. Oocytes injected with this mix responded with larger currents of around 250 nA to 100 μ M acetylcholine and to all the other agonists tested except bephenium and thenium (Fig. 3A–D). Pyrantel was the most potent agonist but with this receptor type, pyrantel and tribendimidine produced the same amplitude of current at 30 μ M. We termed this receptor the *Ode(29–63–38)*, or the *Pyr/Tbd-nAChR*. The potency series of the agonists based on the normalized currents was 30 μ M pyrantel \approx 30 μ M tribendimidine $>$ 100 μ M acetylcholine $>$ 30 μ M nicotine \approx 100 μ M levamisole (Fig. 3 C). The dose-response curves for pyrantel, tribendimidine and acetylcholine are shown in Fig. 3D. The EC_{50} for pyrantel was less than the EC_{50} for tribendimidine and acetylcholine (Table 2). The Hill slopes for tribendimidine and acetylcholine were both close to 1.0 (Table 2), showing little co-operativity between agonist concentration and response. Again interestingly, the two anthelmintics, pyrantel and tribendimidine were more potent than the natural ligand and the anthelmintic levamisole, but with this receptor type, the currents were larger than with the *Ode(29–63)* receptor.

A4.4 Expression of *Ode(29-63-8)*, the *ACh-nAChR*

When we added *Ode-acr-8* and injected *Ode-unc-29:Ode-unc-63:Ode-acr-8* cRNA in the ratio 1:1:1 along with the three *H. contortus* ancillary factors into the oocytes, we observed even bigger receptor responses to 100 μ M acetylcholine. We also observed responses to all the agonists we tested, including bephenium and thenium (Fig. 3E–H), which

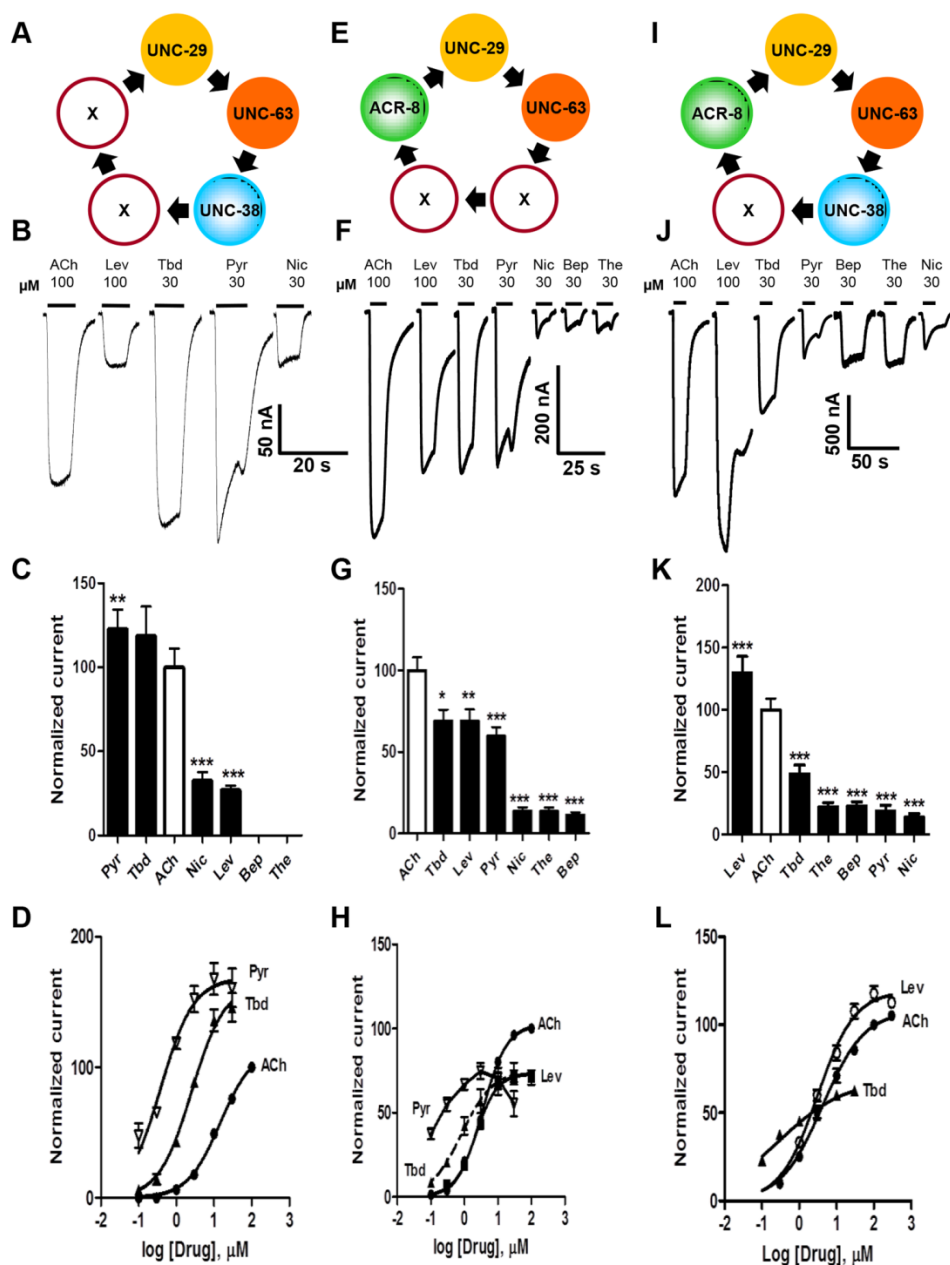


Figure 3. Voltage-clamp of oocytes injected with different combinations of the four *O. dentatum* nAChR subunits. (A) Depiction of a possible arrangement of *O. dentatum* UNC-29, UNC-63 & UNC-38. 'X' represents any of the subunits. Pyr, pyrantel; Tbd, tribendimidine, ACh, acetylcholine; Nic, nicotine; Bep, buprenorphine; The, thenium. (B) Representative traces of inward currents elicited by the various agonists in oocytes injected with 1:1:1 *Ode-unc-29:Ode-unc-63:Ode-unc-38*. Pyr & Tbd were the most potent agonists on this receptor subtype. (C) Bar chart (mean \pm se) of currents elicited by the different agonists in the *Ode-(29 - 38 - 63)* Pyr/Tbd-nAChR (paired *t*-test, ** $p < 0.01$, *** $p < 0.001$). (D) Dose-response of normalized currents vs log concentration for Pyr (inverted Δ , $n=6$), Tbd (\blacktriangle , $n=6$) and ACh (\bullet , $n=5$) in the Pyr/Tbd-nAChR. (E) Diagrammatic representation of the three subunits, *unc-29*,

unc-63 and *acr-8* injected into oocytes. 'X' could be any of the three subunits. (F) Representative traces of inward currents produced by the different agonists in oocytes injected with 1:1:1 *Ode-unc-29:Ode-unc-63:Ode-acr-8*. (G) Bar chart (mean \pm se) of normalized currents elicited by the different agonists in the *Ode(29-63-8)* receptor subtype. All currents normalized to 100 μ M ACh currents; comparisons made with the ACh currents (*paired t-test*, * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$). (H) Dose-response plot of normalized currents vs log. Concentration of Pyr (inverted Δ , $n=6$), Tbd (\blacktriangle , $n=6$), ACh (\bullet , $n=6$) and Lev (\blacksquare , $n=6$). (I) Representation of a possible arrangement of the four *O. dentatum* subunits injected into *Xenopus* oocytes. (J) Representative traces of inward currents elicited by the different agonists on the *Ode(29-63-38-8)* or Lev-nAChR. (K) Bar chart (mean \pm se) of normalized currents elicited by the different agonists on the Lev-nAChR subtype. Comparisons were made with 100 μ M ACh currents, which was used for the normalization (*paired t-test*, *** $p < 0.001$). (L) Dose-response plot of normalized currents against log of Tbd (\blacktriangle , $n=6$), ACh (\bullet , $n=18$) and Lev (\circ , $n=5$) concentrations.

suggests that *Ode-acr-8* introduces buphenium and thenium binding sites. 100 μ M acetylcholine produced the largest current responses, always greater than 800 nA and sometimes greater than 1 μ A. We termed this receptor type: *Ode(29-63-8)*, or the ACh-nAChR.

For the *Ode(29-63-8)* receptor, the potency series of the agonists (anthelmintics) based on the normalized currents, was 100 μ M acetylcholine > 30 μ M tribendimidine ≈ 100 μ M levamisole ≈ 30 μ M pyrantel > 30 μ M nicotine ≈ 30 μ M thenium ≈ 30 μ M buphenium (Fig. 3G). Here, the least potent agonists were nicotine, buphenium and thenium with average currents $< 20\%$ of the acetylcholine currents. The dose-response curves (Fig. 3H) show that at the highest concentrations tested, levamisole and tribendimidine current responses were less than that of acetylcholine. Despite this, the EC_{50} values of both tribendimidine and levamisole were lower than acetylcholine on this receptor type. The EC_{50} values are summarized in Table 2. The levels of co-operativity (slope) were similar for these three agonists, but I_{max} for acetylcholine (100.0%) was bigger than I_{max} for tribendimidine (75.0 \pm 6.2%) and levamisole (73.0 \pm 2.4%).

Two characteristic features of the response of the *Ode(29–63–8)* receptor to pyrantel suggest the presence of open-channel block which is more pronounced with *Ode(29–63–8)* than with the other types. Firstly, the maintained application of 30 μM pyrantel produced a response that declined rapidly despite the concentration being maintained, and secondly, on wash-out of pyrantel the response ‘rebounded’ or increased temporally before declining. Pronounced open-channel block with pyrantel has been observed at the single-channel level [30]. Altogether, these results highlight for the first time the reconstitution of a new functional receptor with distinct pharmacological profile made of the UNC-29, UNC-63 and ACR-8 subunits.

A4.5 Expression of *Ode(29-63-8-38)*, the *Lev-nAChR*

Finally, we injected all our subunits in a mix of *Ode-unc-29:Ode-unc-63:Ode-acr-8:Ode-unc-38* cRNA in the ratio 1:1:1:1 along with the three *H. contortus* ancillary factors. These subunits reconstituted a receptor type on which 100 μM levamisole produced the biggest responses of $>1.5 \mu\text{A}$, sometimes reaching $>4.5 \mu\text{A}$, Fig. 3I–L. We termed this receptor type: *Ode(29–63–8–38)* or the *Lev-nAChR*. The potency series of the agonists based on the normalized currents, was 100 μM levamisole $>100 \mu\text{M}$ acetylcholine $>30 \mu\text{M}$ tribendimidine $>30 \mu\text{M}$ thenium $\approx 30 \mu\text{M}$ buphenium $\approx 30 \mu\text{M}$ pyrantel $>30 \mu\text{M}$ nicotine (Fig. 3K). Here, the least potent agonists were thenium, buphenium, pyrantel and nicotine with average currents $<25\%$ of the acetylcholine currents. The EC_{50} for tribendimidine was less than the EC_{50} for levamisole and acetylcholine (Table 2). The dose-response curves were rather shallow with Hill slopes less than one for acetylcholine, levamisole and tribendimidine (Table 2). We have shown that expression of *Ode-UNC-29*, *Ode-UNC-63*, *Ode-ACR-8* and *Ode-UNC-38* produced large currents, and that the receptor, *Ode(29–63–8–38)*, was most

sensitive to levamisole. It is clear from the observations above that each of the four subunits: Ode-UNC-29, Ode-UNC-63, Ode-ACR-8, and Ode-UNC-38 may combine and be adjacent to different subunits as they form different pentameric nAChRs.

A4.6 Antagonistic effects of derquantel

We tested the antagonist effects of derquantel on the levamisole and pyrantel concentration-response plots of *Ode (29-63-38-8)* and *Ode (39-63-38)*, Fig. 4A–D. Recall that levamisole is more potent as an agonist on *Ode(29-63-8-38)* and pyrantel is more potent on *Ode(39-63-38)*. Fig. 4A shows that derquantel behaves like a potent competitive antagonist of levamisole, with 0.1 μM producing a right shift in EC_{50} dose-ratio of 1.7 (the antagonist negative log dissociation constant from the Schild equation, pK_B , was 6.8 ± 0.1). When we tested the antagonist effects of derquantel on *Ode(29-63-8-38)* using pyrantel as the agonist, we saw mixed non-competitive and competitive antagonism: there was a right-shift in the EC_{50} and a reduction to 41% of the maximum response by 0.1 μM derquantel, Fig. 4 B. One explanation for these mixed effects of derquantel is that co-expression of UNC-29, UNC-63, UNC-38, ACR-8 subunits produces a mixture of receptors: mostly *Ode(39-63-38-8)* receptors that are preferentially activated by levamisole and which are competitively antagonized by derquantel and; a smaller number of receptors like *Ode(39-63-38)* that are preferentially activated by pyrantel and antagonized non-competitively by derquantel. To test this further we examined the antagonist effects of derquantel on pyrantel and levamisole activation of *Ode (39-63-38)*. Derquantel antagonized both agonists non-competitively, Fig. 4 C & D. We interpret these observations to suggest that expression of *Ode(39-63-38-8)* receptors can give rise to expression of a smaller number of other receptors

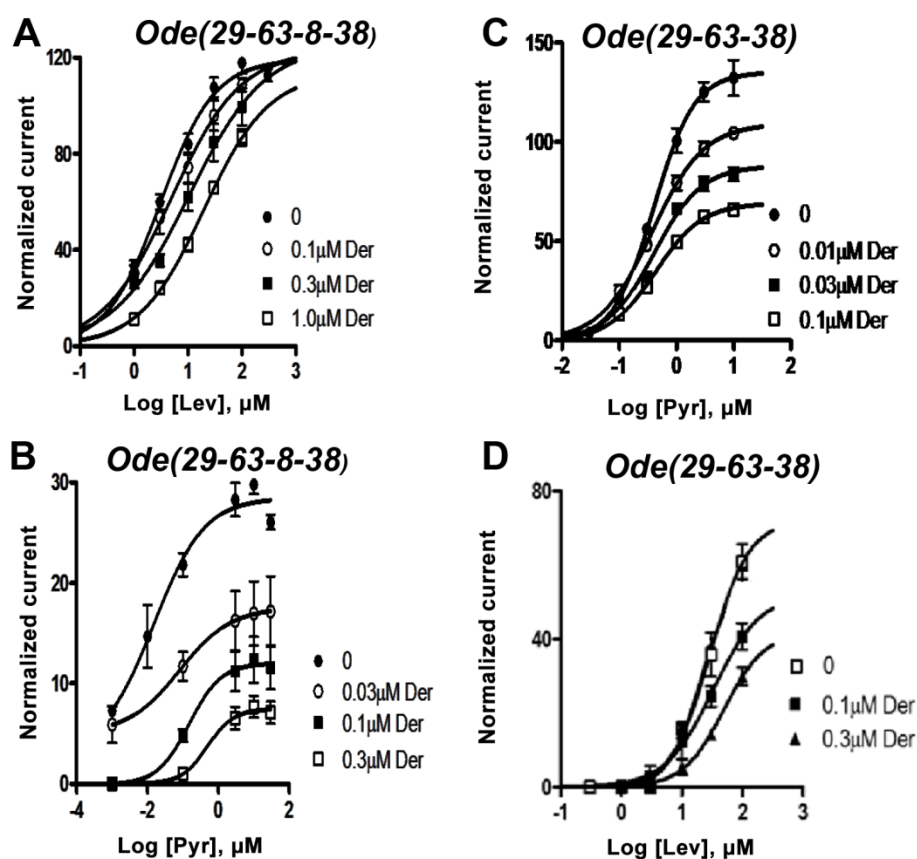


Figure 4. Effects of derquantel on levamisole-activated and pyrantel-activated expressed *Ode(29-63-8-38)*, the *Lev-nAChR*, and on pyrantel-activated and levamisole-activated *Ode(29-63-38)*, the *PyR/Trbd-nAChR* subtypes. Der: derquantel; Lev: levamisole; Pyr: pyrantel. (A) Antagonistic effects of varying derquantel concentrations on levamisole currents of *Ode(29-63-8-38)*. Levamisole evokes supramaximal normalized currents and derquantel competitively inhibited levamisole currents. (B) Derquantel antagonism of pyrantel currents of *Ode(29-63-8-38)*. Here, derquantel produced mixed non-competitively competitive antagonism. Pyrantel did not activate supramaximal currents. (C) Antagonism of pyrantel by derquantel on the *Ode(29-63-38)*, Pyr/Tbd-nAChR. Derquantel is a potent non-competitive antagonist. (D) Derquantel non-competitively antagonized levamisole responses on the *Ode(29-63-38)* receptor.

including *Ode(39-63-38)*. We comment further on these observations in our discussion.

Nonetheless, the competitive and non-competitive antagonism of derquantel when levamisole is used on the two different receptor subtypes, Fig. 4 A & D, illustrates that derquantel effects are subtype selective.

A4.7 The receptor types have different calcium permeabilities

The EC_{50} concentrations of acetylcholine for the different expressed receptors varied (Table 2), suggesting that there are different physiological functions for the different nAChR types. One physiological difference may be the permeability to the second messenger, calcium. To examine this we measured the relative permeability of calcium in *Ode(29-63-38)*, *Ode(29-63-8)* and *Ode(29-63-8-38)*, receptors which produced large enough currents to determine reversal potentials.

We observed two different effects of increasing calcium from 1 mM to 10 mM on the acetylcholine currents. One effect was potentiation of the current amplitudes, an effect that was voltage-dependent (Fig. 5A, B & C). The voltage-dependent increases in acetylcholine currents was prominent in *Ode(29-63-8-38)*, and less in the other two receptor types. The potentiating effect of calcium on the acetylcholine currents indicates the presence of positive allosteric binding sites on one or more subunits of the pentameric nAChR [31]. The second effect was a positive shift to the right of the current-voltage plot indicating that the channels are permeable to calcium [32]. A shift in reversal potential of 1.7 mV was recorded for the *Ode(29-63-8)* (Fig. 5A). Using the Goldman Hodgkin Katz constant field equation (Text S1 Legend), we calculated this change in reversal potential corresponds to a relative calcium permeability ratio, P_{Ca}/P_{Na} of 0.5. The reversal potential shift for *Ode(29-63-38)* was similar, 1.3 mV, also giving a permeability ratio P_{Ca}/P_{Na} of 0.4 (Fig. 5B). For *Ode(29-63-8-38)*, the shift was 16.0 mV (Fig. 5C), corresponding to a calcium permeability ratio, P_{Ca}/P_{Na} , of 10.3. The *Ode(29-63-8-38)* receptor, was therefore much more permeable to extracellular calcium and positively allosterically [31] modulated by extracellular calcium than the other two receptor types, a physiologically significant observation.

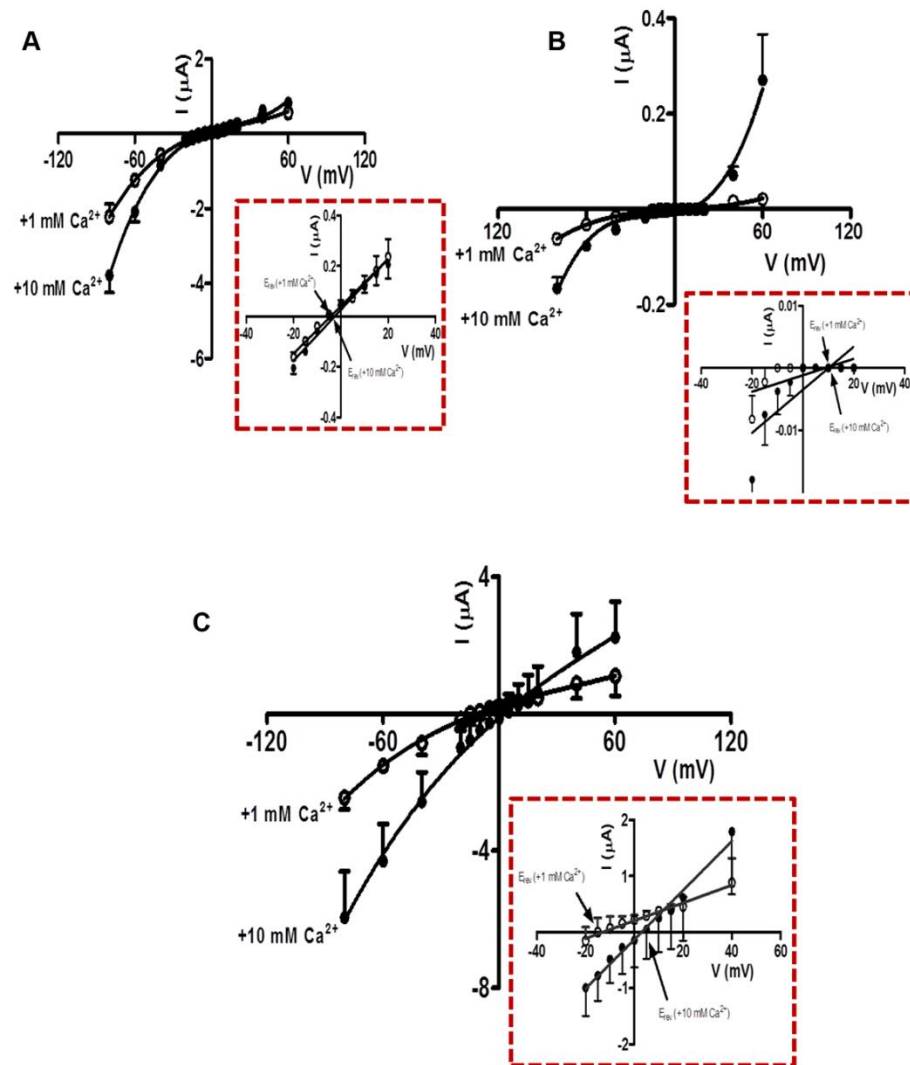


Figure 5. Ca^{2+} permeability of the *O. dentatum* receptor subtypes with large ACh currents. (A) Current-Voltage plot for oocytes injected with *Ode(29-63-8)*, showing the change in current with voltage in 1 mM and 10 mM Ca^{2+} recording solutions. *Insert*: Magnified view of current-voltage plot from -20 mV to $+40$ mV showing the E_{rev} in 1 mM and 10 mM extracellular Ca^{2+} . (B) Current-Voltage plot for oocytes injected with *Ode(29-63-38)* showing the current changes in 1 mM and 10 mM Ca^{2+} recording solution under different voltages. *Insert*: Magnified view of current-voltage plot from -20 mV to $+40$ mV showing the E_{rev} in 1 mM and 10 mM extracellular Ca^{2+} . (C) Current-Voltage plot for oocytes injected with *Ode(29-63-38-8)* in 1 mM and 10 mM Ca^{2+} recording solutions. *Insert*: Magnified view of current-voltage plot from -20 mV to $+40$ mV showing the E_{rev} in 1 mM and 10 mM extracellular Ca^{2+} . The calcium permeability was calculated using the GHK equation (Text S1 Legend).

A4.8 *Ode(29-63-8-38)*, *Lev-nAChR* channels have a mean conductance of 35 pS

Single-channel studies in *Oesophagostomum dentatum* body muscle have demonstrated the presence of different nAChR types with conductances of 25, 35, 40 and 45 pS, showing the presence of four or more receptor types. We have shown in experiments here, that combinations of four nAChR subunits from this parasite can produce four pharmacologically different receptor types. We found that the expressed *Ode(29-63-38-8)* *Lev-nAChR* type was most sensitive to levamisole and had a high permeability to calcium and hypothesized that this type may be the G35 type. Accordingly we investigated the single-channel properties of this type under patch-clamp using 10 μ M levamisole as the agonist. In control oocytes injected with only the ancillary proteins, we recorded no nAChR-like channel currents in 4 oocytes. We found however, that in patches from oocytes expressing the *Ode(29-63-8-38)* type, that more than 90% of patches contained active, recognizable nAChR channels with one main conductance level. Fig. 6A shows representative channel currents from one of these patches and its current-voltage plots which had a conductance of 36.6 ± 0.5 pS (mean \pm SE). The mean conductance of channel from patches made from five different oocytes was 35.1 ± 2.4 pS. We did not test the effects of different cholinergic anthelmintics on channel conductance. The reversal potentials of all plots were close to 0 mV, an indication that the channel was nonselective and permeable to Cs^+ (reversal potential of 0 mV).

We measured the mean open times, τ , at the different potentials and observed values of 2.4 ± 0.4 ms at +100 mV and 2.9 ± 0.5 ms at -100 mV (Fig. 6B). The mean open times are comparable to the mean open times recorded *in vivo* in *O. dentatum* with the same concentration of levamisole.

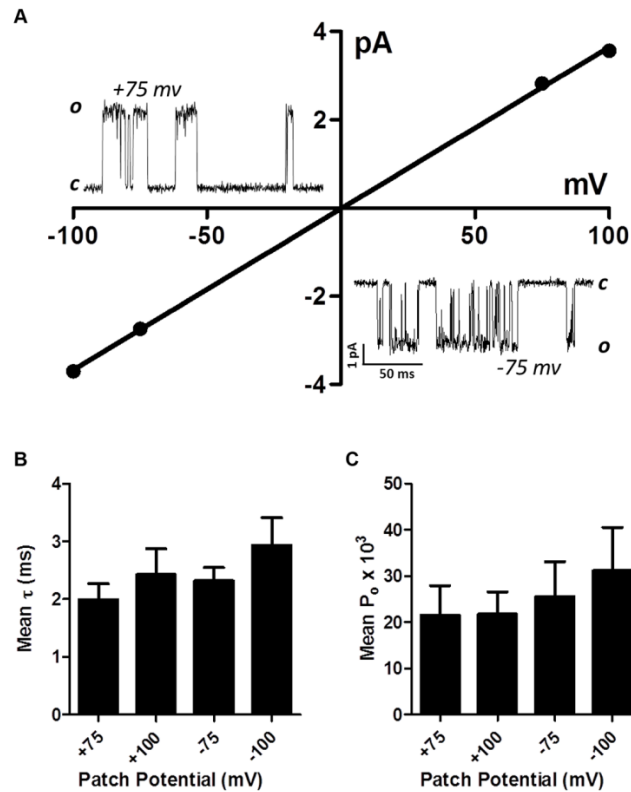


Figure 6. Single-channel properties of the *Lev-nAChR* subtype. (A) Representative current-voltage plot from oocyte-attached patch with 10 μ M levamisole. Inserts are representative channel openings at +75 mV and -75 mV membrane potentials. Even with 10 μ M levamisole, we sometimes observed ‘flickering’ channel block events; note the ‘flickering’ channel block shown by openings at -75 mV. (B) Bar chart (mean \pm se) of the mean open times (τ) at the different patch potentials. (C) Bar chart (mean \pm se) of the probability of channel opening, P_o , at the different patch potentials.

A4.9 The three ancillary proteins affect expression levels

We tested the requirements for the ancillary proteins, RIC-3, UNC-50 and UNC-74, by removing each of the ancillary proteins in turn when expressing the *Ode(29-63-8-38)* receptor. We found that the requirement for all the ancillary proteins was not essential and that each protein, when absent reduced currents produced by the expressed receptors (Fig. S3). When all the ancillary factors were removed, we observed no measurable currents in response to acetylcholine. Here, we have observed that unlike in *C. elegans*, robust

functional *O. dentatum* receptors can be reconstituted when one of these three ancillary factors is omitted and that the ancillary proteins can affect the balance of the pharmacology of the receptors expressed (Fig. S3)

A5.0 Discussion

A5.1 The origin of diverse nAChR types in parasitic nematodes

We have shown previously in the parasitic nematodes, *O. dentatum* [24] and *A. suum* [13], that there are diverse types of nAChR on body muscle of parasitic nematodes which may be activated by cholinergic anthelmintics. In *A. suum* we found that these types have different sensitivities to different cholinergic anthelmintics like levamisole and derquantel. In *O. dentatum* there are four types that can be distinguished by their single-channel conductance, with reduced numbers of the G 35 pS type in levamisole resistant isolates. Here we explored and tested the hypothesis that the receptor subtypes may be due to different combinations of subunits. We found that four main pharmacology types could be produced and separated by expressing in *Xenopus* oocytes different combinations of the α -subunits Ode-UNC-38, Ode-UNC-63 and Ode-ACR-8 together with the non- α subunit Ode-UNC-29. The types could be separated on the basis of their EC_{50} and amplitude of response to the natural ligand acetylcholine, permeability to calcium and anthelmintic profiles (rank order potency and/or concentration-response relationships). We have not tested the possibility that post-translational modification may serve as an additional mechanism to produce different receptor types.

A5.2 The different AChR types have different functional properties

Ode(29-63-38-8), *Ode(29-63-8)* and *Ode(29-63-38)* produce the largest current responses to acetylcholine. On the basis of the larger size of the currents responses to

acetylcholine and the smaller currents of *Ode(29–63)* mixture, we speculate that the other three receptor types have more important physiological roles in the worm. *Ode(29–63–38)* was the most sensitive type to acetylcholine with an EC_{50} of $3.5 \pm 0.2 \mu\text{M}$ but it had a lower calcium permeability, P_{Ca}/P_{Na} of 0.5, than *Ode(29–63–38–8)* that had an acetylcholine EC_{50} of $4.2 \pm 0.2 \mu\text{M}$. However, *Ode(29–63–38–8)* had greater responses to levamisole and a calcium permeability, P_{Ca}/P_{Na} of 10.4. Thus the addition of ACR-8 is responsible for increasing the calcium permeability and the response to levamisole. Since the *Ode(29–63–38–8)* receptor produced the biggest current to levamisole and had a single-channel conductance of $35.1 \pm 2.4 \text{ pS}$, close to the *in vivo* G 35 pS type that is reduced with levamisole resistance, we suggest that *Ode(29–63–38–8)* subunit combinations give rise to the *in vivo* G 35 pS channel in *O. dentatum*. There may also be pH regulatory effects on channel activity of *Ode(29–63–38–8)*. The presence of histidine (pK_a 6.0) in the ACR-8 (Fig. S1D, position 282) channel pore entrance on TM2 region is predicted to produce a pH sensitive channel that is less permeable to cations and calcium at pH 6.0 than 7.5. ACR-8 may provide a functional mechanism of reducing depolarization and muscle contraction at low pHs that can occur in an anaerobic environment. It would also have been of interest to look at the single-channel properties of the other receptor types when activated with levamisole to compare with the *in vivo* channel properties. Unfortunately, the smaller size of the levamisole currents due to the presence of fewer receptors on the oocytes, made single-channel recording less tractable than for *Ode(29–63–38–8)*.

A5.3 Different nAChR types and sensitivities to levamisole, pyrantel, tribendimidine and derquantel

The different nAChR types have different sensitivities to cholinergic anthelmintics: for example *Ode(29-63-38-8)* produces the biggest response to levamisole, while *Ode(29-63-38)* produces the biggest response to pyrantel. If these two types of receptors exist together in the nematode parasite, our observations suggest that combinations of levamisole and pyrantel will produce a bigger therapeutic response than either of the two anthelmintics given alone and that combination therapy may be advantageous. However, very few reports of combining levamisole and pyrantel for treatment are available. In one report [33] using *T. muris* infected mice, combination of levamisole and pyrantel treatment produced antagonism but these authors did not determine the EC_{50} dose for pyrantel pamoate and used a very high dose of 300 mg/Kg dose, above the normal therapeutic dose. At this level we anticipate the presence of open-channel block limiting the effects of the therapeutic combination [32].

We tested the effects of derquantel on the *Ode(29-63-38-8)*, the *Lev-nAChR*, and on *Ode(29-63-38)*, the *Pyr/Trbd-nAChR*. Interestingly, the mode of action of derquantel varied (competitive or non-competitive) with the receptor subtypes when activated by the same agonist, levamisole. The difference in the mode of action will relate to the preferred non-equivalent binding sites of derquantel, of levamisole and of pyrantel on the receptor subtypes. The competitive antagonism of levamisole suggests a common binding site for derquantel on the *Ode(29-63-38-8)* receptor; the non-competitive antagonism of pyrantel and levamisole by derquantel on *Ode(29-63-38)* suggests negative allosteric modulation and different non-equivalent binding sites for derquantel and the agonists, levamisole and derquantel, on this receptor. Interestingly the loss of the ACR-8 subunit, which reduces the

levamisole sensitivity of the *Ode(29-63-38)* receptor, changes the antagonism of levamisole from competitive to non-competitive. Thus ACR-8 may contribute to a high affinity binding site of levamisole and a competitive site of derquantel. When ACR-8 was not present derquantel behaved non-competitively. We have interpreted the mixed non-competitive competitive antagonism of pyrantel by derquantel on *Ode(29-63-38-8)* to be due to a mixed expression of receptor subtypes with mostly the levamisole sensitive *Ode(29-63-38-8)* receptors being present and a smaller proportion of other receptors like *Ode(29-63-38)* being present. This is certainly possible because, as we have shown, the subunits can and do combine in different ways to form 4 types of receptor. Although less likely, it may be that: 1) expression of *Ode(29-63-38-8)* produces only one receptor type, 2) levamisole and pyrantel bind to separate sites on this receptor, 3) derquantel acts competitively, binding at the levamisole site but; 4) derquantel acts as a negative allosteric modulator when pyrantel binds to its receptor. Further study is required to elucidate details of binding sites on the different receptor types. Despite these possibilities we have seen potent antagonist effects of derquantel on both the *Ode(29-63-38-8)* and the *Ode(29-63-38)* subtypes suggesting that derquantel could still be active against levamisole resistance associated with reduced ACR-8 expression.

We were also interested in the effects of the novel cholinergic anthelmintics tribendimidine [6] and to compare their effect with the other anthelmintics. We found that tribendimidine was a potent cholinergic anthelmintic on the *Ode(29-63-38)*, *Ode(29-63-8)* and *Ode(29-63-38-8)* types. Thus tribendimidine could remain an effective anthelmintic if levamisole resistance in parasites were associated with null mutants or decreased expression of *acr-8* and/or *unc-38*.

A5.4 Regulation of AChR type expression

The different functional properties of the nAChR types indicate that each type may have different physiological roles to play in the parasite and the proportion of the different types present at the membrane surface is likely to be regulated. This regulation could allow changes in calcium permeability, desensitization, receptor location, receptor number and anthelmintic sensitivity. The control is expected to include dynamic physiological processes and developmental process that take place over different time scales. An adaptable and diverse receptor population may allow changes, even during exposure to cholinergic anthelmintics. We know little about these processes, their time-scales and how they may be involved in anthelmintic resistance in parasitic nematodes but some information is available from *C. elegans*.

In *C. elegans* there are a number of genes involved in processing and assembly of the subunits of AChR; specific examples include *Cel-ric-3*, *Cel-unc-74* and *Cel-unc-50* [34], [35], [36]. *Cel-RIC-3* is a small transmembrane protein, which is a chaperone promoting nAChR folding in the endoplasmic reticulum [37]. The gene *Cel-unc-74* encodes a thioredoxin-related protein required for the expression of levamisole AChR subunits [38]. The gene *Cel-unc-50* encodes a transmembrane protein in the Golgi apparatus [35]. In *Cel-unc-50* mutants, levamisole nAChR subunits are directed to lysosomes for degradation. We found that acetylcholine currents and pharmacological profile of the receptors were sensitive to the presence of the accessory proteins, RIC-3, UNC-74 & UNC-50, suggesting the possibility that the expression level of these proteins could contribute to anthelmintic resistance in parasitic nematodes.

A5.5 Species differences

We show here that four *O. dentatum* receptor subunits can be used to reconstitute different functional levamisole receptor types and that levamisole is a full agonist in one of the main types. All of the four main *O. dentatum* receptor types responded to nicotine, which supports our use of the term nAChR. In contrast, in the expressed levamisole-sensitive AChRs of *C. elegans*, levamisole is a partial agonist, requires five subunits (Cel-UNC-38:Cel-UNC-29:Cel-UNC-63:Cel-LEV-1:Cel-LEV-8) and does not respond to nicotine. The *C. elegans* nicotine-sensitive muscle receptor is a separate homopentamer of ACR-16 [39]. We also saw differences between the expressed receptors of *O. dentatum* and the expressed AChR of *H. contortus* [16]: only two types of AChRs were produced in *Xenopus* oocytes expressing *H. contortus* subunits. Furthermore, we saw differences and similarities between the expressed *O. dentatum* receptors and the expressed *A. suum* receptors [14]. Only two subunits were used to reconstitute the *A. suum* AChR, such that varying the amounts of the subunit cRNAs injected changed the pharmacology of the expressed receptors. This is similar to the *Ode(29–63)*, in that only two subunits were used to reconstitute a *Pyr-nAChR* and varying the amount of injected subunit cRNAs affected the pharmacology of the receptor. Whereas no ancillary factors were used to reconstitute the *A. suum* nAChRs, we observed that the three ancillary factors were required to reconstitute the *O. dentatum* receptors. Another observation is that the amounts of cRNA we injected to reconstitute the *O. dentatum* receptors were far less than what was injected to reconstitute the *A. suum* receptors. These demonstrate differences between the expressed receptors of nematodes in the same clade (*O. dentatum*, *C. elegans* and *H. contortus*) and/or in different clades (*O. dentatum* and *A. suum*). In addition we have also demonstrated tribendimidine's effect on all four *O. dentatum*

receptor types and in two of the receptor types, the EC_{50} values show tribendimidine was more potent than the other agonists across the types. We found that pyrantel was the most potent agonist of two types of *O. dentatum* receptors but it is only most potent in one of the types of *H. contortus*. The real and significant differences between the effects of pharmacological agents on the model nematode *C. elegans* and on the parasitic nematode *O. dentatum*, both Clade V nematodes, shows that species variation requires that effects of anthelmintics on the relevant nematode parasite are tested as a vital reality check.

A6.0 Materials and Methods

A6.1 Ethical Concerns

All animal care and experimental procedures in this study were in strict accordance with guidelines of good animal practice defined by the Center France-Limousin ethical committee (France). The vertebrate animals (pig) studies were performed under the specific national (French) guidelines set out in the Charte Nationale portant sur l'éthique de l'expérimentation animale of the Ministère De L'enseignement Supérieur et de la Recherche and Ministère De L'Agriculture et de la Pêche experimental agreement 6623 approved by the Veterinary Services (Direction des Services Vétérinaires) of Indre et Loire (France).

A6.2 Nematode isolates

These studies were carried out on the levamisole-sensitive (SENS) isolate of *O. dentatum* as previously described [40]. Large pigs were experimentally infected with 1000 infective larvae (L3s) and infection was monitored 40 days later by fecal egg counts every 3 days. The pigs were slaughtered after 80 days at the French National Institute for Agricultural Research (Nouzilly) abattoir and adult nematodes (males and females) were collected from the large intestine and stored in RNA later (Qiagen®) at -80°C .

A6.3 Molecular biology

Ten adult males from *O. dentatum* SENS isolate were used for total RNA preparation using TRIzol (Invitrogen) according to the manufacturer's instructions. First-strand cDNA synthesis on resuspended and DNase-treated total RNA was carried out with the oligo (dT) RACER primer and superscript III reverse transcriptase (Invitrogen, Carlsbad, CA, USA) as previously described [16]. To identify full-length cDNA sequences of *O. dentatum unc-29*, *unc-63* and *acr-8* homologues, 5'- and 3'- rapid amplification of complementary ends (RACE) polymerase chain reactions (PCR) were performed using the splice leader sequence primer (SL1) with internal reverse primers and internal forward specific primers with reverse transcription 3'-site adapter primers, respectively. PCR products were cloned into the pGEM-T vector (Promega). Positive identifications were made by BLAST analysis against all *Haemonchus contortus* entries in the *H. contortus* information resource data base. Primers designed on *unc-29* sequence from *H. contortus* and *C. elegans* (*unc-29-F0* GGACGAGAAAGATCAAGTTATGCA, *unc-29-XR2* TCATCAAATGGGAAGAAAYTCGACG) allowed PCR amplification of a 288 bp fragment corresponding to partial *O. dentatum unc-29* homologue. New gene specific primer sets were designed on this sequence for the 5'- and 3'-RACE-PCR providing the full-length cDNA sequence of *Ode-unc-29*. To identify the *unc-63* homologue from *O. dentatum*, degenerate primers were designed based on the *Ode-unc-38* mRNA sequence (accession number GU256648) and the *unc-63* and *unc-38* sequences of cDNAs available from multiple nematode species (*Ode-unc-63-F1* GCGAATCGCGAYGCGAATCGKCT, *F2* AARAGYATGTGYCAAATWGAYGT, *R3* ATATCCCAYTCGACRCTGGGATA, *R4* TAYTTCCAATCYTCRATSACCTG). An 861 bp partial coding sequence of *Ode-acr-8*

cDNA was amplified using a sense primer (Hco-acr-8-FT1 TATGGTTAGAGATGCAATGGTT) and an antisense primer (Hco-acr-8-RE8 GTGTTTCGATGAAGACAGCTT) from *H. contortus* *Hco-acr-8*. The product of this reaction was cloned and sequenced, and the data were used to design primers to get the 5' and the 3' ends of the target transcript. To amplify the full-length coding sequence of *Ode-unc-38*, *Ode-unc-63*, *Ode-unc-29* and *Ode-acr-8*, we used the Phusion DNA polymerase (Finnzymes) and gene specific primer pairs containing *HindIII* or *XhoI* and *ApaI* restriction enzyme sites (Table S1 in Text S1) to facilitate directional cloning into the pTB-207 expression vector that is suitable for *in vitro* transcription. PCR products were then digested with *XhoI* and *ApaI* restriction enzymes (except *Ode-unc-29*, digested with *HindIII* and *ApaI*), purified using the NucleoSpin Gel and PCR Clean-up kit (Macherey-Nagel), ligated into the respective corresponding sites of the pTB-207 expression vector with T4 DNA Ligase (New England Biolabs), and resulting constructs were transformed into *E. coli* DG1 cells (Eurogentec) [26]. Three clones of each gene were sequenced using the standard primers T7 and polyT-V. Each of the reported sequences in supplementary figures S1A–D is from one of the nearly identical clones. The mMessage mMachine T7 transcription kit (Ambion) was used for *in vitro* cRNA synthesis from linearized plasmid DNA templates. The cRNAs were precipitated by lithium chloride, resuspended in RNase-free water and stored at -80°C .

A6.4 Sequence analysis and accession numbers

Database searches, prediction of conserved motifs and phylogenetic analyses for the cDNAs were carried out as already described [16]. Maximum likelihood analysis was performed on full-length AChR subunit cDNA sequences as follows: sequences were aligned

with Geneious 6.1.6 (Biomatters Ltd) using the translation align MAFFT plugin [41] that aligns the nucleotide sequences as codons based on amino acid sequences. The resulting nucleotide alignment was used to generate phylogenetic trees with the PhyML plugin for Geneious [42]. The HK85 substitution matrix was selected in order to optimize the tree topology and branch lengths. Branch support was evaluated using the chi2 option of PhyML. The accession numbers for cDNA and protein sequences mentioned in this article are *C. elegans*: UNC-29 NM_059998, UNC-38 NM_059071, UNC-63 NM_059132, ACR-8 JF416644; *H. contortus*: *Hco-unc-29.1* GU060980, *Hco-unc-38* GU060984, *Hco-unc-63a* GU060985, *Hco-acr-8* EU006785, *Hco-unc-50* HQ116822, *Hco-unc-74* HQ116821, *Hco-ric-3.1* HQ116823; *O. dentatum*: *Ode-unc-29* JX429919, *Ode-unc-38* JX429920, *Ode-unc-63* HQ162136, *Ode-acr-8* JX429921.

A6.5 Voltage-clamp studies in oocytes

Xenopus laevis ovaries were obtained from NASCO (Fort Atkinson, Wisconsin, USA) and defolliculated using 1–2 mg/ml collagenase type II and Ca²⁺-free OR2 (mM: NaCl 100, KCl 2.5, HEPES 5, pH 7.5 with NaOH). Alternatively, defolliculated oocytes were purchased from Ecocyte Bioscience (Austin, Texas, USA). Oocytes (animal pole) were microinjected with ~36 nL of a cRNA injection mix containing 50 ng/μL of each subunit cRNA, as described in [26]. Equal amounts of the *H. contortus* ancillary factors *ric-3*, *unc-50* and *unc-74* were added to each mix. Microinjected oocytes were incubated at 19°C for 2–5 days. The oocytes were incubated in 200 μL of 100 μM BAPTA-AM for ~3 hours prior to recordings, unless stated otherwise. In control experiments, we recorded from un-injected oocytes. Recording and incubation solutions used are reported in [26]. Incubation solution was supplemented with Na pyruvate 2.5 mM, penicillin 100 U/mL and streptomycin 100

$\mu\text{g/ml}$. All drugs applied, except tribendimidine and derquandel, were purchased from Sigma Aldrich (St Louis, MO, USA). Oocytes were voltage-clamped at -60 mV with an Axoclamp 2B amplifier; all data were acquired on a desktop computer with Clampex 9.2.

A6.6 Single-channel studies

Oocyte-attached (outside-out) patch-clamp procedure was used to obtain all recordings at room temperature (20°C – 25°C). Oocytes were prepared for the recordings by removal of the vitelline membrane with forceps after placing in hypertonic solution, as already described [43]. The oocytes were transferred to the recording chamber and bathed in a high Cs solution with no added Ca^{2+} (composition in mM: CsCl 140, MgCl_2 2, HEPES 10, EGTA 1, pH 7.3) to reduce K^+ currents and lower opening of Ca^{2+} -activated Cl^- channels. Patch electrodes were pulled from thin-walled capillary glass tubing (Warner Instruments, Hamden, CT), coated close to the tip with sylgard and fire-polished. The electrodes were filled with a high pipette solution {composition in mM: CsCl 35, CsAc 105, CaCl_2 1, HEPES 10} containing $10\ \mu\text{M}$ levamisole. Axopatch 200B amplifier (Axon Instruments, Union City, CA) was used to amplify currents which were sampled at 25 kHz with Digidata 1320A (Axon Instruments) and filtered at 1.5 kHz (3-pole Bessel). The linear least squares regression was used to estimate the conductances of the channels since the slopes were linear and did not show rectification.

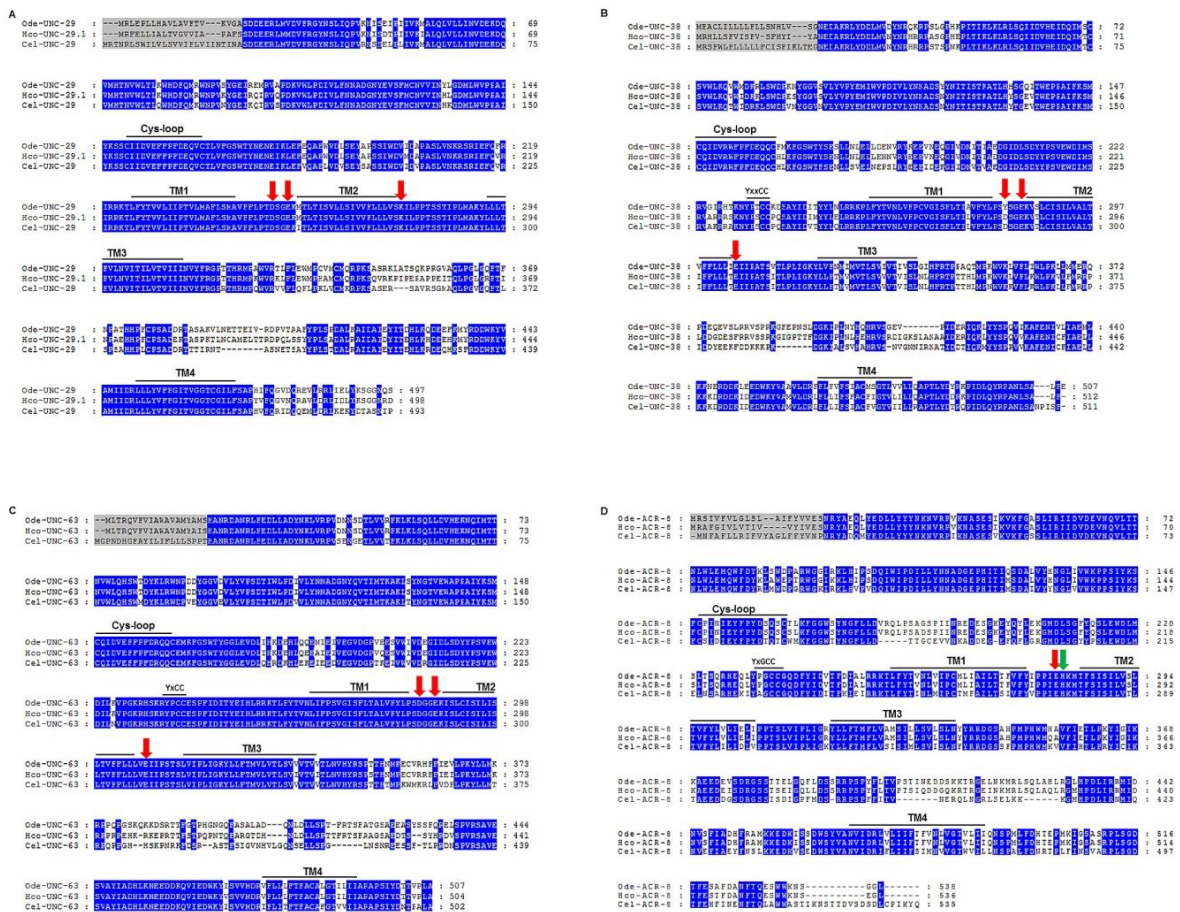
A6.7 Data analysis

Acquired data were analyzed with Clampfit 9.2 (Molecular Devices, Sunnyvale, CA, USA) and Graphpad Prism 5.0 software (San Diego, CA, USA). The peak of currents in BAPTA-soaked oocytes was measured. The response to $100\ \mu\text{M}$ ACh was normalized to 100% and the responses to the other agonists normalized to that of ACh. For all dose-

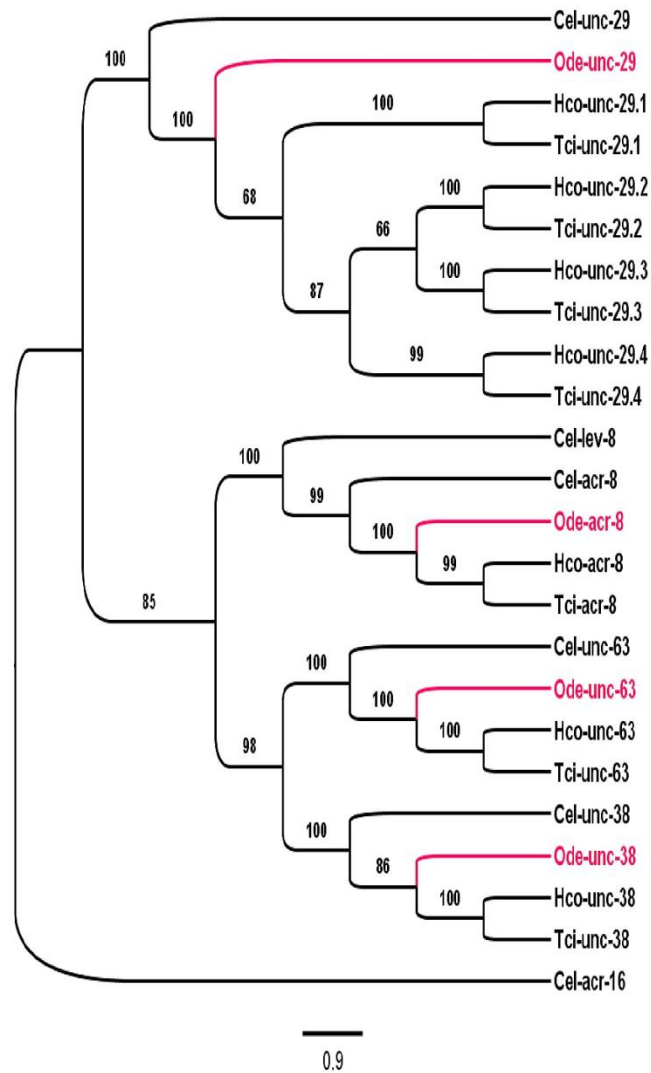
response relationships, the mean ± s.e of the responses is plotted. Dose-response data points were fitted with the Hill equation as described previously [26]. To calculate the pK_B values, the graphs were fitted with the Gaddum/Schild EC_{50} shift and the bottom of the curves were set to zero.

A7.0 Supporting Information

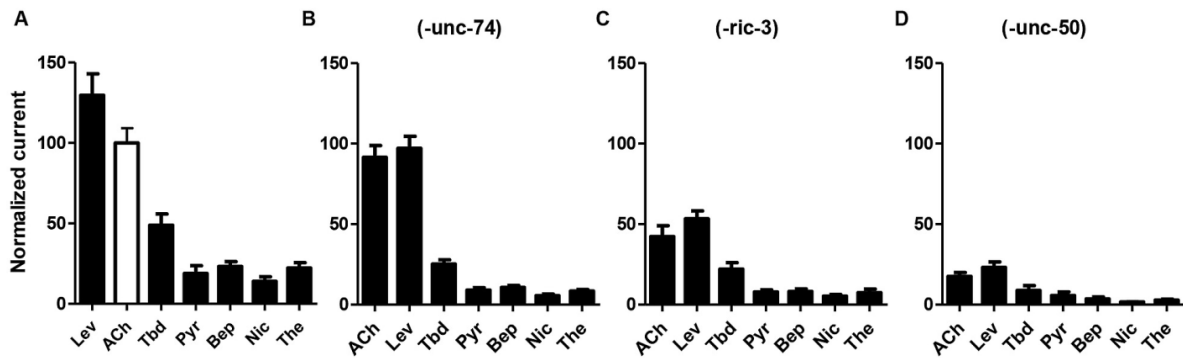
A7.1 Supplementary figures



Supplementary **Figure S1**. A–D. Amino acid alignments of the four *O. dentatum* nAChR subunits with the *H. contortus* and *C. elegans* homologues. The sequences were aligned with the MUSCLE algorithm [44] and processed further with GeneDoc. Shaded in grey are the predicted signal peptides and in blue are the amino acids conserved between all three species. Noted above the aligned sequences are the cys-loop, Yx(x)CC motif and transmembrane domains. Noted with red arrows (S1 A–C) are the amino acids, on either side of the transmembrane region (TM2) that are predicted to contribute to the permeability of the channel to calcium [45], [46]. Green arrow in S1 D shows a histidine which implies pH sensitivity around pH 6.5 to channel permeability.



Supplementary **Figure S2**. Distance tree showing relationships of nicotinic acetylcholine receptors (nAChR) subunit sequences in *Oesophagostomum dentatum* (Ode, highlighted in red), *Caenorhabditis elegans* (Cel), *Haemonchus contortus* (Hco) and *Teladorsagia circumcincta* (Tci). Numbers at each branch indicate percentage bootstrap values corresponding to 1000 replicates. The scale bar represents substitutions per site. The *C. elegans* *acr-16* nAChR subunit was used as an outgroup. Distance analyses were performed on full-length cDNA sequences. Multiple alignment was performed using Muscle program with standard parameters [47]. Relationships between sequences were determined using the neighbor-joining method and the HKY substitution model [48]. One thousand bootstrap replicates were performed to test the support of nodes.



Supplementary **Figure S3**. Effect of the ancillary proteins on receptor reconstitution. (A) Bar chart (mean \pm se) of agonist-elicited currents in the *Ode(29-63-38-8)* or Lev-nAChR subtype. This receptor subtype was used to test the effect of sequentially removing the ancillary proteins on the reconstitution. All responses were normalized to control 100 μ M ACh (unfilled bar) currents in oocytes expressing this receptor subtype with all the ancillary proteins (A). (B) Effect of removing *unc-74* from the mix on the *Ode(29-63-38-8)/Lev*-nAChR subtype. Note the relative change in ACh and Lev responses. (C) Effect of removing *ric-3* on the *Ode(29-63-38-8) : Lev*-nAChR subtype. The ACh current responses were reduced to <50% of the control. (D) Effect of removing *unc-50* on the *Ode(29-63-38-8)* or Lev-nAChR subtype. Note the dramatic decrease in currents elicited by all agonists.

A7.2 Supplementary Results

A7.2.1 Supplementary results S1. UNC-74 is a gene that encodes a transmembrane thioredoxin that can affect expression of nAChRs [26]. When we expressed the *Ode(29-63-8-38)* receptor with RIC-3 and UNC-50 but without UNC-74, the oocytes responded with acetylcholine currents that were only slightly reduced (mean 9%, S2-B). However, the order of the agonist potency series changed from 100 μ M acetylcholine > 100 μ M levamisole to 100 μ M acetylcholine \approx 100 μ M levamisole (S2-A, B). We tested the agonist potency series of all the anthelmintic agonists and found that their normalized responses were significantly different ($p < 0.0001$, F-test). Thus, UNC-74 was not an absolute requirement for expression of *Ode(29-63-8-38)* but affected the pharmacological profile of the expressed receptors suggesting that it changed the balance of the receptor subtypes types present. RIC-3 is an

endoplasmic reticulum resident protein that acts as a nAChR chaperone. RIC-3 enhances functional expression of some nAChRs, whilst inhibiting expression of other nAChRs [49,50,51]. RIC-3 stabilizes receptor intermediates and promotes maturation of receptors through subunit-specific interactions with nAChR subunits [52]. When we removed just RIC-3 from the mix, the acetylcholine and levamisole currents were reduced to < 60 % of control (S2-A, C). When we compared the acetylcholine-normalized responses of all the agonists we found that they were significantly different ($p < 0.0001$, F-test) suggesting that the balance of the receptor types present had changed.

The most striking decrease in current amplitude was obtained when just UNC-50 was removed. The acetylcholine current amplitudes obtained were < 20 % of control (S2-D). UNC-50 is a Golgi resident protein that is required to prevent some nAChR types from being trafficked to and degraded by the lysosomal system [53]. In the absence of UNC-50, it is reasonable to postulate that only a few synthesized receptors make it to the cell membrane. When we compared the acetylcholine-normalized responses of all the anthelmintic agonists to the control, we again found that they were significantly different ($p < 0.0001$, F-test), suggesting that the balance of the receptor types expressed was changed.

A7.3 Supplementary text

A7.3.1 Text S1 Materials and Methods: Ca²⁺-permeability measurements. For these set of experiments, we increased external Ca²⁺ in the recording solution from 1 mM to 10 mM without changing the concentration of the other ions. We used the GHK equation to calculate the permeability ratio, PCa/PNa . Due to BAPTA treatment before recordings, we assumed the internal [Ca²⁺] to be negligible; we also assumed permeability to Na and K, PNa and PK , are equal. Ionic activities were used for the calculations (activity coefficients:

0.56 for Ca²⁺ and 0.72 for Na⁺ and K⁺). Below is the GHK equation used to calculate the calcium permeability ratio, with the activity coefficients for Na⁺, K⁺ and Ca²⁺ inserted:

$$E_{rev} = RT/F$$

$$\ln\left\{\frac{P_{Na} \cdot 0.72[Na]_o + P_K \cdot 0.72[K]_o + 4P' \cdot 0.56[Ca]_o}{P_{Na} \cdot 0.72[Na]_i + P_K \cdot 0.72[K]_i}\right\}.$$

Where R is the universal gas constant (8.314 JK⁻¹mol⁻¹); F is Faraday's constant (96485 Cmol⁻¹); T is the temperature (room temperature, 298 K); and P' =

$$P_{Ca}/P_{Na}\{1/(1+e^{FE_{rev}/RT})\}.$$

A7.3.2 Table S1.0 Primers used for the PCR and cloning of *O. dentatum* AChR subunits

Gene name	Primer name	Primer sequence
<i>Ode-unc-29</i>	F-Hind3	AAAAAGCTTATGCGTCTCGAACCGTTACTTC
	R-Apa1	TTTGGGCCCTAAACCCGTACAGTCATAAAACAAT
<i>Ode-unc-38</i>	F-Xho1	AAACTCGAGATAGCTGGTTGCAAGTGCGTATT
	R-Apa1	TTTGGGCCCTCTCAACAAAATTGGCCTAATATAC
<i>Ode-unc-63</i>	F-Xho1	AAACTCGAGATGCTGACGCGACAAGTGTTTC
	R-Apa1	TTTGGGCCCTACCCAGCCGGCTGCTCGC
<i>Ode-acr-8</i>	F-Hind3	AAACTCGAGCTTGGCTAGCTTAAACTAAGATT
	R-Apa1	TTTGGGCCCAACCATAATACTATACATATCTCAGA

A8.0 Acknowledgements

We are grateful to Debra J Woods, Zoetis Animal Health, Kalamazoo, MI for the generous supply of derquantel. We would like to thank Prof. Shu Hua Xiao, National Institute of Parasitic Diseases, Shanghai, Peoples' Republic of China for the gift of tribendimidine. The authors would like to thank Dr. Robin Beech, McGill University, Canada for his help and comments concerning the phylogenetic analysis. We particularly thank Elise Courtot, INRA, Nouzilly, France and Dr. Jeff Beetham, Department of Vet Pathology, Iowa State University for assistance cloning the receptor subunits.

A9.0 Author Contributions

Conceived and designed the experiments: SKB CLC CN APR RJM. Performed the experiments: SKB CLC JCo MA APR. Analyzed the data: SKB CLC CN APR RJM.

Contributed reagents/materials/analysis tools: CLC CN NP APR RJM EC. Wrote the paper:

SKB CLC CN JCa APR NP RJM.

**APPENDIX B. ANTHELMINTICS: THE BEST WAY TO PREDICT THE FUTURE
IS TO CREATE IT**

A paper published in *Veterinary Parasitology* (2015)¹

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B1.0 Abstract

‘The best way to predict the future is to create it.’ When we look at drugs that are used to control parasites, we see that new knowledge has been created (discovered) about their modes of action. This knowledge will allow us to predict combinations of drugs which can be used together rationally to increase the spectrum of action and to slow the development of anthelmintic resistance. In this paper we comment on some recent observations of ours on the modes of action of emodepside, diethylcarbamazine and tribendimidine. Emodepside increases the activation of a SLO-1 K⁺ current inhibiting movement, and diethylcarbamazine has a synergistic effect on the effect of emodepside on the SLO-1 K⁺ current, increasing the size of the response. The combination may be considered for further testing for therapeutic use. Tribendimidine is a selective cholinergic nematode B-subtype nAChR agonist, producing muscle depolarization and contraction. It has different subtype selectivity to levamisole and may be effective in the presence of some types of levamisole resistance. The new information about the modes of action may aid the design

of rational drug combinations designed to slow the development of resistance or increase the spectrum of action.

B1.1 Keywords

Anthelmintic; mode of action; tribendimidine; emodepside; diethylcarbamazine

B2.0 Introduction

‘The best way to predict the future is to create it.’ This quote is usually ascribed to Abraham Lincoln and leads to some interesting thoughts when applied to different research fields including our own field of study, that is, anthelmintics. What are we creating and what can we see for the future for anti-parasitic drugs? We are creating new techniques for the screening of anthelmintic drugs, we are creating new methods for studying the modes of actions of anthelmintics and we are creating new ways for detecting anthelmintic resistance (Gilleard and Beech, 2007 and Lanusse et al., 2014). We are also creating better awareness of the ‘neglected tropical diseases’ (Hotez et al., 2008) of humans which include ascariasis, hookworm and trichuriasis and better awareness of the link between human and animal medicine, the ‘One Health’ concept. Our western economic system has also produced a more favorable economic environment for the development of animal anthelmintics, than anthelmintics for humans. Currently, we limit the damage done by nematode parasites of animals with pasture management, and improved targeted metaphylactic and therapeutic use of anthelmintics; for humans, clean water and sanitation are limiting factors (like clean pasture for animals) while mass drug administration (MDA) has similarities to the regular metaphylactic use of anthelmintics for animals. Vaccinations against parasites for both humans and animals are very desirable but so far they have limited efficacy.

The advances and creations listed above lead to a number of logical predictions for the future use and development of anthelmintics. We are confident that the development and better understanding of anthelmintic properties will continue, at a steady but modest pace, driven by economic, human and animal needs. We think that the economic pressures associated with animal medicine will remain greater than for human medicine and focused on the development of novel ‘resistance-busting’ anthelmintics. Success in research can be limited by funding as was said by the father of modern drug development, Paul Ehrlich, Fig. 1 (1854–1915), who recognized success required the four Gs: *Gluck, Geduld, Geschick und Geld* (luck, patience, skill and money, (Perutz, 1988). The ‘money’ for animal anthelmintics comes from the market for anti-parasitic drugs and chemicals for small animals and livestock which was estimated at \$11 billion (Evans and Chapple, 2002). This contrasts with the market for human anthelmintics which is only \$0.5 billion despite some 2 billion humans being infected in developing countries, around 25 cents per person annually! Given that the out of pocket costs of new human drugs may be \$403 million (at year 2000 valuations (DiMasi et al., 2003) or more, we can see that the commercial development of human anthelmintic drugs is not favorable. It seems more likely that the economics of animal health will drive the development and advance of the knowledge base of animal anthelmintics and that these developments will be applied and adapted for human use (ivermectin and perhaps emodepside) unless private charities, governments and foundations overcome the financial limitations. In addition to the gradual development of resistance-busting anthelmintics we see: developments in our understanding of the modes of action of anthelmintics; we see more logical combinations of anthelmintics to slow down or counter the development of resistance and; also new methods for detecting anthelmintic resistance.



Fig. 1. Paul Erlich in his Frankfurt office, *circa* 1900, the father of modern chemotherapy, who worked on trypanosome diseases and popularized the concept of the ‘magic bullet’ (magische Kugel, the perfect therapeutic agent).

Our lab has focused on understanding of the modes of action of anthelmintics and in this paper we illustrate some of our recent observations and developments in our understanding of the actions of emodepside, diethylcarbamazine and tribendimidine. The mode of action of these anthelmintics involves effects on membrane ion-channels and has required us to use electrophysiological techniques for their study (Martin et al., 1996b). We think that better knowledge of the mode of action of these compounds will allow rational combination with other anthelmintics to increase potency, spectra and allow a slowing of the speed of development of resistance in animal and human parasites. This paper is based on a lecture given to the World Association for the Advancement of Veterinary Parasitology (WAAVP) in Liverpool, 2015 and covers: (1) emodepside, an anthelmintic used for small animals, which has the potential for being used for human use to control filarial parasites; (2)

diethylcarbamazine, a long serving anthelmintic still used for the control of filariasis in humans and; (3) tribendimidine, a recent anthelmintic developed by China for human use.

B3.0 Emodepside

Emodepside is a cyclooctadepsipeptide developed by Bayer, Fig. 2, which is related to its parent compound, PF1022A (Martin et al., 1996a) which has broad-spectrum anthelmintic activity. Emodepside has an inhibitory effect on locomotion that allowed (Guest et al., 2007) to use a *C. elegans* mutagenesis screen to find that *slo-1* (a Ca^{2+} -dependent K^+ channel) mutant alleles were resistant to the inhibitory effects of emodepside. (Crisford et al., 2011) also described transgenic experiments in which *C. elegans* SLO-1a channels were swapped for KCNMA1, the human orthologue of SLO-1 channels. These studies found that the sensitivity to emodepside in the rescues depended upon the origin of the SLO-1 channel: the human KCNMA1 channel was 10–100 times less sensitive to emodepside than the rescues expressing *C. elegans* SLO-1a channel. These experiments suggested that SLO-1 Ca^{2+} -dependent K^+ channels of nematodes are a major part of the target site of emodepside. Expression of *C. elegans* SLO-1a channels in *Xenopus* oocytes have revealed that emodepside can directly open these channels (Kulke et al., 2014) and that emodepside action on this splice variant of the channel does not require the presence of additional receptors like the latrophilin receptors for an emodepside effect (Willson et al., 2004). It does not however, rule out a contribution of latrophilin receptors to the overall mode of action of emodepside in parasites as indicated by the interaction of Lat-1 and emodepside (Saeger et al., 2001).

SLO-1 K^+ channels have large (~ 200 pS) single-channel conductances and are also known as ‘big’ potassium (BK) channels. These channels serve to clamp the membrane potential near the potassium reversal potential and inhibit electrical excitability. The SLO-1 K^+ channel, has a different function to the high conductance Ca^{2+} -dependent Cl^- channel

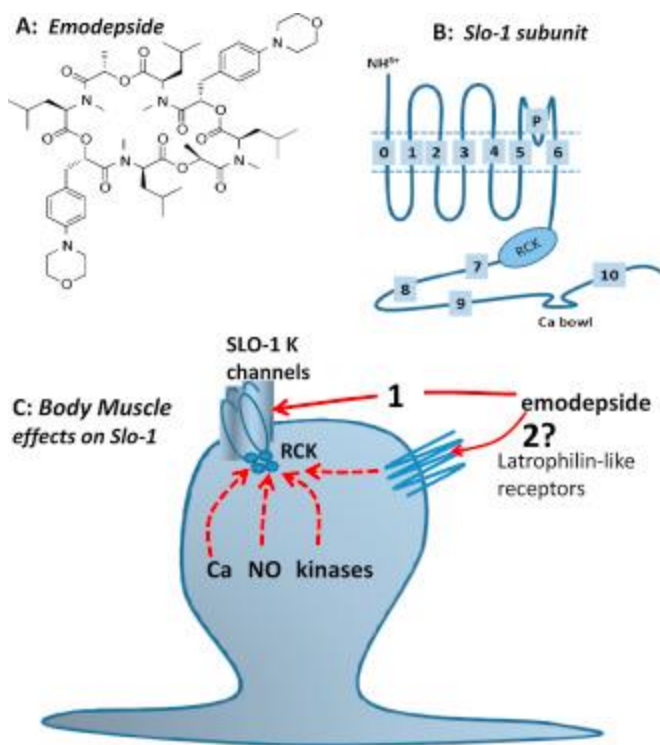


Fig. 2. Summary diagrams of emodepside structure, Slo-1 subunit and a model of the mode of action of emodepside on nematode body muscle. A: Emodepside. B: Line diagram of structure of one SLO-1 subunit; each SLO-1 K^+ channel is made up of 4 of these subunits. C: Putative mode of action of emodepside on SLO-1 K^+ channels in the muscle: act directly (1) or indirectly by stimulating latrophilin-like receptors (2) and signaling cascades that may involve NO, protein Kinase C and/or calcium. It is unlikely that emodepside acts at the extracellular surface of the SLO-1 K^+ channel because of the slow time course of its action. It is very lipophilic and could act in the lipid membrane phase on the SLO-1 K^+ channel or move into the cytoplasm and act intracellularly. A SLO-1 K^+ channel (C) is shown composed of 4 subunits along with the 'RCK' cytoplasmic regulatory region of the channel. (Martin et al., 2012).

(Thorn and Martin, 1987) which is associated with the transport of carboxylic acids from anaerobic metabolism of glucose (Valkanov and Martin, 1995). Subunits homologous to the vertebrate SLO-1 K^+ channels are found in *C. elegans* and *Ascaris suum* (Buxton et al., 2011). The SLO-1 K^+ channels are composed of 4 α -subunits; α -subunits have seven (S0–S6) transmembrane regions, a P-loop between S5 and S6, a large intracellular domain (S7-S10) and a well conserved 'calcium bowl' between domains S9 and S10, Fig. 2. In addition, the regulator of the K^+ channel conductance (RCK) domains (S7, S8) contains high and low affinity calcium binding sites. The SLO-1 α -subunits show alternative splicing, producing

channels with different calcium sensitivities; in *C. elegans* there are up to 15 splice variants (including SLO-1a, SLO-1b and SLO-1c (Kulke et al., 2014 and Wang et al., 2001)). Each α -subunit of the channel has at least two high affinity calcium binding sites and one low affinity calcium/magnesium binding site. The channel also combines with secondary, regulatory β -subunits in vertebrates (Knaus et al., 1994) but these subunits have not yet been identified in *C. elegans*. However, *Drosophila*, which also lacks β subunits, has Slob proteins, which appear to carry out similar functions to the vertebrate β -subunits and these may be present in nematodes (Claridge-Chang et al., 2001).

The suggested function of the SLO-1 K^+ channels is that they adjust the resting membrane potential of electrically excitable cells and adjust the level of excitability, up or down, and so affect the response to other inputs. The opening of the SLO-1 K^+ channel, Fig. 2, is regulated by at least ten factors including: (1) membrane potential; (2) calcium; (3) magnesium; (4) NO; (5) CO; (6) arachidonic acid; (7) propagandist; (8) phosphorylation by cAMP-dependent protein kinase A; (9) phosphorylation by diacylglycerol/ Ca^{2+} -dependent protein kinase C; and (10) phosphorylation by cGMP-dependent protein kinase G (Salkoff et al., 2006). The kinases allow SLO-1 to be coupled to multiple and quite diverse signaling cascades permitting different ways of adjusting the excitability of the cells. The different nematode neuropeptides could affect cAMP and cGMP levels (e.g., AF1, AP2, and PF1 and PF2) could then affect SLO-1 channels (Muhlfeld et al., 2009, Verma et al., 2007 and Verma et al., 2009). A selective agonist for the PF1 and/or a selective antagonist of the AF1 receptor would activate a SLO-1 K^+ -like current and increase the efficacy of emodepside. The neuropeptides AF1, AF10 and PF2 also bind with low affinity to the latrophilin-like receptor, HC110-R of *Haemonchus contortus*, suggesting that emodepside could also have an indirect

mode of action on SLO-1 K⁺ channels through these latrophilin-like receptors (Fig. 2) that are neuropeptide receptors (Muhlfeld et al., 2009).

We found (Buxton et al., 2011 and Martin et al., 2012 that *Asu-slo-1* is an evolutionarily conserved homologue of the *slo-1* genes, expressed in adult *A. suum* body muscle flaps. Using a two-micro-electrode current-clamp and voltage-clamp technique, Fig. 3A, we found in the nematode parasite *A. suum*, that emodepside activates SLO-1-like K⁺ channels to produce hyperpolarization under current-clamp, Fig. 3B1, and an outward current when under voltage-clamp, Fig. 3B2. We also found that emodepside increased voltage-activated K⁺ currents, Fig. 3C and D, in a time dependent manner. Emodepside, Fig. 3C, unlike PF1 did not decrease calcium currents and so emodepside does not work by releasing PF1 as has been hypothesized. We found that the effects of emodepside on the voltage-activated K⁺ channels is Ca²⁺-dependent and were inhibited by 5 mM 4-aminopyridine, Fig. 4A. The membrane hyperpolarization and increase in voltage-activated K⁺ current produced by emodepside, Fig. 3B, are very slow in onset and increase over a period of more than 10 min (Buxton et al., 2011); the slow onset effect of emodepside might be due to its very lipophilic nature and a membrane partitioning effect. It may also be because the effects of emodepside are indirect and produced by activation of a slow signaling cascade. Fig. 4B and C shows that the effects of emodepside are potentiated by sodium nitroprusside (a NO donor), antagonized by iNOS inhibitors (NNLA), and inhibited by 1 μM staurosporine, an inhibitor of protein kinase (Buxton et al., 2011). Interestingly, these signaling molecules are known as activators of SLO-1 in other cells (Bolotina et al., 1994b, Holden-Dye et al., 2007, C shows that the effects of emodepside are potentiated by sodium nitroprusside (a NO donor), antagonized by iNOS inhibitors (NNLA), and inhibited by 1 μM staurosporine, an

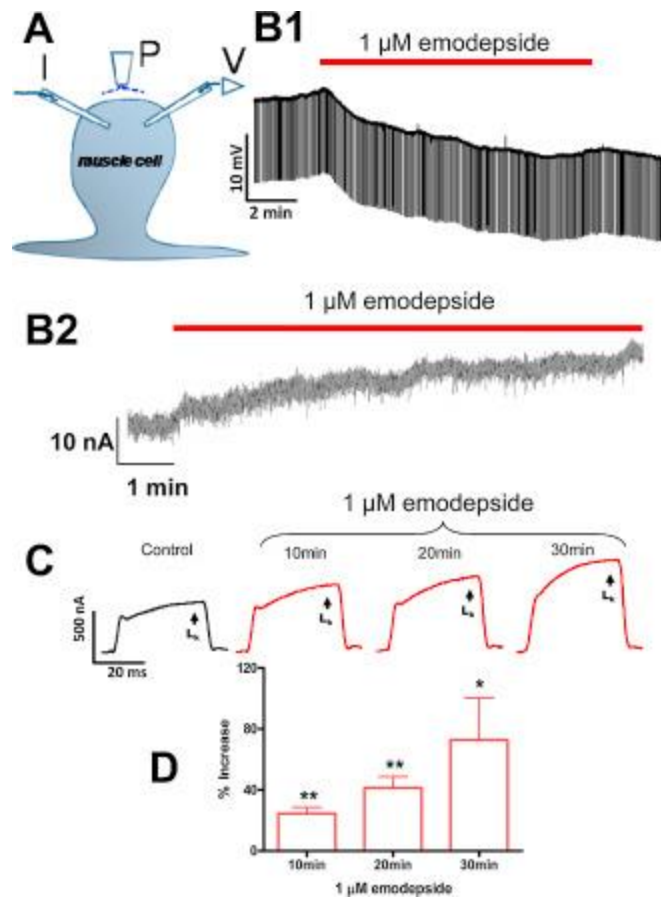


Fig. 3. Electrophysiological techniques (two micropipette current-clamp and voltage-clamps) for recording from *Ascaris suum*. A: *A. suum* muscle bag showing the current (I) and voltage (V) micropipettes in the bag, and the perfusion needle (P). B1: Representative current-clamp trace showing the slow hyperpolarizing membrane potential during and after 10 min application of 1 μM emodepside. B2: Outward current response to 1 μM emodepside at higher time resolution. Holding potential -35 mV. Notice that emodepside produces a gradually increasing current after a delay of some 30 seconds. The response does not plateau in the time period of this recording. C: Voltage-clamp traces of control K^+ current and the time-dependent effects of 1 μM emodepside on the K^+ currents, all to a step potential of 0 mV from a holding potential of -35 mV. D: Bar chart (mean \pm S.E.) of 1 μM emodepside effect on steady state (LK) currents. Comparison was made between the control 0 mV step current at 30–40 ms and the corresponding current increased by emodepside at 10, 20 and 30 min. Emodepside increased LK currents at 10 min ($p < 0.01$, $n = 4$, paired t -test), 20 min ($p < 0.01$, $n = 4$, paired t -test) and 30 min ($p < 0.05$, $n = 4$, paired t -test). (Martin et al., 2012).

inhibitor of protein kinase (Buxton et al., 2011). Interestingly, these signaling molecules are known as activators of SLO-1 in other cells (Bolotina et al., 1994b, Holden-Dye et al., 2007, Mistry and Garland, 1998 and Wang et al., 1999) and therefore encourage the view that emodepside could act through either or both of these signaling cascades and the signaling

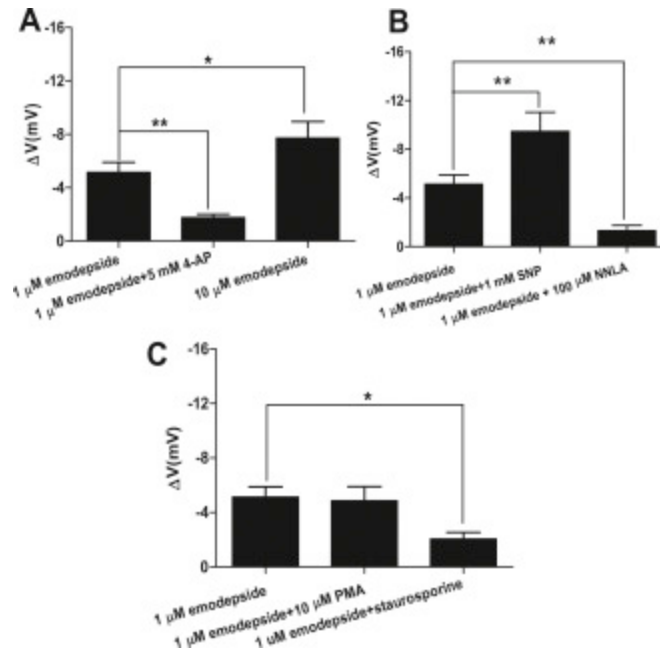


Fig. 4. Effect of 1 μ M emodepside on membrane potential. A: Comparison was made between membrane potential before and during emodepside application. 1 μ M emodepside caused a significant membrane hyperpolarization ($p < 0.001$, $n = 10$, paired t -test) which was reduced in the presence of 5 mM 4-aminopyridine ($p < 0.01$, $n = 8$, unpaired t -test). 10 μ M emodepside caused an increased hyperpolarization in comparison to 1 μ M emodepside ($p < 0.05$, unpaired t -test). B: Bar chart (mean \pm s.e) of NO influence on emodepside-induced hyperpolarization. In the presence of 1 mM SNP, 1 μ M emodepside caused an increased hyperpolarization ($p < 0.01$, $n = 4$, paired t -test). 100 μ M NNLA decreased the hyperpolarization caused by 1 μ M emodepside ($p < 0.01$, unpaired t -test). C: Bar chart (mean \pm s.e) of effect of protein kinase modulators on emodepside-induced hyperpolarization. 10 μ M PMA had no significant effects on the hyperpolarization caused by 1 μ M emodepside. However, 1 μ M staurosporine decreased the hyperpolarization caused by 1 μ M emodepside ($p < 0.05$, unpaired t -test). (Martin et al., 2012).

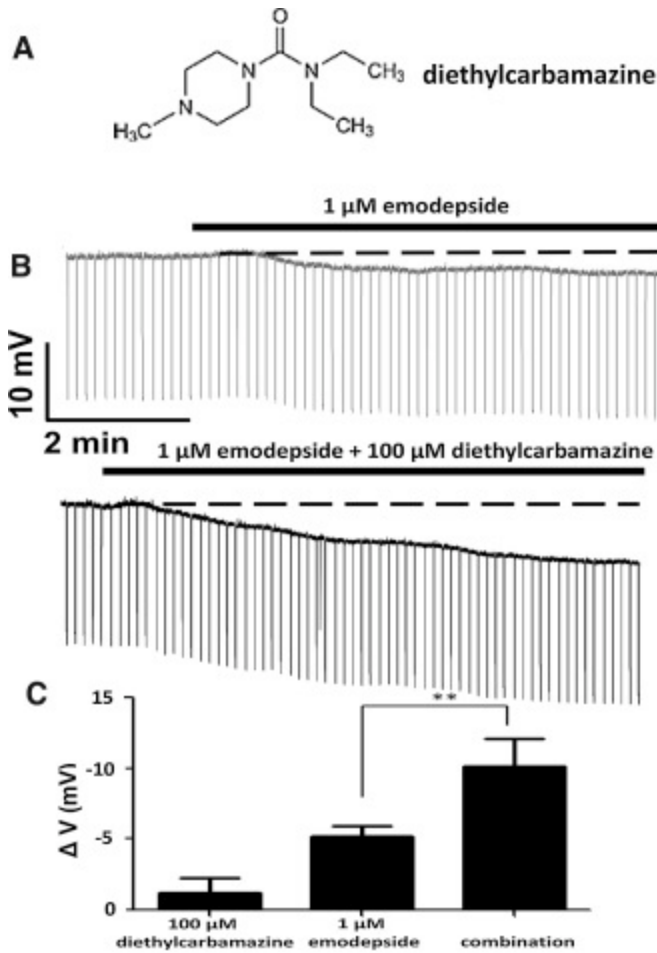
cascades may be in series or parallel, Fig. 2C. A number of studies on the mammalian orthologues of SLO-1 show that they are directly and alternately regulated by complex, multiple signaling cascades, involving NO and diacylglycerol or PKC activation (Ghatta et al., 2006 and Salkoff et al., 2006). It is pointed out that NO signaling pathways in mammals may not be conserved in all species of nematode.

Thus emodepside appears to selectively activate the SLO-1 K^+ current that is present in nematodes but has less effect on the SLO-1 K^+ currents of vertebrates. This can explain the selective toxicity of the drug. The existence and mechanisms of resistance to emodepside

in nematode parasites remain to be studied but could involve several different mechanisms including changes in the splice forms of the SLO-1 K⁺ channel or its regulation by different signaling cascades. However, such resistance, depending on the specific mechanism, might be countered (Verma et al., 2007 and Verma et al., 2009) by a selective agonist for the FMRFamide PF1 receptor and/or a selective antagonist of the FMRFamide AF1 receptor which would activate a SLO-1 K⁺-like current and increase the efficacy of emodepside. An increased knowledge of the physiology of target site of emodepside provides a new way of designing drug combinations. The complex nature of SLO-1 K⁺ regulation suggests that if there were resistance to emodepside it would be complex in nature and therefore likely to be polygenic involving multiple mechanisms.

B4.0 Diethylcarbamazine

Diethylcarbamazine, Fig. 5A, is an antifilarial drug that has been used since 1947 against lymphatic filariasis and loiasis. It is still an important and effective antifilarial drug but its mode of action is not fully described. Diethylcarbamazine has been suggested to have an indirect, host mediated mode of action: it appears to alter host arachidonic acid, nitric oxide metabolic pathways and inhibits NF-κB, which together in an unknown way leads to immobilization and sequestration of the microfilariae (Maizels and Denham, 1992 and Peixoto and Silva, 2014). Diethylcarbamazine activity against *B. malayi* microfilariae is abolished in inducible nitric oxide synthase knockout mice (iNOS^{-/-}), suggesting that diethylcarbamazine activity is dependent on host inducible nitric oxide synthase (iNOS) and nitric oxide (McGarry et al., 2005).



DEC potentiates emodepside

Fig 5. The combined effect of emodepside and diethylcarbamazine is greater than the effect of emodepside alone on *A. suum* membrane potential. A: Chemical structure of diethylcarbamazine. B: Representative current-clamp traces showing the membrane potential before, during 1 μM emodepside application (top trace) and during application of 1 μM emodepside plus 100 μM diethylcarbamazine (lower trace). The time delay between the end of the application of 100 μM diethylcarbamazine and 1 μM emodepside plus 100 μM diethylcarbamazine was 10 min. The change in membrane potential between the beginning of the 100 μM diethylcarbamazine and application of 1 μM emodepside plus 100 μM diethylcarbamazine was a hyperpolarization of 1.5 mV. C: Bar chart (mean ± i.e.) of diethylcarbamazine effect on emodepside-induced hyperpolarization. 100 μM diethylcarbamazine increased the hyperpolarization caused by 1 μM emodepside ($p < 0.01$, $n = 5$, unpaired *t*-test. (Buxton et al., 2014a).

We were interested to determine how diethylcarbamazine would affect calcium-dependent SLO-1 K⁺ currents in isolated *A. suum* muscle flap preparations, and how diethylcarbamazine interacts with emodepside. The interest was prompted by observations in vertebrates (Bolotina et al., 1994a) which show that nitric oxide activates SLO-1 K⁺ channels and observations on *A. suum* indicating the presence of nitric oxide synthase and of SLO-1 K⁺ channels which show positive modulation by a nitric oxide pathway (Buxton et al., 2011). We hypothesized that diethylcarbamazine, with effects on arachidonic acid and nitric oxide pathways, would increase activation of SLO-1 K⁺ currents in *A. suum* muscle and potentiate effects of emodepside on membrane potential (Buxton et al., 2014a). We conducted current-clamp and voltage-clamp electrophysiological experiments, using *A. suum* body muscle in the presence of sufficient calcium to allow activation of the SLO-1 K⁺ currents. We found that indeed diethylcarbamazine, by itself, can increase activation of SLO-1 K⁺ currents and potentiate the hyperpolarizing effects of emodepside. This to us was very interesting since it showed that diethylcarbamazine has a direct effect on the nematode parasite and its effects are not exclusively mediated via the host as has been suggest by earlier experiments. It seems likely that the effects of diethylcarbamazine may involve effects on NO or arachidonic acid metabolites both in the host and in the parasite. Although the mechanism of action of diethylcarbamazine remains to be further defined, the synergistic effect of emodepside and diethylcarbamazine suggests that the combination of the two drugs could be considered for therapeutic use for the treatment of filarial nematode infections.

B5.0 Tribendimidine

Tribendimidine, Fig. 6, is a symmetrical diamidine derivative, of amidantel which was developed in China for use in humans in the mid-1980s. It is a broad-spectrum

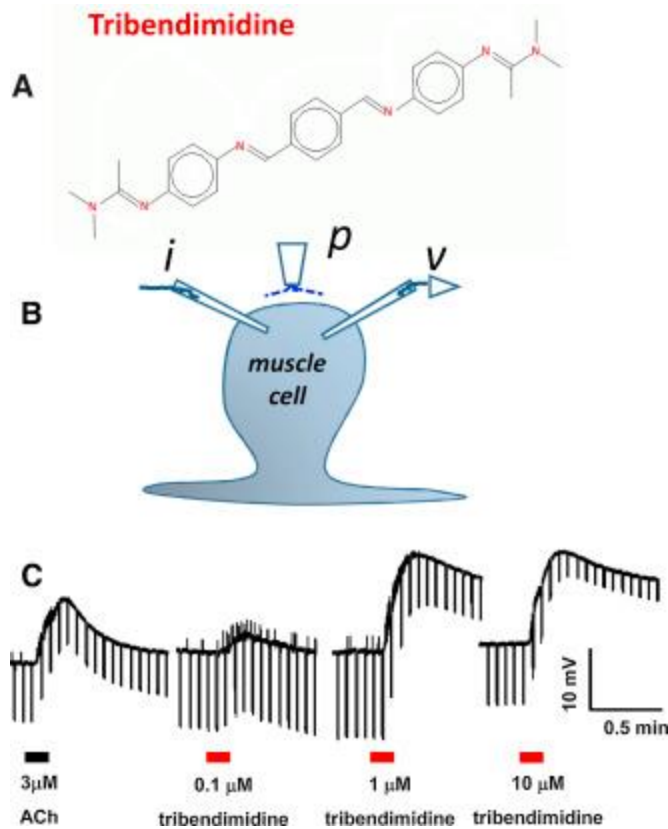


Fig. 6. A: Chemical structure of tribendimidine. B: Diagram of the two-micropipette current-clamp technique used to record the membrane potential (v) and to inject 40 nA hyperpolarizing 500 ms current pulses (i) at 0.3 Hz. p is the microperfusion pipette used to apply and wash off the drugs. C: Application of 3 μ M acetylcholine and then 0.1, 1 and 10 μ M tribendimidine to the same preparation. 1 μ M tribendimidine produces a bigger depolarization response (upward movement) and conductance increase (reduction in the voltage responses to current injection, producing a narrowing of the width of the trace) than 3 μ M acetylcholine (Robertson et al., 2015).

anthelmintic effective against soil-transmitted helminthiasis including hookworm, pinworms, roundworms, *Strongyloides* and flatworms (Xiao et al., 2005 and Xu et al., 2014) of humans.

Molecular studies (Hu et al., 2009) on *C. elegans* using null-mutants of the levamisole receptor subunits strongly suggested that tribendimidine is a cholinergic agonist that is selective for the same nematode muscle nAChR as levamisole. When we looked at these studies we found that there are no direct electrophysiological observations in nematode parasites that had been made to test this hypothesis and we were aware that sometimes

observations on the model Clade V nematode were not always the same in parasitic nematodes, particularly for the parasites from a different Clade. We were also interested in trying to explain why tribendimidine is effective against some nematode parasites when levamisole is not.

We tested the effects of tribendimidine on the electrophysiology, Fig. 6, and contraction of *A. suum* muscle (Robertson et al., 2015) and found that tribendimidine produces a dose-dependent depolarization associated with an increase in the conductance of the muscle membrane as the nicotinic receptors (nAChRs) open, Fig. 6. We found that tribendimidine was more potent than acetylcholine and had an EC_{50} of 0.8 μM . We also tested the effects of the nicotinic antagonist mecamylamine, a potent antagonist of muscle nAChRs of parasitic nematodes and found that 3 μM was potent against tribendimidine; the antagonist effects of mecamylamine confirmed the cholinergic action of tribendimidine on the nAChRs of the parasite *A. suum*.

We characterized the pharmacological profile of tribendimidine using our *Ascaris* muscle contraction assay systems (Qian et al., 2006 and Robertson et al., 2002) with tribendimidine as the agonist and methyllycaconitine, paraherquamide and derquantel as antagonists to calculate the potency, pA_2 , of the antagonists and the subtype of the selectivity of tribendimidine. We found that tribendimidine was more selective for the **B**-subtype (bephenium preferring) nAChRs than the **L**-subtype (levamisole preferring) or the **N**-subtype (nicotine preferring). These observations showed the selectivity for the different groups of nAChRs present on the *Ascaris* muscle was not the same as levamisole and it was possible that levamisole-resistant parasites would remain sensitive to tribendimidine. To test this we used, *Oesophagostomum dentatum* L_3 larval migration inhibition assays with levamisole-

sensitive isolates and levamisole-resistant isolates and tested the effects of tribendimidine on motility. Levamisole was less effective ($p < 0.001$, F -test) in inhibiting migration of levamisole-resistant larvae than the migration of levamisole-sensitive larvae. We tested the effects of tribendimidine to the limits of its solubility, $\sim 30 \mu\text{M}$, and found that tribendimidine was actually more potent on the levamisole-resistant isolate than on the levamisole-sensitive isolates ($p < 0.001$, F -test). The larger effect of tribendimidine on the levamisole-resistant, than the levamisole-sensitive isolates at lower tribendimidine concentrations, supports the view that levamisole and tribendimidine do not activate identical nAChR receptor subtypes. The higher efficacy of tribendimidine on the levamisole resistant *O. dentatum* isolate might indicate a case of negative cross resistance (Miltch et al., 2013)

We have been able to express, in *Xenopus* oocytes a range of different nAChR receptor subtypes derived from anthelmintic sensitive *Oesophagostomum dentatum* clones of their nAChR receptor subunits (Buxton et al., 2014b). Fig. 7 shows a diagram of the subunit composition of two nAChR subtypes expressed in oocytes, one composed of Ode-UNC-29:Ode-UNC-63:Ode-UNC-38, the other composed of Ode-UNC-29:Ode-UNC-63:Ode-UNC-38:Ode-ACR-8 subunits. The Ode-UNC-29:Ode-UNC-63:Ode-UNC-38 receptor was more sensitive to tribendimidine and pyrantel but not to levamisole or nicotine. We can see that the receptor subunit arrangements affect their pharmacology and that not all cholinergic anthelmintics have the same selectivity.

Our understanding to date is that there are a range of pharmacologically different nAChR subtypes present in parasitic nematodes and the pharmacology of the receptor subtypes varies with the subunit composition of the receptor which varies with the tissue and

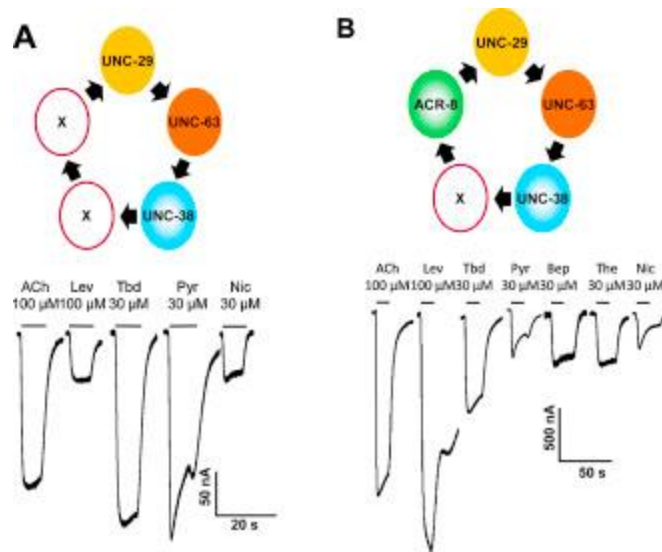


Fig. 7. Tribendimidine as an agonist of Ode-(29 – 8 – 38 – 63) and Ode-(29-63-38) receptors expressed in oocytes, currents recorded under voltage-clamp at -60 mV (Buxton et al., 2014b) A: Tribendimidine and pyrantel at $100 \mu\text{M}$ is more potent than levamisole on the Ode(29 – 38 – 63) receptor. B: Levamisole at $100 \mu\text{M}$ is more potent than acetylcholine, tribendimidine, pyrantel and nicotine on the expressed Ode(29 – 8 – 38 – 63) receptor. Note that derquantel produces competitive antagonism of the effects of levamisole but a non-competitive antagonism of pyrantel, suggesting that the mode of action of levamisole and pyrantel are not identical.

species of the nematode parasite. There will therefore be cholinergic anthelmintics that act on different nAChR subtypes and it is therefore possible that there will not always be cross-resistance between the cholinergic anthelmintics.

B6.0 Discussion

Diethylcarbamazine is used mostly for treatment of filariasis in humans but has effects against hookworm and ascariasis, intestinal nematode parasites (Meyrowitsch and Simonsen, 2001). In addition to the treatment of filariasis, diethylcarbamazine, as a single dose treatment, has modest effects on intestinal nematode parasite infections including ascariasis and trichuriasis but is more effective when combined with ivermectin or albendazole (Belizario et al., 2003). We have seen in our experiments that emodepside increases a Slo-1 K^+ current in the parasite and that diethylcarbamazine can potentiate the

effect of emodepside. Both of these compounds have been used separately as single anthelmintics but we do not have data on their therapeutic effect when used in combination. This information is desirable to obtain and if therapeutic combination of emodepside and diethylcarbamazine is safe and more potent than either compound in isolation, such synergism could slow the development of resistance and extend the spectrum of action of the therapy.

Levamisole and tribendimidine have different selectivities for nAChR subtypes. In *Ascaris* tribendimidine is more selective for the B-subtype rather than the L-subtype of nAChR. Tribendimidine is more potent on expressed *O. dentatum* receptor subtypes composed of Ode-UNC-29:Ode-UNC-63:Ode-UNC-38 subunits, than on subtypes composed of Ode-UNC-29:Ode-UNC-63:Ode-UNC-38:Ode-ACR-8 subunits (Buxton et al., 2014b). The difference in selectivity suggests that tribendimidine has the potential to be effective against nematode parasites that are not sensitive to levamisole, including those parasites that have developed resistance. A careful combination of different cholinergic anthelmintics has the potential to extend the spectrum of action of the drug treatment. Tribendimidine has an interesting and promising pharmacology and has the potential for single-dose MDA with its broad-spectrum of action. Although tribendimidine appears safe and has broad-spectrum activity, a large-scale clinical study is advocated to further verify human safety.

B7.0 Conclusion

We have been excited by our discovery of further details of the modes of action of the different anthelmintics that we work on and believe that the information will be useful for defining mechanisms of resistance to the anthelmintic drugs that we have studied. We also think that the improved understanding of their mechanisms of action will lead to better use of

these compounds and logical design of synergistic combinations. We do not look back, but *forward*, to the future.

B8.0 Funding

The research project culminating in this paper was funded by the National Institute of Allergy and Infectious Diseases (NIH) grant R01 A1047194 to RJM and R21 AI092185 to APR. The funders had no role in study design, data collection and analysis, decision to publish, or preparation of the manuscript.

**APPENDIX C. THE *ASCARIS SUUM* NICOTINIC RECEPTOR, ACR-16, AS A
DRUG TARGET: FOUR NOVEL NEGATIVE ALLOSTERIC MODULATORS
FROM VIRTUAL SCREENING**

A paper published in *International Journal for Parasitology: Drugs and Drug Resistance*
(2016)¹

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C1.0 Abstract

Soil-transmitted helminth infections in humans and livestock cause significant debility, reduced productivity and economic losses globally. There are a limited number of effective anthelmintic drugs available for treating helminths infections, and their frequent use has led to the development of resistance in many parasite species. There is an urgent need for novel therapeutic drugs for treating these parasites. We have chosen the ACR-16 nicotinic acetylcholine receptor of *Ascaris suum* (Asu-ACR-16), as a drug target and have developed three-dimensional models of this transmembrane protein receptor to facilitate the search for new bioactive compounds. Using the human $\alpha 7$ nAChR chimeras and *Torpedo marmorata* nAChR for homology modeling, we defined orthosteric and allosteric binding sites on the Asu-ACR-16 receptor for virtual screening. We identified four ligands that bind to sites on

Asu-ACR-16 and tested their activity using electrophysiological recording from Asu-ACR-16 receptors expressed in *Xenopus* oocytes. The four ligands were acetylcholine inhibitors (SB-277011-A, IC_{50} , $3.12 \pm 1.29 \mu\text{M}$; (+)-butaclamol Cl, IC_{50} , $9.85 \pm 2.37 \mu\text{M}$; fmoc-1, IC_{50} , $10.00 \pm 1.38 \mu\text{M}$; fmoc-2, IC_{50} , $16.67 \pm 1.95 \mu\text{M}$) that behaved like negative allosteric modulators. Our work illustrates a structure-based in silico screening method for seeking anthelmintic hits, which can then be tested electrophysiologically for further characterization.

C1.1 Keywords

Asu-ACR-16; Structure-based drug discovery; Homology modeling; Orthosteric site; Allosteric modulator; *Xenopus* expression

C1.2 Abbreviations

ECD, extracellular domain; TID, transmembrane and intracellular domain; (+), principal subunit; (−), complementary subunit; NAM, negative allosteric modulator; nAChR, nicotinic acetylcholine receptor; AChBP, acetylcholine-binding protein

C2.0 Introduction

Soil-transmitted gastrointestinal nematodes, namely roundworms, whipworms and hookworms, infect approximately two billion people worldwide and pose a significant health challenge to humans and animals (de Silva et al., 2003 and Bethony et al., 2006). The infections with the soil-transmitted helminths can cause malnutrition, iron-deficiency anemia and impaired cognitive performance (Crompton, 2000 and Hotez et al., 2007). Currently, there are no effective vaccines available (Hewitson and Maizels, 2014), and sanitation is not adequate in many countries. The World Health Organization (WHO) recommends four anthelmintics for treatment and prophylaxis of soil-transmitted nematode infections: albendazole, mebendazole, levamisole and pyrantel (Keiser and Utzinger, 2008). The

repeated use of a limited number of anthelmintic drugs has led to an increase in drug resistance in animals and there are similar concerns for humans. It is therefore important to identify novel therapeutic compounds that selectively target receptors of parasitic nematodes so that we maintain effective therapeutics.

The nicotinic acetylcholine receptors (nAChRs) are pentameric ligand-gated ion channels that mediate synaptic transmission at neuromuscular junctions of vertebrates and invertebrates (Changeux and Edelstein, 1998). The neurotransmitter, acetylcholine, activates nAChRs by binding to orthosteric binding sites on the extracellular domain of the receptor and triggers the opening of the channel pore in the transmembrane domain. The opening of the nicotinic receptors leads to an influx of sodium and calcium depending on the receptor subtypes, as well as an output of potassium ions, followed by membrane depolarization and muscle contraction.

Nicotinic anthelmintics are selective agonists of nematode muscle nAChRs which cause spastic paralysis of the parasites (Martin and Robertson, 2010 and Buxton et al., 2014). There are three different pharmacological subtypes of nAChRs present on muscle of *Ascaris suum*. The anthelmintics, levamisole and pyrantel are selective agonists of L-subtypes of nAChRs in *A. suum* (Martin et al., 2012). Bephenium selectively activates B-subtypes of nAChRs. Nicotine and oxantel selectively activate N-subtypes of nAChRs in *A. suum* (Qian et al., 2006). The anthelmintic monepantel activates nAChRs which are composed of DEG-3-like subunits (*Haemonchus contortus* MPTL-1, *Caenorhabditis elegans* ACR-20 and *H. contortus* ACR-23 subunits (Rufener et al., 2010 and Buxton et al., 2014). We have selected the N-subtype of nAChR that is composed of ACR-16 subunits (Ballivet et al., 1996 and Polli et al., 2015) for a drug target, because it is pharmacologically different to the

other nicotinic receptor subtypes (Raymond et al., 2000), for further study. Asu-ACR-16 transcript has been found in *A. suum* muscle and may be involved in locomotion.

The ACR-16 nicotinic acetylcholine receptor of *A. suum* (Asu-ACR-16) is a homomeric receptor made up of five identical α subunits. Homomeric nAChRs have five identical orthosteric binding sites where agonists and competitive antagonists bind at the interface of two adjacent subunits. The orthosteric site is in the extracellular domain and is formed by the loops A, B & C of the principal subunit and by the loops D, E & F on the complementary subunit (Galzi et al., 1991 and Arias, 2000). In addition, three allosteric binding sites close to the orthosteric binding sites in the extracellular domain have been observed in the $\alpha 7$ nAChR-AChBP chimera (Spurny et al., 2015). In the transmembrane domain, an intrasubunit allosteric binding site has been found in *Rattus. norvegicus* $\alpha 7$ nAChR (Young et al., 2008), while an intersubunit allosteric binding site has been found in *C. elegans* glutamate-gated chloride channel (GluCl) (Hibbs and Gouaux, 2011). These well-studied binding sites in nAChRs or other Cys-loop receptors provided our framework for characterizing putative orthosteric and allosteric sites in Asu-ACR-16.

Because of the lack of a crystal structure for Asu-ACR-16, we used homology modeling to predict the protein structure, based on the observations that proteins with similar sequences usually have similar structures (Cavasotto and Phatak, 2009). In this study, we used homology modeling to predict the three-dimensional structure of Asu-ACR-16, based on the observed experimental structures of the human $\alpha 7$ nAChR chimeras and the *Torpedo marmorata* nAChR as templates. Virtual screening was performed for the ACR-16 orthosteric binding sites, using the predicted structure to identify the potential candidates of agonists and competitive antagonists. Allosteric binding sites were also used to examine the

binding properties of the virtual screening hits. Subsequently, we tested the pharmacological profiles of virtual screening hits on Asu-ACR-16 receptors expressed in *Xenopus laevis* oocytes, using a two-electrode voltage clamp to test the activity of the hits on the receptors.

C3.0 Materials and methods

C3.1 Identification of template structures

We selected the extracellular domain of Asu-ACR-16 (ECD-Asu-ACR-16) because it forms a homologomer that allows homology modeling. In addition, many of the agonists that activate Asu-ACR-16, acetylcholine, nicotine, cytosine, epibatidine (Abongwa et al., 2016), are also known to bind to the orthosteric binding sites of extracellular domain of *Lymnaea stagnalis* AChBP or *A. californica* AChBP (Celie et al., 2004, Li et al., 2011, Rucktooa et al., 2012 and Olsen et al., 2014a). In addition to the orthosteric binding site, three separate allosteric binding sites in the extracellular domain of $\alpha 7$ nAChR are now recognized (Bertrand et al., 2008, Pan et al., 2012 and Spurny et al., 2015), increasing the possibility of identifying allosteric modulators.

The amino acid sequence of Asu-ACR-16 (Fig. 1) was obtained from the UniProtKB/SwissProt database with the accession number F1KYJ9 (Wang et al., 2011). Structural templates were identified by using BLASTP on NCBI network service (Altschul et al., 1997) and PSI-BLAST on the ProtMod server (Rychlewski et al., 2000) by searching in the Protein Data Bank (Berman et al., 2000). Three crystal structures of human $\alpha 7$ nAChR chimeras with different co-crystal ligands in orthosteric binding site were used: epibatidine bound (PDB code: 3SQ6; Li et al., 2011), no ligand (PDB code: 3SQ9; Li et al., 2011), and α -bungarotoxin bound (PDB code: 4HQP; Huang et al., 2013). These structures were selected as the templates for three different bound-forms of the ECD-Asu-ACR-16. The three

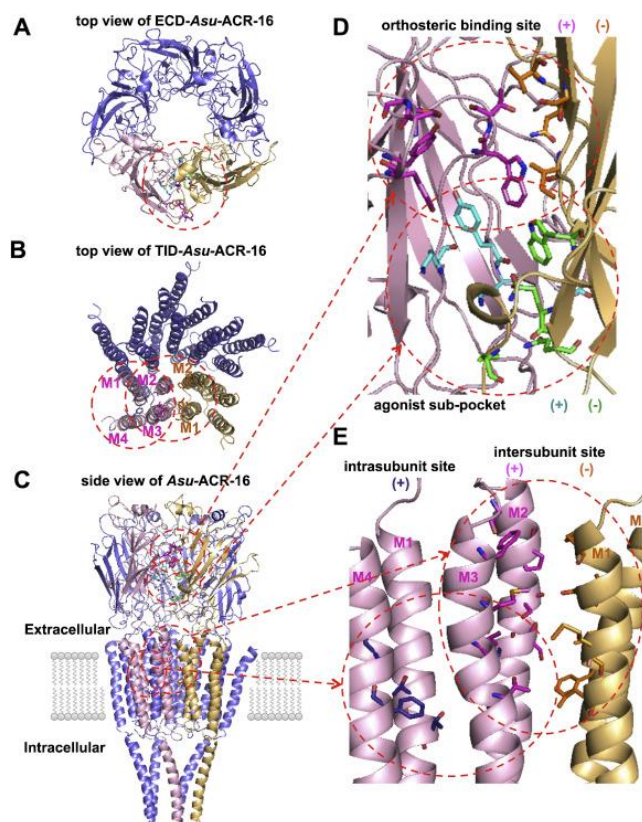


Fig. 2. (A) Ribbon diagram of the antagonist-bound model of ECD-Asu-ACR-16 viewed from the synaptic cleft, showing the location of the orthosteric binding site and agonist sub-pocket. For clarity, only the front two subunits are highlighted (principal subunit, light pink; complementary subunit, yellow). The residues that contribute to the orthosteric binding site (principal side, pink; complementary side, orange) and the agonist sub-pocket (principal side, turquoise; complementary side, green) are represented by sticks and highlighted inside the red dotted circle. (B) Ribbon diagram of the antagonist-bound model of TID-Asu-ACR-16 viewed above the membrane, showing the location of two transmembrane allosteric binding sites. For clarity, only the front two subunits are highlighted (principal subunit, light pink; complementary subunit, yellow). The residues that contribute to the intersubunit site (principal side, pink; complementary side, orange) and intrasubunit site (principal side, purpleblue) are represented by sticks and highlighted inside the red dotted circle. (C) Ribbon diagram of the antagonist-bound model of full-length Asu-ACR-16 viewed parallel to the membrane plane, showing the location of the orthosteric binding site and the agonist sub-pocket in the extracellular domain, the intersubunit and intrasubunit binding sites in the transmembrane domain. For clarity, only the front two subunits are highlighted (principal subunit, light pink; complementary subunit, yellow). The residues that contribute to the ligand binding sites are represented by sticks (orthosteric site: (+), pink; (-), orange; agonist sub-pocket: (+), turquoise; (-), green; intersubunit transmembrane site: (+), pink; (-), orange; intrasubunit transmembrane site: purpleblue) and highlighted inside the red dotted circle. (D) Detailed view of the orthosteric binding site and agonist sub-pocket in the antagonist-bound model of ECD-Asu-ACR-16. The principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the orthosteric binding site (principal side, pink; complementary side, orange) and the agonist sub-pocket (principal side, turquoise; complementary side, green) are represented by sticks and highlighted inside the red dotted circle. Carbon is in either turquoise or green. Nitrogen is in blue. Oxygen is in red. (E) Detailed view of the transmembrane allosteric binding sites in the antagonist-bound model of TID-Asu-ACR-16. The principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to intersubunit site (principal side, pink; complementary side, orange) and intrasubunit site (principal side, purpleblue) are represented by sticks and highlighted inside the red dotted circle. Carbon is in either pink or orange or purpleblue. Nitrogen is in blue. Oxygen is in red. Sulfur is in yellow. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

models were: the agonist-bound form ECD-Asu-ACR-16; the apo form ECD-Asu-ACR-16 and; the antagonist-bound form ECD-Asu-ACR-16 (Fig. 2A).

We modeled the transmembrane and intracellular domains of Asu-ACR-16 (TID-Asu-ACR-16, Fig. 2B) because of the presence of an intrasubunit allosteric binding site that is found in $\alpha 7$ nAChR and an intersubunit allosteric binding site that is demonstrated in a Cys-loop receptor, GluCl crystal structure in complex with ivermectin (Young et al., 2008, Bertrand et al., 2008 and Hibbs and Gouaux, 2011). Ivermectin is a known allosteric modulator of $\alpha 7$ nAChRs (Krause et al., 1998). The *T. marmorata* nAChR (PDB code: 2BG9 chain A; Unwin, 2005) is the only pentameric nAChR structure with the transmembrane domains and partial intracellular domains determined. Therefore, the transmembrane and intracellular domains of *T. marmorata* nAChR (TID-Tma-nAChR) were selected as the template for our TID-Asu-ACR-16 model.

The sequence of the ECD-Asu-ACR-16 and the human $\alpha 7$ nAChR chimera (SwissProt ID: P36544; Peng et al., 1994) were aligned using CLUSTALW multiple alignment (Thompson et al., 1994). The sequence of the TID-Asu-ACR-16 and TID-Tma-nAChR (SwissProt ID: P02711; Devillers-Thiery et al., 1983 and Devillers-Thiery et al., 1984) were aligned using CLUSTALW.

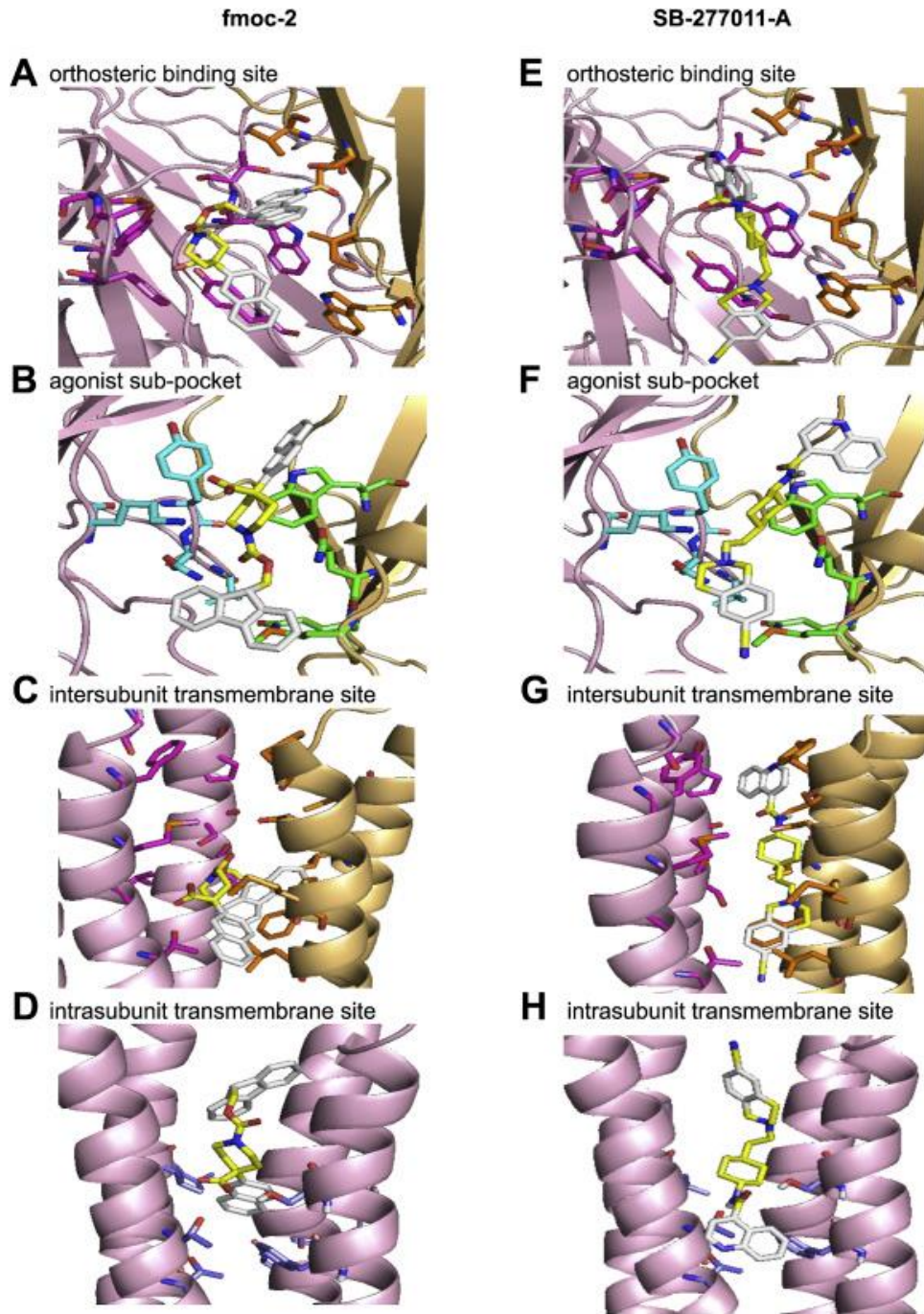
C3.2 Homology modeling of Asu-ACR-16

We used Modeller (Eswar et al., 2007) to build a three-dimensional model of ECD-Asu-ACR-16 and used JACKAL (http://wiki.c2b2.columbia.edu/honiglab_public/index.php/Software:Jackal) to build the model of TID-Asu-ACR-16 for each of the five subunits. These five subunits were then assembled to generate the pentamer using COOT software (Emsley and Cowtan, 2004). The

model geometry was first refined manually, and then optimized by PHENIX software (Adams et al., 2010). Each of the TID-Asu-ACR-16 subunits were then merged into the ECD-Asu-ACR-16 model by using COOT to edit and alter the C_{α} coordinates of residues around the outer membrane regions. The final optimized pentameric model was then visualized using the program PyMol (The PyMOL Molecular Graphics System, Version 1.7.4, Schrödinger, and LLC., Figs. 2C & S1).

C3.3 Structure-based virtual screening

Smiles strings of ligands were downloaded from the lead-like subset of commercially available compounds in the ZINC Database (Irwin et al., 2012) and were converted initially to PDB formats using the PHENIX-eLBOW program (Moriarty et al., 2009). The ligand and receptor input files were then prepared in PDBQT format for AutoDock Vina by using the AutoDock Tools package (Morris et al., 2009). For initial screening, a docking area was defined visually around the orthosteric binding site of ECD-Asu-ACR-16 (Fig. 2D S2A & S2B) by a grid box of $40 \text{ \AA} \times 40 \text{ \AA} \times 40 \text{ \AA}$ using 0.375 \AA grid point spacing in AutoGrid. The conformations of ligands in the binding sites of the receptor were searched with GALS (Genetic Algorithm with Local Search; Morris et al., 1998). The binding free energies between the ligands and receptor were calculated by the combination of the knowledge-based and empirical scoring function in AutoDock Vina (Trott and Olson, 2010). The best nine binding modes of the ligand based on the binding affinities on the three bound-forms of ECD-Asu-ACR-16 models were implemented by AutoDock 20 runs for each ligand. Each docked ligand was then ranked by its highest binding affinity to the orthosteric binding site of the apo, agonist-bound, or antagonist-bound model. From the 60,000 screened molecules, we selected the top 9 ligands (0.015%) with the highest predicted affinities that had



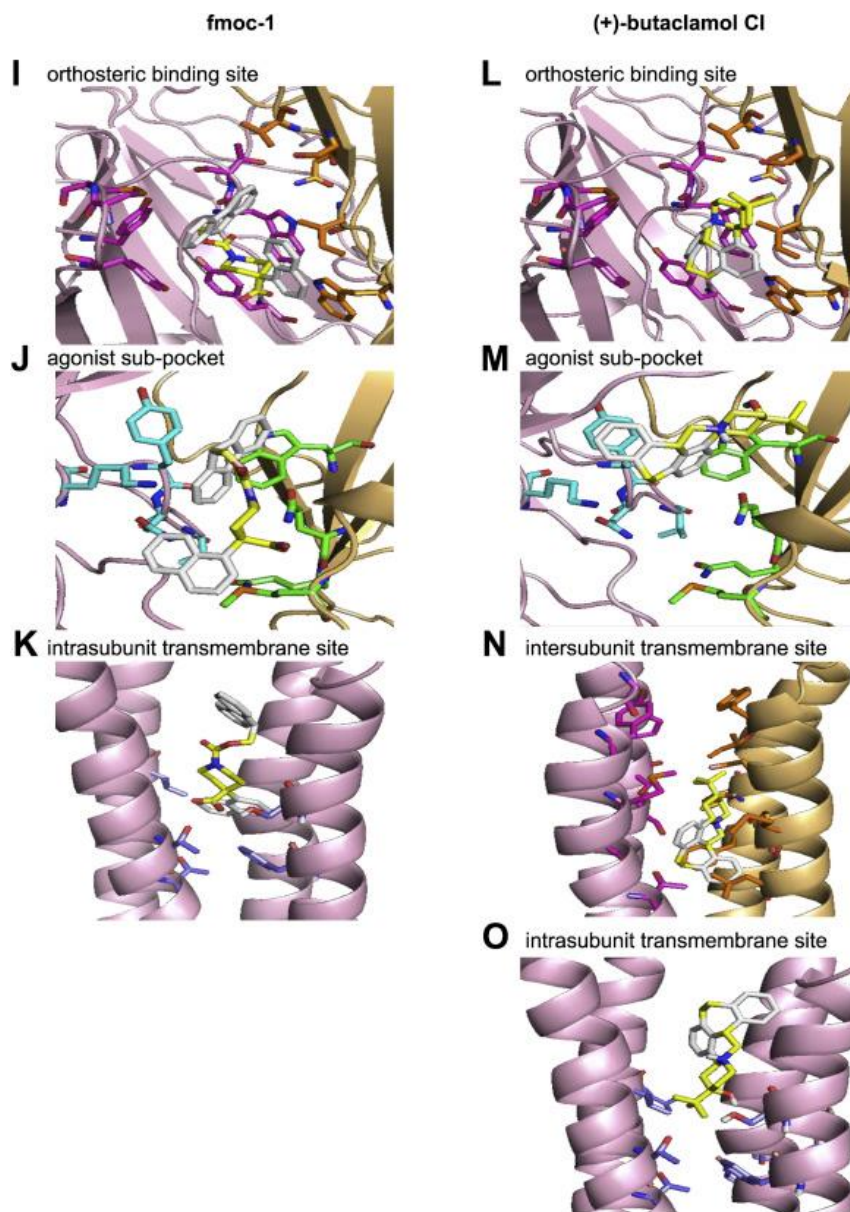


Fig. 3. Binding modes of four virtual screening hits in the orthosteric binding site, the agonist sub-pocket, the intersubunit and intrasubunit transmembrane allosteric binding pockets of the antagonist-bound model of Asu-ACR-16: (A), (B), (C), (D) fmc-2; (E), (F), (G), (H) SB-277011-A; (I), (J), (K) fmc-1; (L), (M), (N), (O) (+)-butaclamol Cl. Hits docked into the binding pockets are represented by sticks (carbon in yellow; ring in white; nitrogen in blue; oxygen in red). (A), (E), (I) and (L) show the four hits bound in the orthosteric binding site of the antagonist-bound model of ECD-Asu-ACR-16. The front two subunits are highlighted (principal subunit, light pink; complementary subunit, yellow). The residues in the orthosteric binding site are labeled (principal side, pink; complementary side, orange) to show the location of the orthosteric binding site. (B), (F), (J) and (M) show the four hits bound in the agonist sub-pocket of the antagonist-bound model of ECD-Asu-ACR-16. The front two subunits are highlighted. The residues in the agonist sub-pocket are labeled (principal side, turquoise; complementary side, green) to show the location of the agonist sub-pocket. (C), (G) and (N) show the four hits bound in the intersubunit transmembrane site of the antagonist-bound model of TID-Asu-ACR-16. The front two subunits are highlighted. The residues in the intersubunit transmembrane site are labeled (principal side, pink; complementary side, orange) to show the location of the intersubunit transmembrane binding site. (D), (H), (K) and (O) show the four hits bound in the intrasubunit transmembrane site of the antagonist-bound model of TID-Asu-ACR-16. The residues in the intrasubunit transmembrane site are labeled (purple/blue) to show the location of the intersubunit transmembrane binding site. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

C3.4 *In vitro* synthesis of cRNA and microinjection into *Xenopus laevis* oocytes

We used TRIzol (Invitrogen™) to extract the total RNA samples from a 1 cm muscle flap and dissected the whole pharynx of *A. suum*. The first-strand of cDNA was synthesized with oligo RACER primer, Random Hexamer and superscript III reverse transcriptase (Invitrogen, Carlsbad, CA, USA) from total RNA in the muscle and pharynx by reverse transcription polymerase chain reaction (RT-PCR). Full-length *Asu-acr-16* cDNA was amplified with the forward primer TTGATGTAGTGGCGTCGTGT, ATCACGCATTACGGTTGATG and the reverse primer GCATTGATGTTCCCTCACCT, ATTAGCGTCCCAAGTGGTTG (Boulin et al., 2011). The XhoI and ApaI restriction enzymes were used to digest the amplified product, which was then cloned into pTB207 expression vector (Boulin et al., 2008) and linearized by NheI. We used the mMessage mMachinE T7 kit (Ambion) to *in vitro* transcribe the linearized cDNA to cRNA, which was then precipitated with lithium chloride, re-suspended in RNase-free water, aliquoted and stored at -80°C .

The ancillary protein RIC-3 is required for the expression of ACR-16 in *Xenopus* oocytes (Halevi et al., 2003). A 50 nL cRNA mixture was prepared with 25 ng *Asu-acr-16* cRNA, 5 ng *Asu-ric-3* cRNA (SwissProt ID: F1L1D9; Wang et al., 2011) dissolved in RNase-free water. The nanoject II microinjector (Drummond Scientific, PA, USA) was used to inject the cRNA mixture into the animal pole of the de-folliculated *X. laevis* oocyte (Ecocyte Bioscience, Austin, TX, USA).

The injected oocytes were separated into 96-well culture plates and incubated in the incubation solution (pH 7.5), which is composed of 100 mM NaCl, 2 mM KCl, 1.8 mM $\text{CaCl}_2 \cdot 2\text{H}_2\text{O}$, 1 mM $\text{MgCl}_2 \cdot 6\text{H}_2\text{O}$, 5 mM HEPES, 2.5 mM Na pyruvate, 100 U/mL penicillin,

100 µg/mL streptomycin and changed daily. The injected oocytes were stored at 19 °C for 4–8 days to allow the receptor to be expressed.

C3.5 Two-electrode voltage-clamp oocyte recording

We used two-electrode voltage-clamp electrophysiology to record the inward current generated by the activated Asu-ACR-16 receptors expressed in *X. laevis* oocytes. 100 µM BAPTA-AM (final concentration) was added into the oocyte incubation solution 4 h prior to recording, to prevent the current produced by the endogenous calcium-activated chloride channels during recording. An Axoclamp 2B amplifier (Molecular Devices, CA, USA) was used for recording and oocytes were held at –60 mV. A PC computer with software Clampex 9.2 (Molecular Devices, CA, USA) was used to acquire the recording data. The microelectrodes used to measure current in oocytes were pulled on a Flaming/Brown horizontal electrode puller (Model P-97, Sutter Instruments), filled with 3M KCl and had resistances of 20–30 MΩ. The microelectrode tips were broken back carefully with Kimwipes (Wilmington, NC, USA) to reduce the resistance to 2–5 MΩ. The recording solution was: 100 mM NaCl, 2.5 mM KCl, 1 mM CaCl₂·2H₂O and 5 mM HEPES, pH 7.3 (Buxton et al., 2014). Oocytes were placed into a tiny groove of the narrow oocyte recording chamber. The Digidata 1322A (Molecular Devices, CA, USA) was used to control the switches that controlled the perfusion of the chamber at a speed of 4–6 ml/min.

100 µM acetylcholine was applied initially for 10 s as a control to check the viability of the oocytes and Asu-ACR-16 expression for all the recordings. Recording solution was then used to wash out the drug from the oocytes for 2–3 min before next application of drug perfusion.

C3.6 Drugs

Table 1 lists the compounds used, their chemical properties and structures. Fmoc-4-(naphthalen-2-yl)-piperidine-4-carboxylic acid (fmoc-2), SB-277011-A hydrochloride hydrate (SB-277011-A), fmoc-4-(naphthalen-1-yl)-piperidine-4-carboxylic acid (fmoc-1) and (+)-butaclamol hydrochloride (+)-butaclamol Cl), acetylcholine chloride (ach), methyllycaconitine citrate salt (mla) were purchased from Sigma–Aldrich (St Louis, MO, USA). Levamisole hydrochloride (levamisole) was purchased from MP Biomedicals (Santa Ana, CA, USA). With the exception of ach and mla which were dissolved in the recording solution, the rest of chemicals were dissolved in dimethyl sulfoxide (DMSO) to make stock solutions. Stock solutions of 100 mM were prepared, except for SB-277011-A where a stock solution of 10 mM was prepared due to the solubility; stock solutions were frozen until required. Working solutions were then prepared by dilution on the day of the experiment.

C3.7 Pharmacological characterization of molecules selected by virtual screening

To characterize the four hits (Table 1) selected by our virtual screening, each drug was applied for 10 s to the oocytes expressing Asu-ACR-16 to test if the drugs were agonists. They were then tested as antagonists against ach.

To characterize the antagonistic properties of the four hits, the following protocol was used: a) 10 s of 100 μ M ach alone; b) then 10 s of 100 μ M ach + hit and then; c) 10 s of 100 μ M ach alone. This test procedure was repeated with increasing concentrations of the four hits (Fig. 4A–D), to determine the inhibitory dose–response relationships and IC_{50} by fitting Hill equations to the inhibitory dose–response curves using GraphPad Prism 5.0 (Graphpad Software Inc., CA, USA). As a further study of the antagonism, each of the four hits was applied before and during 10 s test applications of increasing concentrations of ach (Fig. S4).

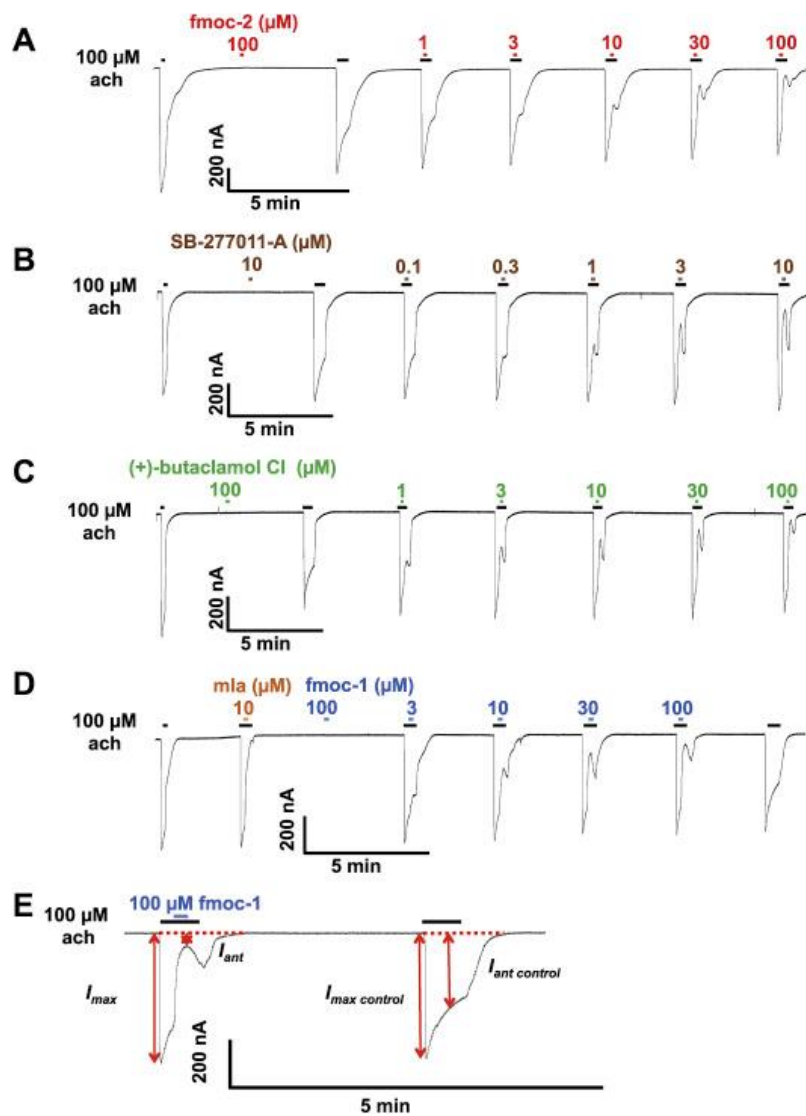


Fig. 4. Effects of four virtual screening hits on Asu-ACR-16 mediated ach responses. Sample traces for: (A) fmoc-2, (B) SB-277011, (C) (+)-butaclamol Cl, (D) fmoc-1 concentration-inhibition relationships on Asu-ACR-16. Mla in (D), which stands for methyllycaconitine citrate salt, was used as an antagonist control of Asu-ACR-16. All four hits did not induce the current response by themselves, while produced the concentration-depended inhibition of ach current response. (E) is the magnified figure of part of (D) as an example to show the four parameters needed to measure the inhibition percentage. $I_{max\ control}$ was the peak current of the control 30 s application of 100 μM ach. I_{max} was the peak current of the 100 μM ach that preceded the 10 s co-application of ach and antagonist. I_{ant} was the minimal current during the co-application of 100 μM ach and antagonist. $I_{ant\ control}$ was the current at the same time point from the beginning of the 30 s application as I_{ant} during the control 30 s application of 100 μM ach.

C3.8 Data analysis

The data from electrophysiological recordings were analyzed using Clampfit 9.2 (Molecular Devices, CA, and USA) and GraphPad Prism 5.0 (Graphpad Software Inc., CA, USA). In all recordings, the peak currents in response to applied drugs were measured, which were later normalized to the control 100 μM ach response, and expressed as mean \pm S.E.M. The mean % inhibition of currents elicited by 100 μM ach \pm S.E.M. was used to determine the inhibition percentage, which was quantified using the following equation:

$$\text{Inhibition}(\%) = \left(1 - \frac{I_{\text{ant}}}{\frac{I_{\text{ant control}}}{I_{\text{max control}}} \times I_{\text{max}}} \right) \times 100\%$$

where $I_{\text{max control}}$ was the peak current of the control 30 s application of 100 μM ach, I_{max} was the peak current of the 100 μM ach that preceded the 10 s co-application of ach and antagonist. I_{ant} was the minimal current during the co-application of 100 μM ach and antagonist. $I_{\text{ant control}}$ was the current at the same point from the beginning of the 30 s application as I_{ant} during the control 30 s application of 100 μM ach (Fig. 4E). Concentration-response relationships or concentration-inhibition (%) relationships were analyzed by fitting data points into the Hill equation, with at least four replicates of each experiment set.

C3.9 Drug treatment of *C. elegans*

The wild-type *C. elegans* strain N2 were obtained from the Caenorhabditis Genetics Center (University of Minnesota, MN, USA). We grew *C. elegans* at 20 °C on nematode growth media (NGM, 3 g/l NaCl, 17 g/l agar, 2.5 g/l peptone, 1 mM CaCl₂, 5 mg/l cholesterol, 1 mM MgSO₄, 25 mM KPO₄ buffer) agar plates, seeded with *Escherichia. coli* OP50 lawn under standard conditions (Brenner, 1974). Ten larvae at L4 stage with active thrashing movement (defined as “normal”) were transferred from NGM plates into M9 buffer

(3 g/l KH_2PO_4 , 6 g/l Na_2HPO_4 , 5 g/l NaCl, 1 mM MgSO_4) in 24-wall plates for each treatment. We counted the number of worms with normal motility in M9 buffer with diluted drugs from the stock solutions ($\leq 1\%$ DMSO) at 0, 5, 10, 15 and 20 min. Five replicates were applied for each treatment. Motility between negative control (1% DMSO, final concentration) and drug treated worms were compared at each time point using student t-test.

C4.0 Results

C4.1 Sequence alignment of *Asu*-ACR-16 and template homologue proteins

The full-length protein sequence of *Asu*-ACR-16 (504 residues) was retrieved from the SwissProt database, of which the ECD-*Asu*-ACR-16 accounts for 234 residues. The first 25 residues of *Asu*-ACR-16 were excluded from alignment with the full length human nAChR $\alpha 7$ chimera (204 residues) because of the shorter length of the template protein sequence. The human $\alpha 7$ nAChR chimera shows 37.6% sequence identity and 72.9% sequence similarity with the ECD-*Asu*-ACR-16, based on the alignment generated by CLUSTALW (Fig. 1A, job ID: 65782ad6ad6d). The TID-Tma-nAChR subunit A shows 22.0% sequence identity and 45.4% sequence similarity with TID-*Asu*-ACR-16, aligned by CLUSTALW (Fig. 1B, job ID: 644888f4f30e). The residues involved in the putative orthosteric and the allosteric binding sites are highlighted in amino acids sequence of *Asu*-ACR-16.

C4.2 Models of the *Asu*-ACR-16 pentamer

The model of the antagonist-bound form of the ECD-*Asu*-ACR-16 subunit starts from an N-terminal α helix followed by seven β strands that comprise an immunoglobulin fold. Loop A (Val114 – Ala122), loop B (Lys169 – Lys179), loop C (Phe213 – Pro220) from the principal subunit, and loop D (Ala78 – Ala83), loop E (Ile143 – Pro144), loop F (Gly185 – Met204) from the complementary subunit are involved in forming the orthosteric binding

site. A disulphide bond between Cys152 and Cys166 contributes to the characteristic component of Cys-loop receptors. The C-terminal continues into the transmembrane domain (Fig. S1A).

The transmembrane domains of the Asu-ACR-16 model are made of four α -helices (M1, M2, M3 and M4). M1 links to the β 7 sheet of the extracellular domain and extends down into the membrane and is followed by the M2 and the M3 helices as the membrane-spanning portions. The MA cytoplasmic loop (helix) connects between M3 and M4. The region between M3 and MA is not modeled due to the poorly defined intracellular domain of the template structure. The C-terminal follows the M4 helix and faces toward the extracellular surface (Fig. S1B).

The pentameric model of Asu-ACR-16 has a five-fold symmetry around the channel pore. The average pairwise Root Mean Square Deviation (RMSD) fit of the C_{α} coordinates of the antagonist-bound ECD-Asu-ACR-16 pentameric model and human α 7 nAChR chimera pentamer (PDB code: 4HQP) was 0.9 Å, which indicates a strong structural conservation between the model and the template structures (Fig. S1C). The C_{α} -RMSD between the TID-Asu-ACR-16 pentamer and the TID-Tma-AChR pentamer was 1.5 Å, which shows the TID fit is still good but not as good as the ECD fit. The membrane-spanning domains are arranged symmetrically. The M2 helix lines the channel pore, while M1, M3 and M4 do not contribute to the channel pore and are arranged peripherally (Fig. S1D).

Since no binding site data of Asu-ACR-16 is available to date, we used the published orthosteric binding site and allosteric binding sites in nAChRs or other Cys-loop receptors to predict the putative binding sites in Asu-ACR-16 (Galzi et al., 1991, Arias, 2000, Young et al., 2008, Hibbs and Gouaux, 2011 and Spurny et al., 2015). The orthosteric binding site is

at the interface between the principal site and the complementary site in two adjacent subunits of the ECD-Asu-ACR-16 pentamer (Fig. 2S2A & S2B). The principal subunit (+) has vicinal cysteines (Cys216, Cys217) that contributes to the loop C of the binding site. The complementary subunit (-) does not use vicinal cysteines as part of the binding pocket and the residues are more variable when nAChRs are compared. The agonist sub-pocket, which we argue is a less significant allosteric binding site in ECD-Asu-ACR-16, is located right below the orthosteric binding site in the extracellular domain (Fig. 2S2C & S2D). The vestibule pocket (Fig. S2E & S2F) and the top pocket (Fig. S2G & S2H) were not high affinity binding sites for the ligands and are not discussed further in this manuscript. The intersubunit allosteric binding sites in TID-Asu-ACR-16 are at the interface region between M2(+), M3(+), M1(-) and M2(-) (Fig. 2S2I & S2J). The intrasubunit allosteric binding sites are at the center of the four transmembrane helices (M1, M2, M3 and M4) in each of the five subunits.

C4.3 Binding properties of virtual screening hits

We carried out virtual screening of the ZINC ligand-database by using the three different bound forms of the ECD-Asu-ACR-16 models. Four molecules were selected as hits based on their high binding affinities and appropriate binding modes within the ligand-binding sites. The 9-fluorenylmethoxycarbonyl group (FMOC) was observed in twelve out of top forty hits ranked by binding affinities and exists in the two out of four hits, which suggests that FMOC could be necessary for the ligand recognition by the receptor. The FMOC group has a low predicted bioavailability due to the biphenyl scaffold, which limits aqueous solubility and may affect distribution to the *A. suum* parasite. Table 1 lists the physicochemical characteristics of four hits. They have relatively high molecular weights and

are more hydrophobic compared to known Asu-ACR-16 agonists. However, they do follow the Lipinski's rule of five, which suggests that these molecules may be orally active (Lipinski et al., 2001 and Lipinski, 2004).

The atomic structure predicts the partition-coefficients (XlogP) of the four hits to be between 4.27 and 6.04 (Table 1). The XlogPs suggest that the four hits are 10,000–1,000,000 times more concentrated in the lipophilic phase of the lipid bilayer than the aqueous phase of the extracellular domain (Cheng et al., 2007). The four hydrophobic hits are, therefore, more likely to bind into the transmembrane allosteric binding pockets rather than to the extracellular ligand binding sites. The four hits which bind in the transmembrane allosteric binding pockets are therefore predicted to be allosteric modulators of the Asu-ACR-16 receptor that alter the activity of the agonists or competitive antagonists that bind to orthosteric binding site. SB-277011-A is known to be a potent and selective dopamine D₃ receptor antagonist with high oral availability (Stemp et al., 2000). (+)-butaclamol Cl is a non-selective dopamine receptor antagonist and a potent antipsychotic agent (Chrzanowski et al., 1985). No paper reporting on the activities of fmoc-2 and fmoc-1 has been published to date.

The four hits (Table 1) were tested for docking into the orthosteric binding sites of the three forms of ECD-Asu-ACR-16 models and the five allosteric binding pockets in the antagonist-bound form of full-length Asu-ACR-16 models. All four hits bound to the orthosteric binding sites of three ECD-Asu-ACR-16 models, but only bound to the three allosteric binding sites out of five: the intersubunit and intrasubunit transmembrane pockets and the agonist sub-pocket (Fig. 3) with high binding affinities.

In the intersubunit transmembrane site of TID-Asu-ACR-16 model, M243 (M1, (-)), L247 (M1, (-)) make hydrophobic interactions with naphthalene of fmoc-2. T312 (M3, (+)), S284 (M2, (+)) form hydrogen bonds with carboxylic acids of fmoc-2. F279 (M2, (-)), I282 (M2, (-)) and make hydrophobic contacts with fluorene of fmoc-2. F279 (M2, (-)), P244 (M1, (-)) make hydrophobic interactions with tetrahydroisoquinoline of SB-277011-A. N240 (M1, (-)) forms a hydrogen bond with carboxamide of SB-277011-A. P288 (M2, (+)) has hydrophobic interactions with quinoline of SB-277011-A. L247 (M1, (-)), F279 (M2, (-)) and makes hydrophobic contacts with dibenzocycloheptene of (+)-butaclamol Cl.

Ach, the natural agonist of Asu-ACR-16 was docked into the ligand binding sites of three forms of Asu-ACR-16 models for comparison. As expected, ach bound to the orthosteric binding site of the agonist-bound Asu-ACR-16 with an affinity (-4.3 kcal/mol), which was higher than the affinities at the other binding sites. The binding pose of ach docked in the orthosteric binding site of the agonist-bound Asu-ACR-16 model was in agreement with the binding pose of ach in the *L. stagnalis* AChBP cocrystal structure (PDB code: 3WIP; Olsen et al., 2014b). The quaternary ammonium of ach faces the basal side of the binding cavity and make cation- π interaction with five aromatic residues from the Asu-ACR-16 ((+): Y89, W143, Y185, Y192; (-): W53), while the carbonyl oxygen of ach faces toward the apical side of the binding cavity. The binding affinities of the selected four compounds were higher than -8.0 kcal/mol in the three different bound forms of Asu-ACR-16, while the binding affinities of ach were lower than -4.5 kcal/mol in three states of Asu-ACR-16 (Table 2).

Table 2

Binding affinities (kcal/mol) of the four hits and ach in the orthosteric binding sites of the three different bound models of ECD-Asu-ACR-16 and three allosteric binding sites of the antagonist-bound model of full-length Asu-ACR-16.

Hits	Binding affinities (kcal/mol)						
	Apo	Agonist-bound		Antagonist-bound		Transmembrane site	
	Orthosteric binding site	Orthosteric binding site	Orthosteric binding site	Agonist sub-pocket	Inter-subunit	Intra-subunit	
fmoc-2	-10.4	-13.0	-10.2	-8.5	-11.4	-10.8	
SB-277011-A	-9.8	-12.3	-9.2	-9.5	-10.8	-9.7	
fmoc-1	-10.6	-12.3	-10.3	-8.9	NA	-11.0	
(+)-butaclamol Cl	-9.5	-11.8	-8.2	-9.2	-10.8	-9.0	
ach	-4.2	-4.3	-3.9	-4.0	-3.7	NA	

C4.4 Pharmacological properties of virtual screening hits

We tested the effects of the putative allosteric modulators on Asu-ACR-16 receptors expressed in *Xenopus* oocyte using two-electrode voltage clamp to observe the currents that flow through Asu-ACR-16 receptors. Representative traces showing the inhibitory dose–response relationships are shown in Fig. 4. Their IC_{50} (Fig. 5A and B) and maximum inhibition (Fig. S3) were determined as described in the methods (Table 3). The most potent antagonist among them was SB-277011-A, which had an IC_{50} of $3.12 \pm 1.29 \mu\text{M}$ and maximum inhibition effect of $96.07 \pm 10.66\%$ ($n = 4$).

The ach concentration-response plots in the presence of $3 \mu\text{M}$ of each putative allosteric modulator (Fig. S4 & Fig. 5C), show the reduced maximum current responses with little shift in EC_{50} of ach (Fig. 5D and E & Table 4), and that the hits were non-competitive antagonists and negative allosteric modulators.

At $10 \mu\text{M}$, SB-277011-A, showed evidence of a mixed competitive and non-competitive antagonism (Fig. S5), characterized by a reduced maximum current response and a right-shift in the EC_{50} of ach (Fig. 5D and E). Thus, $10 \mu\text{M}$ SB-277011-A appears to act at more than one binding site which may include the orthosteric binding sites and additional allosteric binding sites.

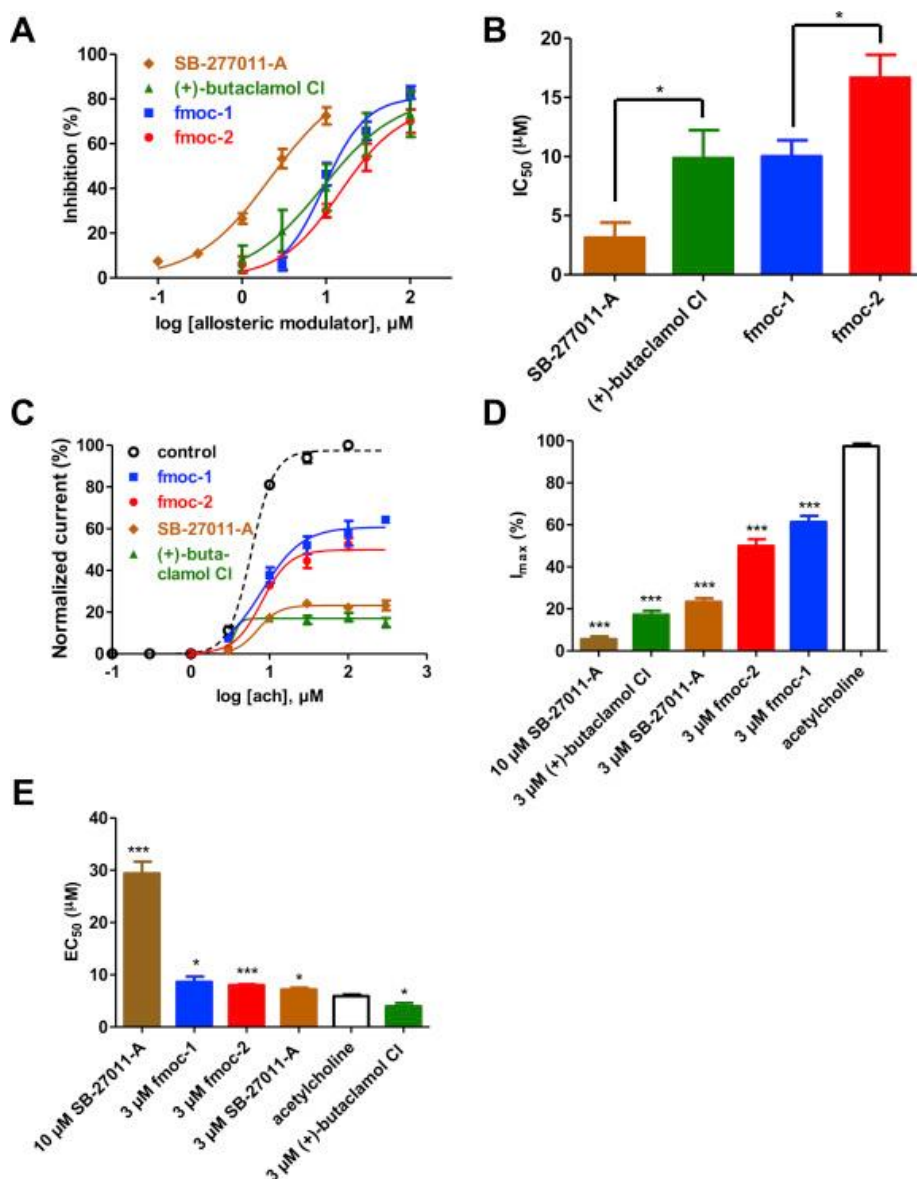


Fig. 5. (A) Effects of four virtual screening hits on Asu-ACR-16 mediated ach responses. Fmoc-2, fmoc-1, (+)-butaclamol Cl and SB-277011-A concentration-inhibition curves for Asu-ACR-16. Results were expressed as mean % inhibition of currents elicited by 100 μM ach ± S.E.M. (B) Bar chart representing the IC₅₀ (mean ± S.E.M, μM) of each plots in (A). The rank order series of inhibition based on IC₅₀ for four hits is: SB-277011-A (3.12 ± 1.29 μM, n = 4) < (+)-butaclamol Cl (9.85 ± 2.37 μM, n = 4) ≈ fmoc-1 (10.00 ± 1.38 μM, n = 4) < fmoc-2 (16.67 ± 1.95 μM, n = 4). * represents p < 0.05 (unpaired t-test). (C) Ach concentration-response plots for Asu-ACR-16 in the absence of hits as a control (ach) and in the continual presence of four hits identified in (A). Ach concentration-response curves for Asu-ACR-16 in the presence of 3 μM of four hits: fmoc-1, fmoc-2, SB-27011-A and (+)-butaclamol Cl. (D) Bar chart (mean ± S.E.M, %) representing the reduced maximum current response of ach concentration-response curves in (C). The series of reduced maximum response of each hits compared to that of ach by unpaired t-test is: 10 μM SB-27011-A (5.51 ± 1.38%, n = 4), 3 μM (+)-butaclamol Cl (17.22 ± 1.94%, n = 4), 3 μM SB-27011-A (23.25 ± 1.80%, n = 5), 3 μM fmoc-2 (49.92 ± 3.27%, n = 4), 3 μM fmoc-1 (61.25 ± 3.08%, n = 4) and ach (97.45 ± 1.19%, n = 4). * represents p < 0.05, ** represents p < 0.01, *** represents p < 0.001. All four hits significantly inhibited the maximum current response induced by ach. (E) Bar chart (mean ± S.E.M, μM) displaying the EC₅₀ of ach concentration-response curves in (C). The series of variable EC₅₀ of each hits compared to that of ach by unpaired t-test is: 10 μM SB-27011-A (29.40 ± 2.27 μM, n = 4), 3 μM fmoc-1 (8.62 ± 1.04 μM, n = 4), 3 μM fmoc-2 (8.01 ± 0.18 μM, n = 4), 3 μM SB-27011-A (7.17 ± 0.33 μM, n = 5), ach (5.92 ± 0.29 μM, n = 4) and 3 μM (+)-butaclamol Cl (3.94 ± 0.66 μM, n = 4). The EC₅₀ of all four hits obviously shift away from the control when applied.

Table 3

Pharmacological profiles of the inhibitory effects of four hits on Asu-ACR-16 mediated ach responses. Results (mean \pm S.E.M.) were expressed as IC_{50} (μ M), Hill slope (n_H), maximum inhibition (%) and the number of repeats (N) of each experiment.

Hits	IC_{50} (μ M)	n_H	Inhibitionmax (%)	N
fmoc-2	16.67 \pm 1.95	1.22 \pm 0.17	80.34 \pm 10.32	4
SB-277011-A	3.12 \pm 1.29	0.99 \pm 0.11	96.07 \pm 10.66	4
fmoc-1	10.00 \pm 1.38	1.97 \pm 0.37	82.49 \pm 4.74	4
(+)-butaclamol Cl	9.85 \pm 2.37	1.34 \pm 0.29	79.53 \pm 12.41	4

Table 4

Pharmacological profiles of EC_{50} shifts and maximum current reductions of Asu-ACR-16 mediated ach responses in the presence and absence of four hits. Results (mean \pm S.E.M.) were expressed as EC_{50} (μ M), Hill slope (n_H) and maximum response (%) and the number of repeats (N) of each experiment.

Hits	EC_{50} (μ M)	n_H	Imax (%)	N
control	5.92 \pm 0.29	3.05 \pm 0.07	97.45 \pm 1.19	4
3 μ M fmoc-2	8.01 \pm 0.18	2.54 \pm 0.18	49.92 \pm 3.27	5
1 μ M SB-277011-A	9.85 \pm 4.80	2.60 \pm 0.71	75.96 \pm 4.40	4
3 μ M SB-277011-A	7.17 \pm 0.33	3.37 \pm 0.28	23.25 \pm 1.80	5
10 μ M SB-277011-A	29.40 \pm 2.27	7.43 \pm 3.30	5.51 \pm 1.38	4
3 μ M fmoc-1	8.62 \pm 1.04	1.76 \pm 0.21	61.25 \pm 3.08	4
1 μ M (+)-butaclamol Cl	4.54 \pm 0.92	9.64 \pm 4.14	30.34 \pm 4.03	4
3 μ M (+)-butaclamol Cl	3.94 \pm 0.66	12.75 \pm 3.63	17.22 \pm 1.94	4

C4.5 SB-277011-A reversibly inhibits locomotion in *C. elegans*

We tested the effects of each allosteric modulator on the locomotion of *C. elegans* L4 larvae. The number of normal worms with thrashing-like movement dropped by 60% in 5 min after exposed to 30 μ M SB-277011-A ($p < 0.01$, $n = 5$, t-test). Paralysis-like movement was observed in the rest of the worms. Interestingly, the number of worms with motility that appeared normal recovered to 50% ($p < 0.05$, $n = 5$, t-test) in 10 min, 85% in 15 min ($p > 0.05$, $n = 5$, t-test) and returned to near negative control values after 20 min (Fig. S6). The recovery may relate to the desensitization properties of the ACR-16 receptor. The reversible inhibition of motility in worms was also observed in 100 μ M (+)-butaclamol Cl, but no significant difference between the number of normal treated worms and negative

control was observed at any time point. No visual effects of 100 μ M fmoc-2 or 100 μ M fmoc-1 were found on the locomotion of worms.

C5.0 Discussion

C5.1 *Asu*-ACR-16 models

We have built up three-dimensional models of full-length structures of *Asu*-ACR-16 at the atomic level for the first time. We used homology modeling based on X-ray crystal structures of human $\alpha 7$ nAChR chimeras and the electron microscopic structure of the *T. marmorata* nAChR as templates for different domains. The quality of our homology models are dependent on the sequence identity of the templates (human $\alpha 7$ nAChR chimeras and *T. marmorata* nAChR) and the target sequence (*Asu*-ACR-16) and the resolutions of template structures (Hillisch et al., 2004 and Cavasotto and Phatak, 2009). Our three ECD-*Asu*-ACR-16 models are likely to be reliable for virtual screening because they have high sequence identities (37.6% identity and 72.9% similarity) with high resolution ($<4 \text{ \AA}$) templates. More errors might be expected in the TID-*Asu*-ACR-16 model, because of the missing loop between M3 and MA in the template structure which reduces sequence identity with the target protein. The missing loop does not include an allosteric binding site, so we can assume that the TID-Tma-nAChR structure is similar to the TID-*Asu*-ACR-16 structure (Bertrand et al., 2008). The overall secondary structures of our models are also consistent with published nAChRs structures (Finer-Moore and Stroud, 1984, Miyazawa et al., 2003 and Unwin, 2005).

We developed the apo, the agonist-bound and the antagonist-bound models of the ECD-*Asu*-ACR-16 on the assumption that these three states of the *Asu*-ACR-16 receptor most closely represent the receptor conformations in the presence and absence of agonists or

antagonists. To produce a realistic dynamic model would require more extensive work (Cavasotto and Orry, 2007 and Spyraakis et al., 2011) and is beyond the scope of this study.

C5.2 Virtual screening

Our structure-based virtual screening approach identified four novel and potent negative allosteric modulators of Asu-ACR-16, which were validated by our electrophysiological studies. The putative ligands were initially selected based on the virtual screening using the orthosteric binding site of the receptor. It was possible that these ligands could have been agonists or competitive antagonists that bind within the orthosteric binding site. In contrast, the pharmacological characterization of the four virtual screening hits shows that they behave as negative allosteric modulators and bind to allosteric sites. This outcome may be due to the hydrophobic properties of the four compounds that impedes their interactions with the orthosteric site in the extracellular domain of the receptor. The high lipid solubility of these compounds increases their concentration in the membrane lipid phase, in the region of the transmembrane allosteric sites.

The binding affinities calculated in the scoring function of AutoDock Vina software usually increase with the number of non-hydrogen atoms, which may be due to the neglect of desolvation in the scoring function (Shoichet et al., 1999, Kuntz et al., 1999 and Park et al., 2006). This leads to a bias of virtual screening methods towards big molecules which are more hydrophobic, concentrated in the lipid bilayer, and less likely to interact with the binding sites in the extracellular domains (Hopkins et al., 2004). It is also pointed out that the simplified force fields used to estimate the binding free energies are unable to evaluate the conformational entropies and other contributions to the free energies (Cosconati et al., 2010). Thus, the success rate of identifying bioactive hits (44%) would be enhanced if we are able to

include these additional parameters into a scoring function for virtual screening. Another approach, which we did not follow here, to enhance the success rate of identifying bio-active hits, is to use the known agonists or antagonists as scaffolds. This would facilitate the identification of low molecular-weight and more hydrophilic agonists or antagonists, and allow further study of the quantitative structure-activity relationships (Sun, 2008).

C5.3 Four negative allosteric modulators of *Asu*-ACR-16

We evaluated the potency of inhibition for the four negative allosteric modulators in our electrophysiology studies on *Xenopus* oocytes: SB-277011-A (IC_{50} $3.12 \pm 1.29 \mu M$) < (+)-butaclamol Cl (IC_{50} $9.85 \pm 2.37 \mu M$) \approx fmoc-1 (IC_{50} $10.00 \pm 1.38 \mu M$) < fmoc-2 (IC_{50} $16.67 \pm 1.95 \mu M$). This rank of inhibition agrees with the level of effects of the four modulators in the motility of *C. elegans*. The most potent modulator SB-277011-A was shown to decrease the motility of *C. elegans* larvae for a duration of about 10 min, yet less effective on adult *C. elegans*. Desensitization of the ACR-16 or other nAChRs in *C. elegans* body muscle may be a reason for the reduced effects of SB-277011-A on worms (Hernando et al., 2012). Treating the *acr-16*-null mutant of *C. elegans* with SB-277011-A can help us to investigate the mode of action of SB-277011-A on *C. elegans* as genetic models to understand SB-277011-A action on the parasitic nematode *A. suum* (Ward, 2015).

C5.4 Allosteric binding sites may offer a better opportunity for drugs that can discriminate between the parasite *Asu*-ACR-16 and mammalian host $\alpha 7$ nAChR

Asu-ACR-16 shows 42.5% sequence identity and 71.2% sequence similarity with the human $\alpha 7$ nAChR (SwissProt ID: P36544) based on the alignment generated by CLUSTALW (Fig. S7, CLUSTALW job ID: cfed4f821eaf). The residues constituting the

orthosteric binding site (pink and orange arrows in Fig. S7) are highly conserved between Asu-ACR-16 and human $\alpha 7$ nAChR, which shows 66.7% identity and 100% similarity (Fig. S8). In contrast, the residues of the four allosteric binding sites have much greater differences (variance) between the nematode parasite and the equivalent sites on the $\alpha 7$ receptor (identities: 62.5%, 45.5%, 66.7%, 62.5% and 40.0% and; similarities: 87.5%, 81.8%, 83.3, 93.8% and 100%). The sequence divergence in the allosteric binding sites between Asu-ACR-16 and host human $\alpha 7$ nAChR indicates that drugs targeted at these sites may be more selective than drugs targeted at orthosteric binding sites. Virtual screening specifically targeting the allosteric binding sites is predicted to offer a better opportunity for development of drugs with much greater receptor subtype selectivity (Nussinov and Tsai, 2013 and Iturriaga-Vasquez et al., 2015).

C5.5 Conclusion

We have developed a structure-based in silico screening approach to search for the bioactive hits that target at a parasitic nematode receptor. This approach allowed us to identify four negative allosteric modulators that were validated using our electrophysiological studies. These four compounds may be useful leads for anthelmintic drug discovery. We point out however, that we have not yet made the structural models for the host human $\alpha 7$ nAChR or other receptors, which would help to distinguish compounds that are active only on the nematode receptors, thereby reducing potential toxicity. It would also be desirable to perform virtual screening for toxicity on a range of host receptors, some structures of which have already been determined and others need to be modeled.

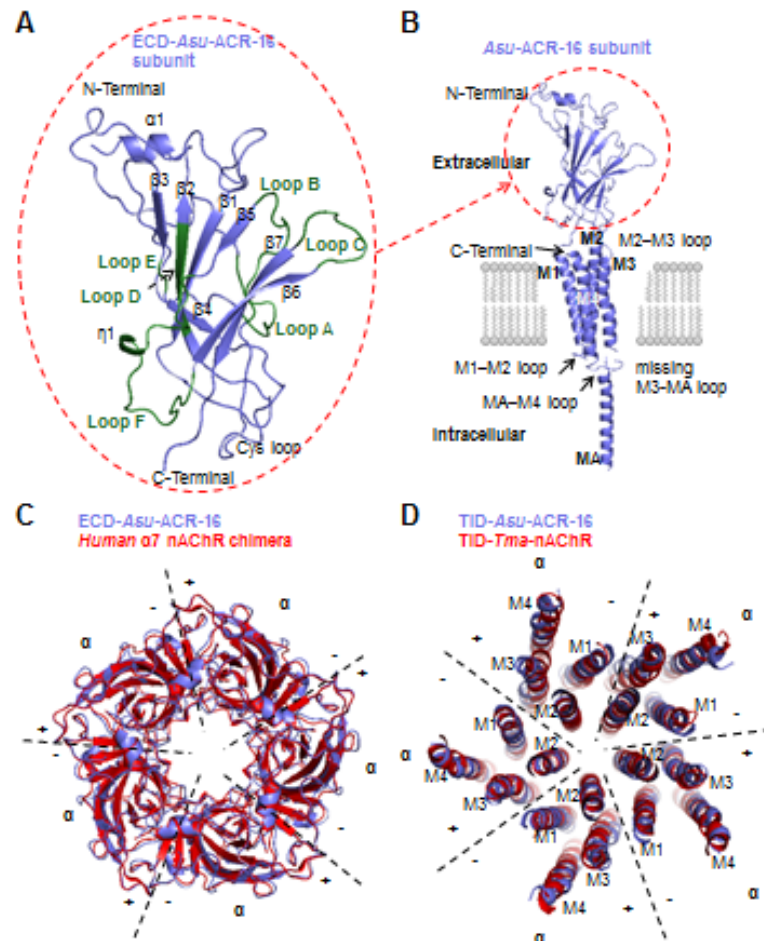
C6.0 Statement of conflict of interest

None identified.

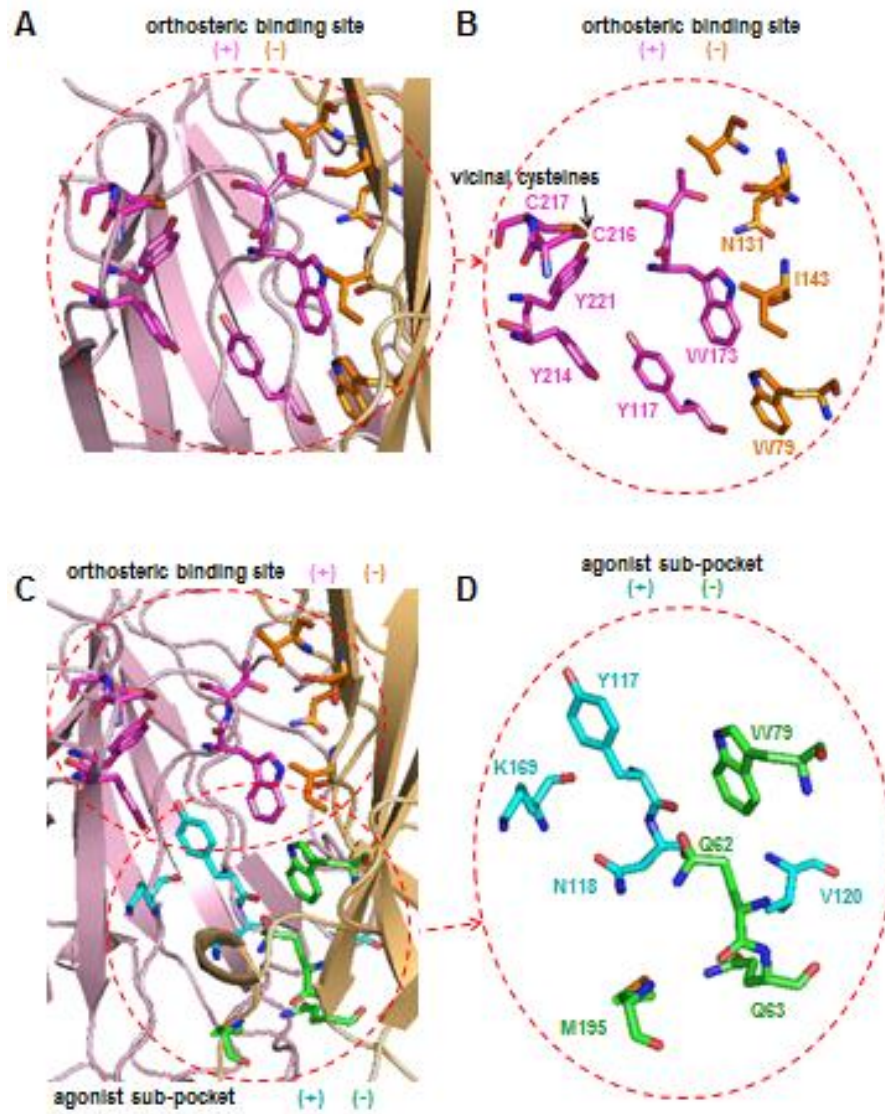
C7.0 Acknowledgements

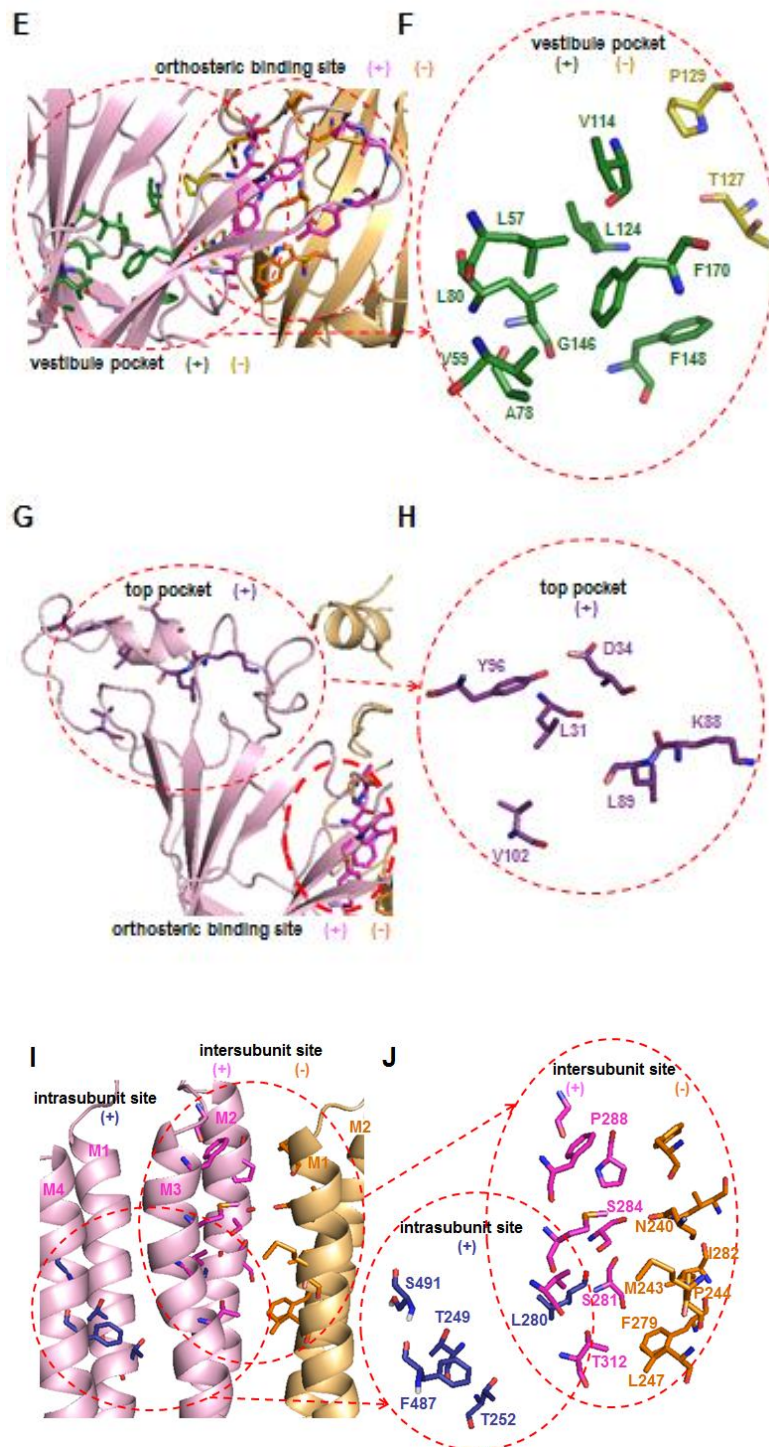
We would like to thank Tsung-Han Chou for the help and advice in modeling and docking. The research funding was by The Hatch Act, State of Iowa, and by NIH grants R01 AI047194 (to RJM) and AI114629 (to EWY) of the National Institute of Allergy and Infectious Diseases. The funding agencies had no role in the design, execution or publication of this study. The content is solely the responsibility of the authors and does not necessarily represent the official views of the National Institute of Allergy and Infectious Disases.

C8.0 Supplementary data

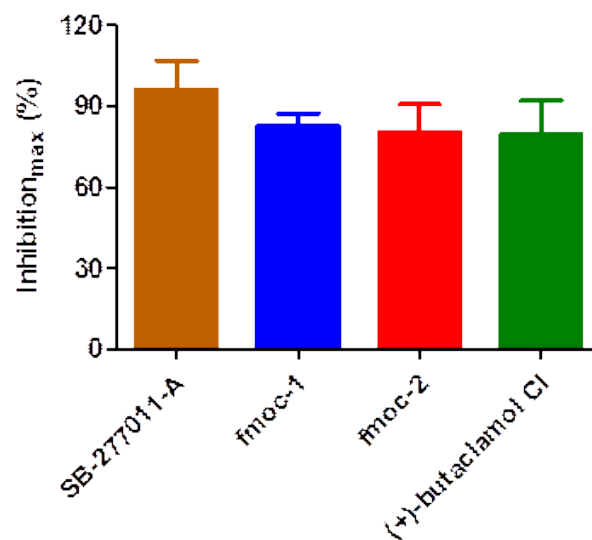


Supplementary Figure S1. (A) Ribbon representation of the ECD-Asu-ACR-16 monomer. Secondary elements are indicated. Loop A, B, C in the principal subunit and loop D, E, F in the complementary subunit which mainly contribute to the orthosteric binding site are labeled by dark green. In the complete structure, the C-terminal would enter the membrane at the bottom and link to M1 helix in the transmembrane domain. (B) Ribbon representation of the full-length Asu-ACR-16 monomer, as viewed parallel to the membrane plane. Four α helices (M1, M2, M3 and M4) that contribute to transmembrane domain and one MA helix that makes up the intracellular domain are indicated. The functionally important M1-M2, M2-M3 and MA-M4 loops are labeled. (C) Superposition of antagonist-bound model of ECD-Asu-ACR-16 pentamer (purple blue) and template human $\alpha 7$ nAChR chimera (red; PDB code: 4HQ9, ligands removed for clarity) viewed from the synaptic cleft. Five homomeric α -subunits are labeled. The interfaces between two vicinal α -subunits are marked by dotted lines. Five orthosteric binding sites are at each interface between the principal side (+) and the complementary side (–) from two vicinal subunits. (D) Superposition of TID-Asu-ACR-16 pentamer (purple blue) and template TID-Tma-AChR (red; PDB code: 2BG9) viewed above the membrane. Five homomeric α -subunits are labeled. The interfaces between two vicinal α -subunits are marked by dotted lines. Five allosteric binding sites are at each interface among the M2, M3 in the principal side (+) and the M1 in the complementary side (–) from two vicinal subunits.

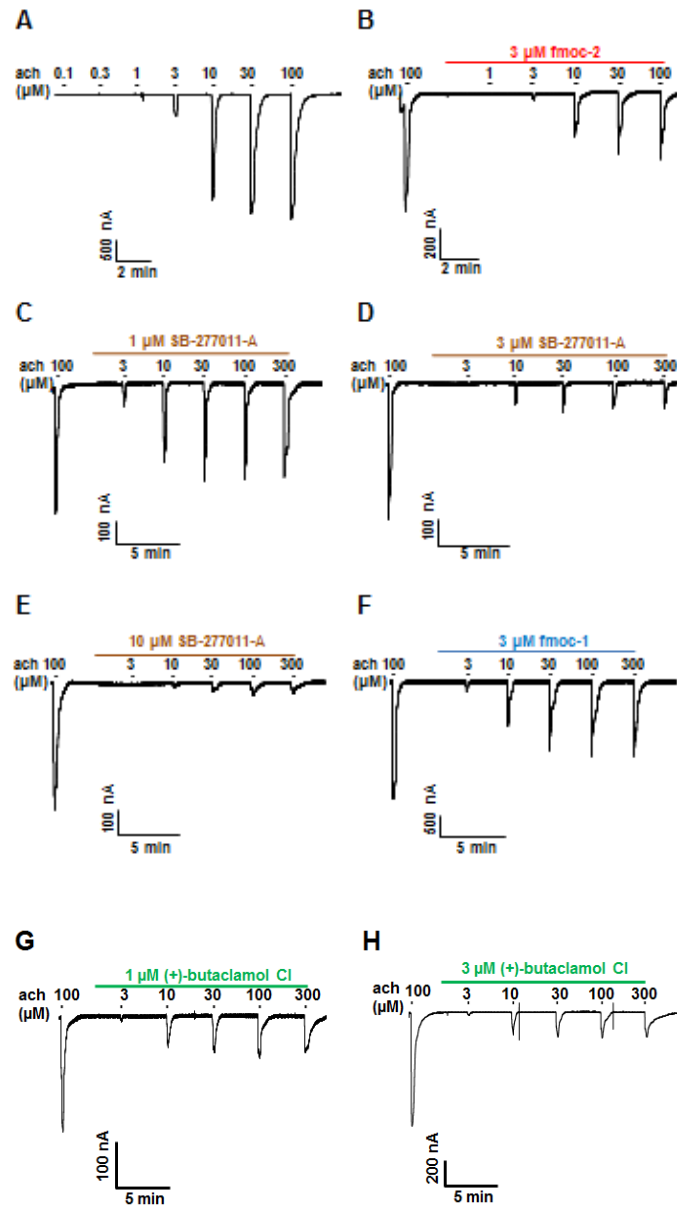




Supplementary Figure S2. (A) Detailed view of the orthosteric binding site in the antagonist-bound model of ECD-Asu-ACR-16. Principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the orthosteric binding site are represented by sticks (principal side (+), pink; complementary side (-), orange) and highlighted inside the red dotted circle. Carbon is in either pink or orange. Nitrogen is in blue. Oxygen is in red. Sulfur is in yellow. (B) Detailed view of the residues involving in the orthosteric binding site in the antagonist-bound model of ECD-Asu-ACR-16. Functionally important amino acids which interact with the ligands bound in this region are labeled. (C) Detailed view of the agonist sub-pocket relative to the location of the orthosteric binding site in the antagonist-bound model of ECD-Asu-ACR-16. Principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the agonist sub-pocket are represented by sticks (principal side (+), turquoise; complementary side (-), green) and highlighted inside the red dotted circle at the bottom. Carbon is in either turquoise or green. Nitrogen is in blue. Oxygen is in red. (D) Detailed view of the residues involving in the agonist sub-pocket in the antagonist-bound model of ECD-Asu-ACR-16. Functionally important amino acids which interact with the allosteric modulators bound in this region are labeled. (E) Detailed view of the vestibule pocket relative to the location of the orthosteric binding site in the antagonist-bound model of ECD-Asu-ACR-16. Principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the vestibule pocket are represented by sticks (principal side (+), dark green; complementary side (-), gold) and highlighted inside the red dotted circle on the left. Carbon is in either dark green or gold. Nitrogen is in blue. Oxygen is in red. (F) Detailed view of the residues involving in the vestibule pocket in the antagonist-bound model of ECD-Asu-ACR-16. Functionally important amino acids which interact with the allosteric modulators bound in this region are labeled. (G) Detailed view of the top pocket relative to the location of the orthosteric binding site in the antagonist-bound model of ECD-Asu-ACR-16. Principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the vestibule pocket are represented by sticks (principal side (+), purple) and highlighted inside the red dotted circle at the top. Carbon is in purple. Nitrogen is in blue. Oxygen is in red. (H) Detailed view of the residues involving in the top pocket in the antagonist-bound model of ECD-Asu-ACR-16. Functionally important amino acids which interact with the allosteric modulators bound in this region are labeled. (I) Detailed view of the two transmembrane allosteric binding sites in the antagonist-bound model of TID-Asu-ACR-16. Principal subunit is colored light pink, whereas the complementary subunit is colored yellow. The residues that contribute to the intersubunit site (principal side, pink; complementary side, orange) and intrasubunit site (principal side, purpleblue) are represented by sticks and highlighted inside the red dotted circle. Carbon is in either pink or orange or purpleblue. Nitrogen is in blue. Oxygen is in red. Sulfur is in yellow. (J) Detailed view of the residues involving in the two transmembrane allosteric binding sites in the antagonist-bound model of TID-Asu-ACR-16. Functionally important amino acids which interact with the allosteric modulators bound in this region are labeled.



Supplementary Figure S3. Bar chart showing effects of the four hits on Asu-ACR-16. Results are expressed as maximum inhibition (mean \pm S.E.M, %) of each plots in (Fig. 5A). The rank order series of inhibition based on maximum inhibition percentage for four hits is: SB-277011-A ($96.07 \pm 10.66\%$, $n = 4$) \approx fmoc-1 ($82.49 \pm 4.74\%$, $n = 4$) \approx fmoc-2 ($80.34 \pm 10.32\%$, $n = 4$) \approx (+)-butaclamol Cl ($79.53 \pm 12.41\%$, $n = 4$) using unpaired t-test.



Supplementary Figure S4. Sample traces showing the effects of four hits on the acetylcholine concentration-response relationships for Asu-ACR-16. Sample trace of acetylcholine concentration-response relationships in the absence of hits is depicted in (A) as a control. 3 μM of each of four hits are applied: (B) fmoc-2, (D) SB-277011, (F) fmoc-1, (H) (+)-butaclamol Cl, to compare the EC₅₀ shifts and the maximum response reduction for four hits. 1 μM SB-277011-A (C), 1 μM (+)-butaclamol Cl (G) and 10 μM SB-277011-A (E) were tested to study the concentration effects on the mode of inhibition.

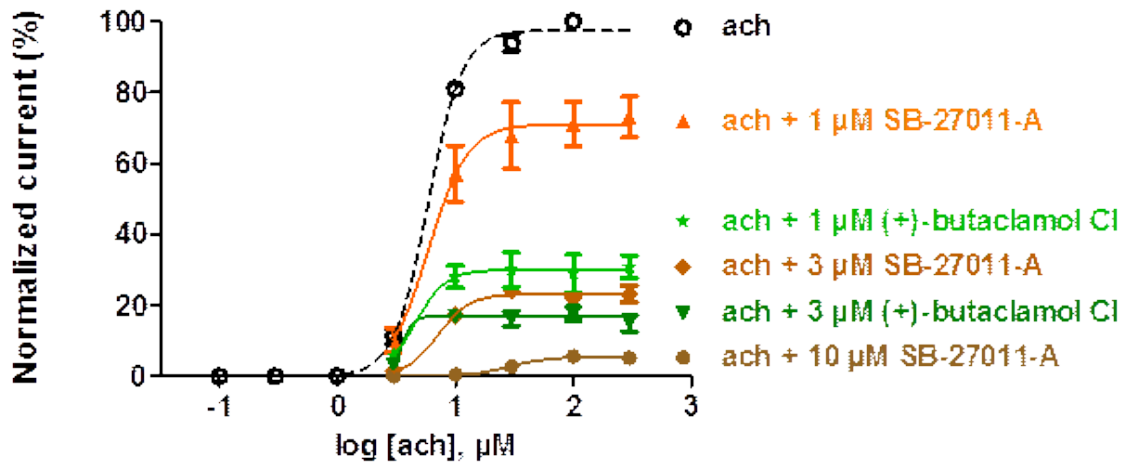
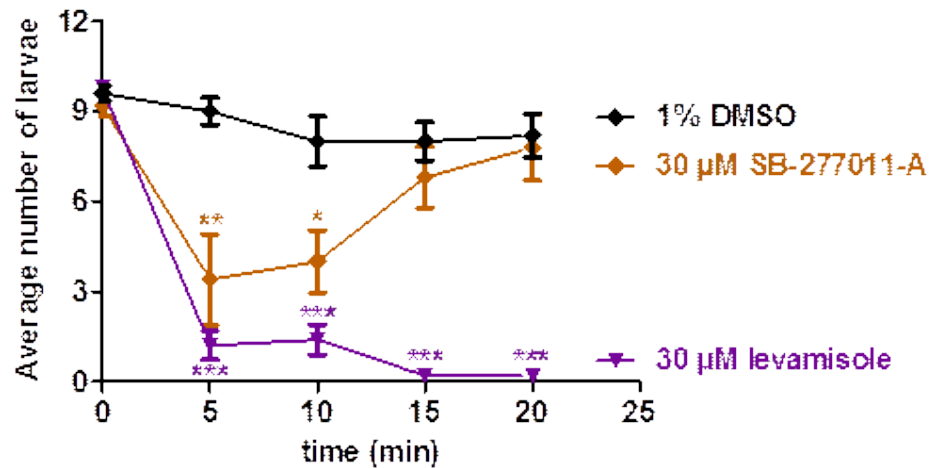
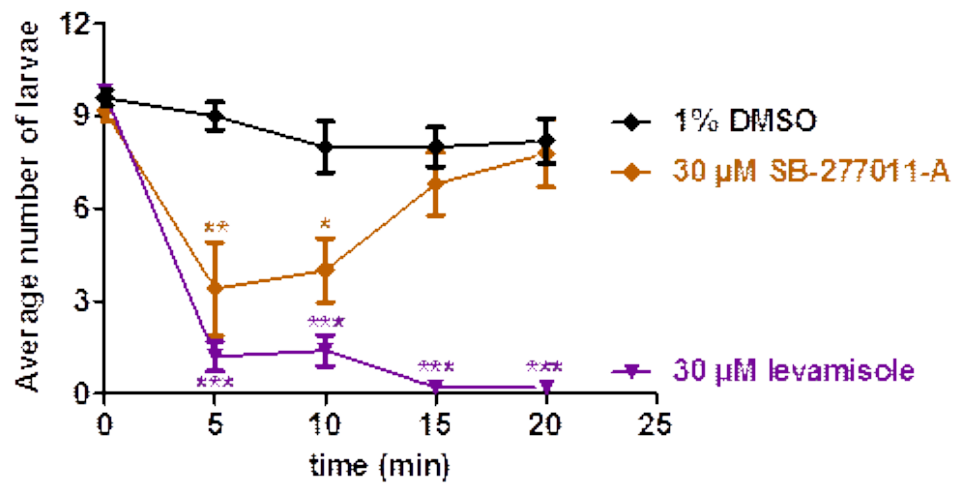


Figure S5. Ach concentration-response curves for Asu-ACR-16 in the absence of hits as a control (ach) and in the continual presence of 1 μ M, 3 μ M, 10 μ M SB-277011-A, 1 μ M, 3 μ M (+)-butaclamol Cl.



Supplementary Figure S6. Plot of average number of L4 *C. elegans* larvae with normal motility (A) vs. time (min) in the absence of drug (1% DMSO, control), presence of 30 μ M SB-277011-A and 30 μ M levamisole. Ten worms were used for each treatment, which was replicated by five times. Comparisons of locomotion were made between control and treated worms at each time point. * $p < 0.05$, ** $p < 0.01$, *** $p < 0.001$. The recovery of normal motility was observed only in the larvae treated with 30 μ M SB-277011-A within 20 min, but not in the larvae treated with 30 μ M levamisole within 24 h.



Supplementary Figure S8. Comparison of residues in the orthosteric binding site and five allosteric binding sites between Asu-ACR-16 and human $\alpha 7$ nAChR.

**APPENDIX D. THE CHOLINOMIMETIC MORANTEL AS AN OPEN CHANNEL
BLOCKER OF THE *ASCARIS SUUM* ACR-16 nAChR**

A paper published in *Invertebrate Neuroscience* (2016)¹

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D1.0 Abstract

Nematode parasite infections pose a significant threat in human and veterinary medicine. At least a third of the world's population is at risk from nematode parasite infections. These infections not only cause health problems, but also cause loss of livestock production and hence, economic losses. Anthelmintic drugs are the mainstay by which control of nematode parasite infections is achieved. Many of the currently available anthelmintics act on nicotinic acetylcholine receptors (nAChRs). However, the detailed mode of action (MOA) of these anthelmintics is not clearly understood. Elucidation of the MOA of anthelmintics is highly desirable; an in-depth knowledge of the MOA will better inform on mechanisms of resistance development and on ways to slow down or overcome resistance. The cholinomimetic anthelmintic, morantel, has a complex MOA involving the activation and block of levamisole-sensitive single nAChR channels (L-type nAChR or L-nAChR). More recently, morantel has been demonstrated to activate *Haemonchus contortus* and *Parascaris equorum* ACR-26/ACR-27 nAChRs expressed in *Xenopus laevis* oocytes. Previous studies in our laboratory, however, have shown morantel does not activate the

nicotine-sensitive nAChR (N-type nAChR or N-nAChR), *Ascaris suum* ACR-16 (*Asu*-ACR-16). In this study, we used two-electrode voltage-clamp (TEVC) electrophysiology to investigate the inhibitory effects of morantel, on expressed *Asu*-ACR-16 nAChRs in *X. laevis* oocytes. Our results show that morantel acts as a non-competitive antagonist on *Asu*-ACR-16. This non-competitive antagonism by morantel was further demonstrated to be voltage-sensitive. We conclude based on our findings that morantel is a non-competitive voltage-sensitive open channel blocker of *Asu*-ACR-16.

D1.1 Keywords

Ascaris suum ACR-16 nAChR Electrophysiology Morantel Open channel block

D1.2 Abbreviations

nAChR	Nicotinic acetylcholine receptor
MOA	Mode of action
TEVC	Two-electrode voltage-clamp
BAPTA-AM	1,2-Bis(2-aminophenoxy)ethane-N,N,N',N'-tetra-acetic acid tetrakis (acetoxymethylester)
HEPES	4-(2-Hydroxyethyl)piperazine-1-ethanesulfonic acid
ach	Acetylcholine
mor	Morantel
DMSO	Dimethyl sulfoxide

D2.0 Introduction

Nematode parasite infections are a significant threat in both human and veterinary medicine, affecting about one-third of the human population and causing significant animal production losses (Bethony et al. 2006; de Silva et al. 2003; Hotez et al. 2006, 2008). The major control strategy for nematode parasite infections involves use of anthelmintic drugs, which are selectively toxic to the parasites (Brooker et al. 2006). Although the mode of action (MOA) of many anthelmintics is not fully understood, some of their sites of action and

biochemical mechanisms are well known. Many of the currently available anthelmintics target nicotinic acetylcholine receptors (nAChRs), which are involved in neuromuscular coordination (Martin et al. 1997; Wolstenholme 2011). Other anthelmintics exhibit their pharmacological effect by interfering with the parasite cell integrity, feeding, or some protective mechanisms against the host which may cause starvation, paralysis and expulsion, or digestion of the parasite (Holden-Dye and Walker 2007, 2014; Lustigman et al. 2014; Morel et al. 2014).

Nematode muscle nAChRs are of significant interest because they are targets for many anthelmintics. nAChRs are pentameric ligand-gated ion channels which mediate rapid synaptic transmission at the neuromuscular and nerve–nerve junctions of vertebrates and invertebrates (Karlin 2002; Zouridakis et al. 2009). The cholinergic anthelmintic agonist, morantel, is a classic example of an anthelmintic that acts on nematode muscle nAChRs (Martin 1997). The published MOA of morantel is that it selectively opens nAChRs present on nematode parasite muscle cells to cause muscle contraction and hence, spastic paralysis and expulsion of the parasite (Martin et al. 1996). However, the agonist effect of morantel has been demonstrated in the levamisole-sensitive nAChRs (L-nAChRs) which are insensitive to nicotine and are heteropentameric, comprising more than one subunit type (Rayes et al. 2007). Morantel has also been shown to cause block of L-nAChRs in addition to its agonist effect on these receptor types (Evans and Martin 1996). At the single-channel level, L-nAChRs have a conductance (G) of 35 pS in *A. suum* (Qian et al. 2006), a Clade III nematode. A similar channel conductance was observed in *Oesophagostomum dentatum* (Buxton et al. 2014), a Clade V nematode.

More recently, morantel was shown to activate the nAChRs, *Haemonchus contortus* ACR-26/ACR-27 (*Hco*-26/27) and *Parascaris equorum* ACR-26/ACR-27 (*Peq*-26/27) expressed in *Xenopus laevis* oocytes, and the sensitivity of *Caenorhabditis elegans* to morantel was increased when these receptors were expressed in body wall muscles (Courtot et al. 2015). The nicotine-sensitive nAChRs (N-nAChRs) which are insensitive to levamisole and are homopentameric, comprising of one subunit type, are not activated by morantel (Raymond et al. 2000). In agreement with this observation, previous studies in our laboratory involving the pharmacological characterization of the N-nAChR, *A. suum* ACR-16 (*Asu*-ACR-16), showed ACR-16 to be insensitive to morantel, in addition to other cholinergic anthelmintic agonists including levamisole, methyridine, thenium, bephenium, tribendimidine, and pyrantel (Abongwa et al. 2016a). In an effort to further elucidate the MOA of morantel, we used the two-electrode voltage-clamp electrophysiology technique to characterize morantel's antagonistic effects on *Asu*-ACR-16 expressed in *X. laevis* oocytes.

D3.0 Materials and methods

D3.1 cRNA preparation

Preparation of the *Asu-acr-16* and *Asu-ric-3* cRNA used in this study has been previously reported (Abongwa et al. 2016a).

D3.2 Expression of *Asu*-ACR-16 in *Xenopus laevis* oocytes

Expression of *Asu*-ACR-16 in *X. laevis* oocytes has been described previously (Abongwa et al. 2016a). Briefly, defolliculated *X. laevis* oocytes obtained from Ecocyte Bioscience (Austin, Texas, USA) were injected with 25 ng *Asu-acr-16* cRNA in combination with 5 ng of the required ancillary factor, *Asu-ric-3* cRNA, in a total volume of 50 nL. Once injected, individual oocytes were transferred to a 96-well culture plate containing 200 μ L of

incubation solution (100 mM NaCl, 2 mM KCl, 1.8 mM CaCl₂·2H₂O, 1 mM MgCl₂·6H₂O, 5 mM HEPES, 2.5 mM Na pyruvate, 100 U/mL penicillin, and 100 µg/mL streptomycin, pH 7.5). Oocytes were then incubated at 19 °C for 5–7 days, with incubation solution changed daily, to allow for protein functional expression.

D3.3 Two-electrode voltage-clamp (TEVC) electrophysiology

At least 2 h prior to recording, 100 µM BAPTA-AM was added to the incubation solution to prevent activation of endogenous calcium-activated chloride channels. Current responses to drug applications were recorded using TEVC electrophysiology (Abongwa et al. 2016b; Robertson et al. 2008). An Axoclamp 2B amplifier (Warner Instruments, USA) was used to record currents from oocytes voltage-clamped at –90, –60, or –30 mV. The data were acquired on a computer with Clampex 9.2 software (Molecular Devices, CA, USA).

Microelectrodes (standard wall borosilicate glass with filament, o.d. 1.5 mm, i.d. 0.86 mm) (G150F-6, Warner Instruments, USA) for impaling oocytes were pulled using a Flaming/Brown horizontal electrode puller (Model P-97, Sutter Instruments). The microelectrodes were then filled with 3 M KCl, and the tips carefully broken with a piece of tissue paper to achieve a resistance of 2–5 MΩ in recording solution (100 mM NaCl, 2.5 mM KCl, 1 mM CaCl₂·2H₂O, and 5 mM HEPES, pH 7.3).

D3.4 Drugs

The drugs used for this study, acetylcholine (ach) and morantel (mor), were purchased from Sigma-Aldrich (St Louis, MO, USA). BAPTA-AM, an intracellular calcium chelator, was also purchased from Sigma-Aldrich (St Louis, MO, USA). Acetylcholine and morantel stock solutions were prepared in recording solution and dimethyl sulfoxide

(DMSO), respectively. The final working DMSO concentration did not exceed 0.1% in all experiments.

D3.5 Drug applications

Oocytes were perfused with drugs by a system controlled by eight valves (VC-8 valve controller) (Warner Instruments, USA) at a flow rate of 4 ml/min. Except otherwise indicated, each concentration of acetylcholine in the absence or presence of morantel was applied for 10 s, followed by a 2-min wash with recording solution in between drug applications. The oocytes were voltage-clamped at -60 mV, except for the voltage sensitivity experiments where the oocytes were voltage-clamped at -90 , -60 , and -30 mV.

Acetylcholine concentration–response relationships in the absence of morantel were generated by applying acetylcholine at concentrations of 0.1 – 300 μM , at semilog intervals. Morantel antagonism was estimated by first applying 100 μM acetylcholine for 30 s as a control, followed by a 2-min wash with recording solution. Thereafter, a test 100 μM acetylcholine was applied for 10 s, followed by a 10-s co-application of 100 μM acetylcholine in the presence of either 0.3 , 1 , 3 , 10 , 30 or 100 μM morantel, and then a final 10-s application of 100 μM acetylcholine. For subsequent experiments, morantel was used at 1 and 3 μM . Acetylcholine concentration–response relationships in the presence of 1 and 3 μM morantel were generated by first applying a control 100 μM acetylcholine for 10 s, followed by a 2-min application of morantel, and 10-s applications of 3 , 10 , 30 , 100 and 300 μM acetylcholine in the continued presence of morantel. Voltage sensitivity experiments were conducted by holding the membrane potential at -90 , -60 , or -30 mV, and applying a control 100 μM acetylcholine for 10 s, followed by a 10-s application of 100 μM acetylcholine in the presence of 3 μM morantel, at each holding potential.

D3.6 Data analysis

Data acquired from the TEVC electrophysiological recordings were analyzed with Clampfit 9.2 (Molecular Devices, CA, USA) and GraphPad Prism 5.0 software (GraphPad Software Inc., CA, USA). Unless otherwise indicated, peak currents in response to applied drugs were measured and normalized to the 100 μM acetylcholine control response and expressed as mean \pm S.E.M. The concentration–response relationships were analyzed by fitting data points with the Hill equation as previously described (Martin et al. 2004). Initial experiments to measure morantel inhibition of acetylcholine responses used a brief (10 s) application of morantel during a longer (30 s) application of acetylcholine (Fig. 2a). In these experiments, inhibition was calculated by measuring the smallest current during the morantel application and the largest current induced by acetylcholine after morantel wash-off began. Percent inhibition was calculated as: (acetylcholine current – morantel current)/acetylcholine current \times 100. In subsequent experiments where morantel was present for sustained period of time, the peak currents in the presence of morantel were used and normalized to acetylcholine currents in the absence of the drug (Figs. 3a, 4a). The voltage-sensitive block effects of morantel were estimated as $1/\tau$, where τ was the mean of a single exponential decay fit to the acetylcholine-induced currents in the presence of morantel:

$$f(t) = \sum_{i=1}^n A_i e^{-t/\tau_i} + C$$

where n = number of components, A = amplitude, t = time, τ = time constant, and C = constant y-offset for each i component.

Statistical comparisons were done using unpaired Student's t test or one-way ANOVA. A p value < 0.05 was considered significant.

D4.0 Results

D4.1 *Asu*-ACR-16 is activated by acetylcholine in a concentration-dependent manner

Figure 1a, b, respectively, show the sample traces (inward currents) and concentration–response relationship for acetylcholine. *Asu*-ACR-16 was not activated by 0.1, 0.3, and 1 μM acetylcholine, but was activated by acetylcholine concentrations $\geq 3 \mu\text{M}$. As previously observed, current responses increased with increasing acetylcholine concentrations, demonstrating activation of the *Asu*-ACR-16 nAChR by acetylcholine is concentration dependent (Abongwa et al. 2016a; Zheng et al. 2016). The EC_{50} for acetylcholine was $6.1 \pm 0.2 \mu\text{M}$, R_{max} $99.4 \pm 0.6\%$, and Hill slope (n_H) 3.4 ± 0.1 ($n = 5$).

D4.2 Morantel is a non-competitive antagonist of the *Asu*-ACR-16 nAChR

We tested the antagonistic effects of morantel on the *Asu*-ACR-16 nAChR by varying the concentration of morantel from 0.3 to 100 μM , while repeatedly applying a constant acetylcholine concentration of 100 μM . The morantel inhibition plot is shown in Fig. 2, with sample traces (a) shown above the plot (b). Inhibition of *Asu*-ACR-16 acetylcholine responses was seen to increase with increasing morantel concentration. Morantel was a potent antagonist of *Asu*-ACR-16 as reflected by its observed IC_{50} value of $5.6 \pm 1.8 \mu\text{M}$ ($n = 4$), n_H 0.9 ± 0.1 ($n = 4$).

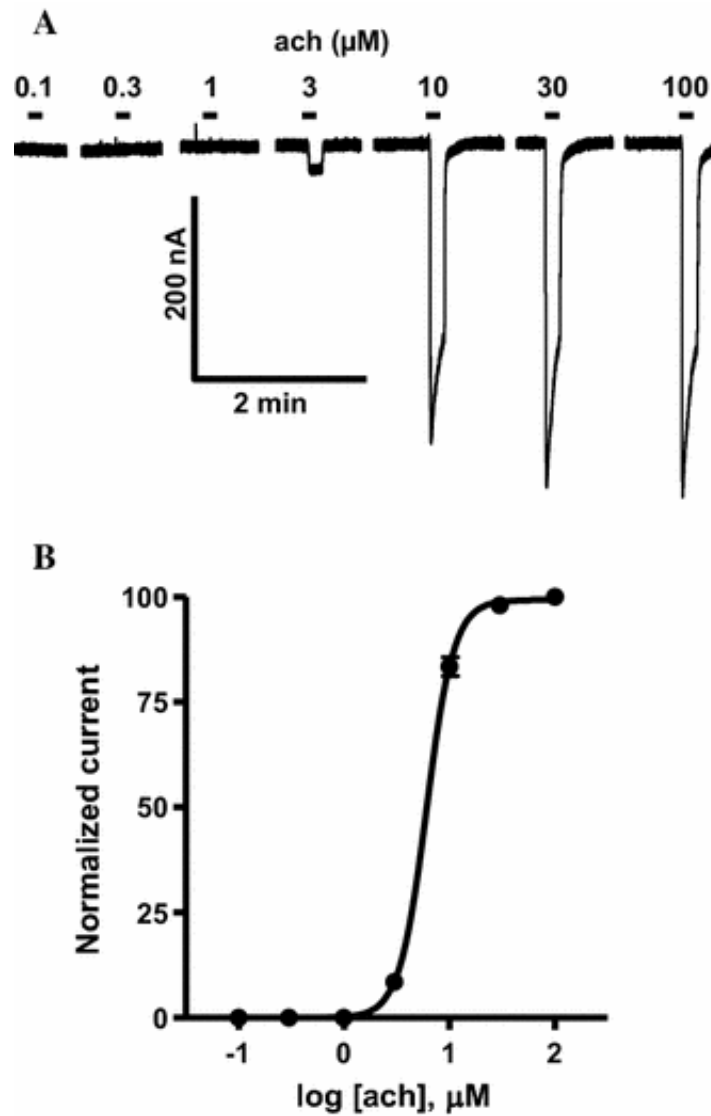


Fig. 1 Acetylcholine concentration–response relationship for *A. suum* ACR-16. **a** Sample traces showing *inward currents* in response to 0.1–100 μM acetylcholine. **b** Acetylcholine concentration–response plot for *A. suum* ACR-16. EC₅₀ for acetylcholine was $6.1 \pm 0.2 \mu\text{M}$, R_{max} $99.4 \pm 0.6\%$, and Hill slope (n_H) 3.4 ± 0.1 ($n = 5$).

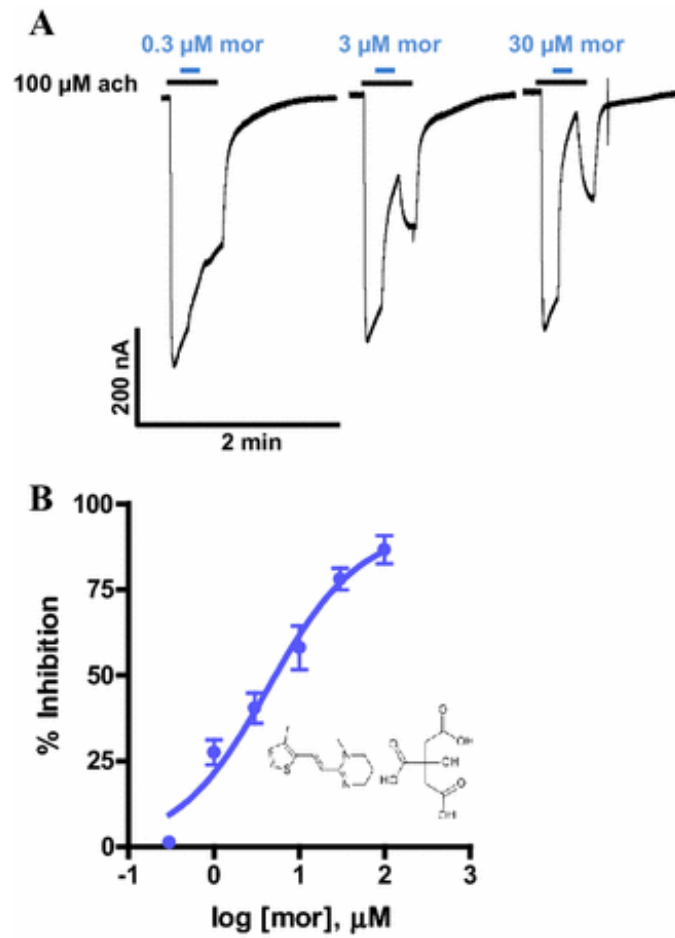


Fig. 2 Inhibition of *A. suum* ACR-16 responses to 100 μM acetylcholine by 0.3–100 μM morantel. **a** Sample traces (*inward currents*) showing a concentration-dependent inhibition of acetylcholine responses by morantel. **b** Concentration–response plot showing percent inhibition of 100 μM acetylcholine by 0.3–100 μM morantel. IC_{50} morantel was $5.6 \pm 1.8 \mu\text{M}$ ($n = 4$), n_H 0.9 ± 0.1 ($n = 4$)

To elucidate the type of antagonism produced by morantel, we first applied 0.3, 1, 3, 10, 30, 100, and 300 μM acetylcholine in the absence of morantel, which served as the control. This was followed by a different set of experiments where we applied 3, 10, 30, 100, and 300 μM acetylcholine in the presence of 1 and 3 μM morantel. Sample traces for these recordings are shown in Fig. 3a. The concentration–response relationships for acetylcholine in the absence and presence of 1 and 3 μM morantel are shown in Fig. 3b. The EC_{50} and R_{max} values were $4.5 \pm 0.1 \mu\text{M}$ and $98.2 \pm 0.1\%$ ($n = 3$) for acetylcholine, $4.5 \pm 0.3 \mu\text{M}$ and $82.6 \pm 3.0\%$ ($n = 4$) in 1 μM morantel, and $4.0 \pm 0.5 \mu\text{M}$ and $39.4 \pm 1.6\%$ ($n = 4$) in 3 μM morantel. Morantel showed a concentration-dependent significant reduction of R_{max} ($p < 0.01$ for 1 μM morantel; $p < 0.001$ for 3 μM morantel), with no change in EC_{50} ($p > 0.05$), which are characteristics of non-competitive antagonism. These results indicate that morantel is a non-competitive antagonist of the *Asu*-ACR-16 nAChR.

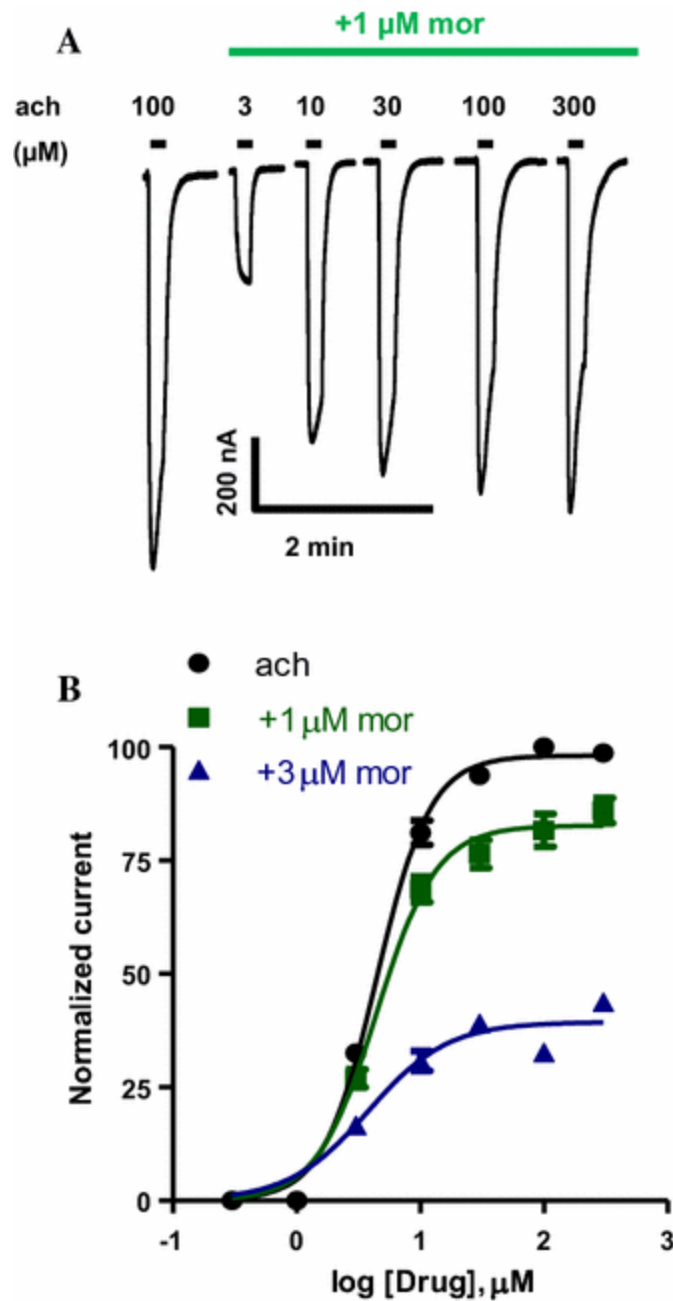


Fig. 3 Concentration–response relationships for acetylcholine in the absence and presence of morantel. **a** Sample traces showing *inward currents* in response to acetylcholine in the presence of 1 μM morantel. **b** Concentration–response plots for acetylcholine alone (*black curve*), acetylcholine in the presence of 1 μM morantel (*green curve*), and acetylcholine in the presence of 3 μM morantel (*blue curve*). EC_{50} and R_{max} values were $4.5 \pm 0.1 \mu\text{M}$ and $98.2 \pm 0.1\%$ ($n = 3$) for acetylcholine, $4.5 \pm 0.3 \mu\text{M}$ and $82.6 \pm 3.0\%$ ($n = 4$) in 1 μM morantel, and $4.0 \pm 0.5 \mu\text{M}$ and $39.4 \pm 1.6\%$ ($n = 4$) in 3 μM morantel.

D4.3 Morantel acts as an open channel blocker to produce antagonism

Voltage sensitivity experiments were performed to further elucidate the mechanism of morantel's non-competitive antagonism. Figure 4a shows sample traces of the effect of morantel on acetylcholine responses at different holding potentials. Figure 4b shows a plot of $1/\tau$ against membrane potential (-90 , -60 and -30 mV). One-way ANOVA revealed a significant effect of voltage on morantel's blocking actions ($p < 0.05$); showing morantel's blocking action is voltage-sensitive. In whole-cell recordings, $1/\tau$ is representative of the mean open time of the channel. The reduction in $1/\tau$ (and therefore mean open-time of the channel) as the holding potential becomes more negative is consistent with the drug acting as an open channel blocker.

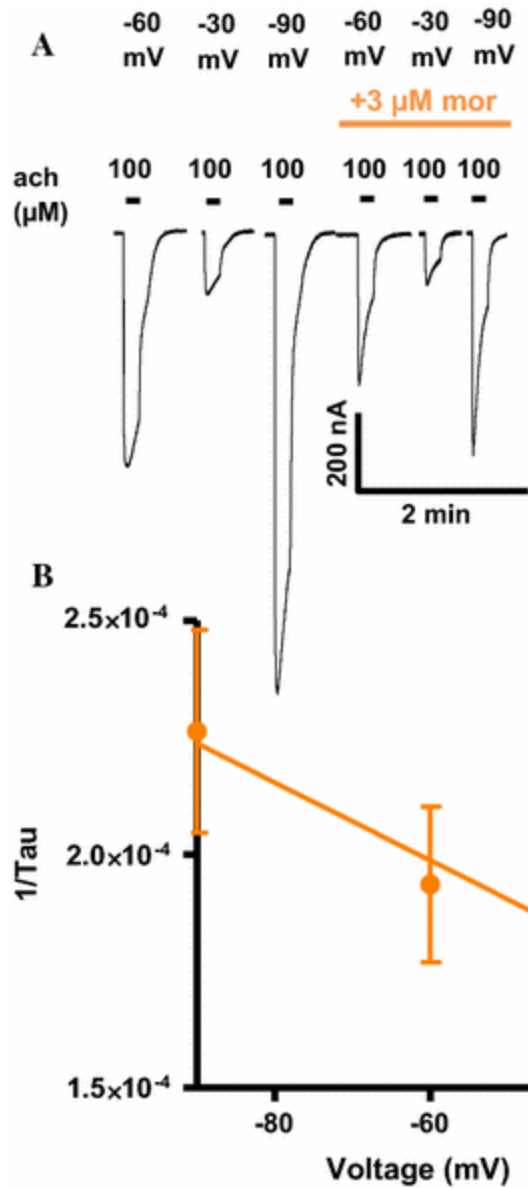


Fig. 4 Voltage sensitivity of morantel's inhibitory effects on *A. suum* ACR-16 responses to acetylcholine. **a** Sample traces (*inward currents*) showing acetylcholine responses in the absence and presence of 3 μM morantel at different holding membrane potentials (-90, -60, -30 mV). **b** $1/\tau$ versus holding potential (mV) showing *line of best fit* by linear regression. Notice morantel's inhibitory effects were higher at more negative membrane potentials, indicating morantel's blocking action is voltage-sensitive.

D5.0 Discussion

The goal of this study was to provide an understanding of the MOA of morantel on the recently characterized *Asu*-ACR-16 nAChR. Like *C. elegans* ACR-16 (*Cel*-ACR-16),

Asu-ACR-16 is a member of the N-type nAChRs that are preferentially activated by nicotine (Abongwa et al. 2016a; Ballivet et al. 1996). It is noteworthy that the characterization of the N-type nAChRs is not as extensive as the L-type channels preferentially activated by levamisole. Furthermore, N-type nAChRs are not activated by the currently used cholinergic anthelmintic agonists (Abongwa et al. 2016a; Raymond et al. 2000). As such, the N-type nAChRs are not well exploited for anthelmintic drug discovery, compared to the L-type. Raymond et al. (2000) showed morantel did not activate *C. elegans* ACR-16 or chicken $\alpha 7$ receptors expressed in *X. laevis* oocytes, voltage-clamped at -100 mV. Rather, morantel inhibited current responses to 1 mM acetylcholine in a dose-dependent manner, with pIC₅₀ values of, respectively, 5.7 and 5.6 for *C. elegans* ACR-16 and chicken $\alpha 7$, which approximates to IC₅₀ values of 2 μ M for *C. elegans* ACR-16 and 2.5 μ M for chicken $\alpha 7$ (Raymond et al. 2000) versus our observed IC₅₀ of 5.6 ± 1.8 μ M for expressed *Asu*-ACR-16 in oocytes voltage-clamped at -60 mV. Notice the IC₅₀ values for *C. elegans* ACR-16 and chicken $\alpha 7$ are lower than that for *Asu*-ACR-16, and this is likely due to more negative holding potential (-100 mV) used in oocytes expressing *C. elegans* ACR-16 or chicken $\alpha 7$, whereas in our experiments, oocytes expressing *Asu*-ACR-16 were held at -60 mV.

By taking advantage of the *X. laevis* oocyte expression system, we have demonstrated using TEVC electrophysiology that morantel acts as a non-competitive antagonist of the *Asu*-ACR-16 nAChR and that the mechanism by which morantel produces its inhibitory effects is consistent with open channel block. This provides new information for the MOA of morantel on the N-type nAChR, *Asu*-ACR-16, in addition to its known agonistic and blocking effects on levamisole receptors (Evans and Martin 1996; Rayes et al. 2007). In our study, however, we found morantel to be more potent on the expressed *Asu*-ACR-16 (IC₅₀ 5.6 ± 1.8 μ M,

$n = 4$) compared to the IC_{50} of $10 \mu\text{M}$ observed in *A. suum* muscle cells at the single-channel level (Evans and Martin 1996). The Hill slope for morantel concentration–response curve in our study ($n_H 0.9 \pm 0.1$, $n = 4$) was also less than that reported by Evans and Martin ($n_H 1.6$). The conductance of *A. suum* muscle nAChRs (32–40 pS, depending on the polarity of the holding potential) reported by Evans and Martin (1996) indicate that they were investigating L-type channels, as described by Qian et al. (2006) rather than the N-type investigated in this study. It is also possible that the study by Evans and Martin (1996) included examples of channels formed by ACR-26/ACR-27 subunits (Courtot et al. 2015) that have not been characterized at the single-channel level to date. According to Raymond et al. (2000), morantel IC_{50} and n_H values for *C. elegans* ACR-16 ($2 \mu\text{M}$ and -0.9) and chicken $\alpha 7$ ($2.5 \mu\text{M}$ and -1.1) were also less than those reported by Evans and Martin (1996) for *A. suum* muscle nAChRs ($10 \mu\text{M}$ and 1.6), implying morantel is also more potent on expressed *C. elegans* ACR-16 and chicken $\alpha 7$ receptors than in *A. suum* muscle cells. Therefore, morantel appears to have different effects on the nicotine and levamisole receptor types.

Multiple sites of action for an anthelmintic are desirable (Martin et al. 1998). Morantel is believed to cause spastic paralysis of the nematode by its action as an L-nAChR agonist. L-nAChRs are involved in muscle contraction; however, ACR-16 may have a paracrine function given its wide distribution in *A. suum* body tissues (Abongwa et al. 2016a). Hence, ACR-16 may not have a distinct role in fast signal transduction at the neuromuscular junction of nematodes, and just as in *C. elegans*, inhibition of *Asu*-ACR16 may have no obvious effect on motility (Touroutine et al. 2005). Therefore, although the inhibition of ACR-16 may be deleterious to the parasite, this anthelmintic effect is uncertain. Regardless, it may not be desirable to use morantel with compounds that act as agonists of

ACR-16. That notwithstanding, a detailed knowledge of drug effects on multiple receptors will inform the selection of compounds to be used in combination therapy, an approach that is increasing in popularity due to its potential for slowing the development of drug resistance, in addition to the obvious potential increase in spectrum of action.

D6.0 Author's contribution

MA, RJM and APR conceived and designed the research study. MA and KEB performed the research. MA, KEB and APR analyzed the data. RJM and APR contributed to reagents/materials/analysis tools. MA, RJM and APR wrote the paper.

D7.0 Funding

This research was funded by the National Institute of Allergy and Infectious Diseases of the National Institutes of Health under Award Number R01AI047194 to RJM, R21AI121831-01 to APR and the Schlumberger Foundation to MA.

D8.0 Compliance with ethical standards

D8.1 Conflict of interest

The authors declare that they have no conflict of interest.

D8.2 Ethical approval

No vertebrate animals were directly used in this study. Adult female *A. suum* worms and defolliculated *Xenopus laevis* oocytes used in this study were obtained from Marshalltown Pork Plant, Marshalltown, Iowa, and Ecocyte Bioscience (Austin, TX, USA), respectively.

APPENDIX E. LIST OF ALL CONFERENCE ABSTRACTS, AWARDS AND FUNDING

CONFERENCE ABSTRACTS

Melanie Abongwa, Fidelis Cho-Ngwa, Godfred Ayimele, Moses Samje, Smith B. Babiaka, Judy Sakanari, Eman Mostafa, Adrian J. Wolstenholme, Richard J. Martin, Alan P. Robertson. "Activity of crude extracts and chromatographic fractions of *Daniellia oliveri* and *Psorospermum febrifugum* against adult *Brugia pahangi*". American Society of Tropical Medicine and Hygiene (ASTMH) 65th Annual Meeting, held at Atlanta Marriott Marquis and Hilton Atlanta, Atlanta, Georgia, USA, November 13-17, 2016.

Melanie Abongwa, Fidelis Cho-Ngwa, Godfred Ayimele, Moses Samje, Smith B. Babiaka, Ann Perera, Eman Mostafa, Adrian J. Wolstenholme, Richard J. Martin, Alan P. Robertson. "Filaricidal activities of extracts of *Daniellia oliveri* and *Psorospermum febrifugum*". International Symposium on Anthelmintics: From Discovery to Resistance II, held at the Marina Village Center, San Diego, California, USA, February 9-12, 2016.

Richard J. Martin, Fudan Zheng, Alan P. Robertson, **Melanie Abongwa** and Edward W. Yu. "The *Ascaris suum* nicotinic receptor, ACR-16, as a drug target: four novel negative allosteric modulators from virtual screening". International Symposium on Anthelmintics: From Discovery to Resistance II, held at the Marina Village Center, San Diego, California, USA, February 9-12, 2016.

Sasa Trailovic, Djorje Marianovic, James G. Tipton, **Melanie Abongwa**, Fudan Zheng, Shivani Choudhary, Richard J. Martin and Alan P. Robertson. "Effects of monepantel on nicotinic acetylcholine receptors from *Ascaris suum* and *Oesophagostomum dentatum*". International Symposium on Anthelmintics: From Discovery to Resistance II, held at the Marina Village Center, San Diego, California, USA, February 9-12, 2016.

Mark McHugh, Saurabh Verma, Shivani Choudhary, **Melanie Abongwa**, Sudhanva Kashyap, JoAnne Powell- Coffman, Alan Robertson, Richard Martin. "Differential expression of four nicotinic acetylcholine receptor subunits (nAChRs) in *Ascaris suum* tissues". International Symposium on Anthelmintics: From Discovery to Resistance II, held at the Marina Village Center, San Diego, California, USA, February 9-12, 2016.

Melanie Abongwa, Fidelis Cho-Ngwa, Godfred Ayimele, Moses Samje, Smith B. Babiaka, Ann Perera, Adrian J. Wolstenholme, Richard J. Martin, Alan P. Robertson. *In vitro* antifilarial activities and metabolomic profiling of extracts of *Daniellia oliveri* and *Psorospermum febrifugum*. American Society of Tropical Medicine and Hygiene (ASTMH) 64th Annual Meeting, held at Philadelphia Marriott Downtown, Philadelphia, Pennsylvania, USA, October 25-29, 2015.

Melanie Abongwa, Alan P. Robertson, Richard J. Martin. "Not just GluCl_s (Glutamate-gated Chloride channels): Abamectin has potent effects on nicotinic acetylcholine receptors of nematode parasites". 25th International Conference of the World Association for the Advancement of Veterinary Parasitology (WAAVP), held at The Arena and Convention Centre, Liverpool, UK, August 16-20, 2015.

Melanie Abongwa, Fidelis Cho-Ngwa, Godfred A. Ayimele, Moses Samje, Smith B. Babiaka, Ann Perera, Richard J. Martin, Alan P. Robertson. "Anthelmintic activity and metabolomic profiling of extracts of *Daniellia oliveri* and *Psorospermum febrifugum*". 25th International Conference of the World Association for the Advancement of Veterinary Parasitology (WAAVP), held at The Arena and Convention Centre, Liverpool, UK, August 16-20, 2015.

Melanie Abongwa, Fudan Zheng, Samuel K Buxton, Elise Courtot, Claude Charvet, Cédric Neveu, Ciaran J McCoy, Saurabh Verma, Alan P Robertson and Richard J Martin. "*Asu*-ACR-16: a homomeric nAChR widely distributed in *Ascaris* tissues". 25th International Conference of the World Association for the Advancement of Veterinary Parasitology (WAAVP), held at The Arena and Convention Centre, Liverpool, UK, August 16-20, 2015.

Melanie Abongwa, Fidelis Cho-Ngwa, Godfred A. Ayimele, Moses Samje, Smith B. Babiaka, Richard J. Martin, Alan P. Robertson. "*In vitro* filaricidal activity, cytotoxicity and phytochemical analysis of crude extracts of *Daniellia oliveri* and *Psorospermum febrifugum*". Society of Toxicology (SOT) 54th Annual Meeting & ToxExpo™, San Diego Convention Center, San Diego, California, USA, March 21-26, 2015.

Claude L Charvet, Samuel K Buxton, Cédric Neveu, Jacques Cabaret, Nicolas Peineau, **Melanie Abongwa**, Elise Courtot, Alan P Robertson, Richard J Martin. "Nematode nicotinic acetylcholine receptor diversity: expression of tribendimidine- & derquantel-sensitive receptors in *Xenopus* oocytes". Joint Meeting of the 16th Drug Design & Development Seminar (DDDS 2015) and WG4 of COST Action CM1307, held at the Robert Koch Institute, Berlin, Germany, March 16-18, 2015.

R. J. Martin, **M. Abongwa**, A. P. Robertson. "Not just GluCl_s (Glutamate-gated Chloride channels): abamectin has potent effects on nicotinic acetylcholine receptors of nematode parasites". Proceedings of the 59th Annual Meeting of the American Association of Veterinary Parasitologists (AAVP), held at The Curtis Hotel, Denver, Colorado, USA, July 26-29, 2014. pp81. Published as an Oral Communication in *Journal of Veterinary Pharmacology and Therapeutics* (2015), **38**: 42-43.

Alan Robertson, **Melanie Abongwa**, Samuel Buxton, Elise Courtot, Claude Charvet, Cedric Neveu, Richard Martin. "Characterization of a homomeric nicotinic acetylcholine receptor, *Ascaris suum* ACR-16, in *Xenopus laevis* oocytes". Proceedings of the 59th Annual Meeting of the American Association of Veterinary Parasitologists (AAVP), held at The Curtis Hotel, Denver, Colorado, USA, July 26-29, 2014. p. 82.

Shivani Choudhary, **Melanie Abongwa**, Samuel K. Buxton, Ciaran J. McCoy, Alan P. Robertson, Saurabh Verma, Richard J. Martin. "*Ascaris suum* ACR-21 forms a homomeric nicotinic acetylcholine receptor with novel pharmacology". Proceedings of the 59th Annual Meeting of the American Association of Veterinary Parasitologists (AAVP), held at The Curtis Hotel, Denver, Colorado, USA, July 26-29, 2014. p. 54.

Charvet, C., Buxton, S. K., Neveu, C., Cabaret, J., Cortet, J., Peineau, N., **Abongwa, M.**, Robertson, A. P., Martin, R. J. (2014). "Nicotinic acetylcholine receptors: expression in oocytes and functional diversity in parasitic nematodes". Presented at NemaTours: Bringing worms together, Tours, FRA (2014-07-17 - 2014-07-18). [<http://prodinra.inra.fr/record/276369>].

M. Abongwa, S. K. Buxton, S. Verma, A. P. Robertson and R. J. Martin. "Pharmacological and electrophysiological characterization of *Ascaris suum* homopentameric nicotinic acetylcholine receptors in *Xenopus laevis* oocytes". Society of Toxicology (SOT) 53rd Annual Meeting & ToxExpoTM, Phoenix Convention Center, Phoenix, Arizona, USA, March 23-27, 2014.

M. Abongwa, S. K. Buxton, C. L. Charvet, C. Neveu, A. P. Robertson and R. J. Martin "Characterization of the *Ascaris suum* homomeric nicotinic acetylcholine receptor, ACR-16, in *Xenopus laevis* oocytes". International Symposium on Anthelmintics: From Discovery to Resistance, held at the Fort Mason Conference Center, San Francisco, California, USA, February 5-7, 2014. p. 27.

R. J. Martin, **M. Abongwa**, S. K. Buxton and A. P. Robertson "Effects of paraherquamide, derquantel, and the macrocyclic lactone, abamectin, on native and expressed receptors of nematode parasites". International Symposium on Anthelmintics: From Discovery to Resistance, held at the Fort Mason Conference Center, San Francisco, California, USA, February 5-7, 2014. 7A.

Alan P Robertson **Melanie Abongwa**, Samuel K Buxton, Sreekanth Puttachary, Nathan Romine, Saurabh Verma, Adrian J Wolstenholme, and Richard J Martin "Cholinergic receptors on the *Ascaris suum* pharynx". International Symposium on Anthelmintics: From Discovery to Resistance, held at the Fort Mason Conference Center, San Francisco, California, USA, February 5-7, 2014. 6D.

M. Abongwa, S. K. Buxton, S. Verma, A. P. Robertson and R. J. Martin "Pharmacological and electrophysiological characterization of *Ascaris suum* homopentameric nicotinic acetylcholine receptors in *Xenopus laevis* oocytes". Central States Regional Chapter Of The Society of Toxicology (CS-SOT) Annual Fall Meeting, held at the Gateway Center and Hotel, Ames, Iowa, USA, October 10-11, 2013. p. 33.

AWARDS

- 2017** (i) Iowa State University Graduate College, Research Excellence Award, Spring 2017.
- (ii) Iowa State University Interdepartmental Toxicology High Impact Publication Award for the academic year 2016 – 2017 (Publication: **Melanie Abongwa**, Samuel K Buxton, Elise Courtot, Claude L Charvet, Cédric Neveu, Ciaran J McCoy, Saurabh Verma, Alan P Robertson and Richard J Martin (2016) "Pharmacological profile of Asu-ACR-16, a new homomeric nAChR widely distributed in Ascaris tissues" British Journal of Pharmacology 173(16): 2463-77. doi: 10.1111/bph.13524).
- 2016** (i) Schlumberger Foundation Faculty for the Future PhD Fellowship Renewal for the academic year 2016 – 2017 (Amount Awarded: \$36,000).
- (ii) Iowa State University Graduate and Professional Student Senate (GPSS) Research Award.
- (iii) Iowa State University Graduate and Professional Student Senate (GPSS) Professional Advancement Grant (PAG) Award.
- 2015** (i) Schlumberger Foundation Faculty for the Future PhD Fellowship Renewal for the academic year 2015 – 2016 (Amount Awarded: \$43,000).
- (ii) American Society of Tropical Medicine and Hygiene (ASTMH) Young Investigator Award – 1st Place Winner for Poster and Oral Presentations.
- (iii) Society of Toxicology (SOT) – Drug Discovery Toxicology Specialty Section (DDTSS) Emil A. Pfitzer Award – 3rd Place Student Poster Contest.
- (iv) Burroughs Wellcome Fund Collaborative Research Travel Award – University of California San Francisco, January 10 – February 14, 2016.
- (v) Iowa State University College of Veterinary Medicine (CVM) Travel Award.
- (vi) Iowa State University Graduate and Professional Student Senate (GPSS) Professional Advancement Grant (PAG) Award.
- 2014** (i) Schlumberger Foundation Faculty for the Future PhD Fellowship for the academic year 2014 – 2015 (Amount Awarded: \$22,684).
- (ii) Toxicologists of African Origin (TAO) Graduate Student Travel Award to attend the Society of Toxicology (SOT) 53rd Annual Meeting in Phoenix, Arizona, USA.
- 2012: Three-year Miller Fellowship, Iowa State University, Ames, USA.

FUNDING

2016-2017	Schlumberger Foundation Faculty for the Future Program. Amount Awarded \$36,000.
2015-2016	Schlumberger Foundation Faculty for the Future Program. Amount Awarded \$43,000.
2014-2015	Schlumberger Foundation Faculty for the Future Program. Amount Awarded \$22,684.
2015	Burroughs Wellcome Fund Collaborative Research Travel Award. Amount Awarded \$1,500.
TOTAL	\$103,184