# Identification of Angiostrongylus cantonensis and other nematodes using the SSU rDNA in Achatina fulica populations of Metro Manila 

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#### Abstract

Angiostrongylus cantonensis is a parasitic nematode that causes eosinophilic meningitis in humans. Accidental infection occurs by consumption of contaminated intermediates, such as the giant African land snail, Achatina fulica. This study surveyed the presence of $A$. cantonensis juveniles in A. fulica populations from 12 sites in Metropolitan Manila, Philippines using the SSU rDNA. Fourteen distinct sequences from 226 nematodes were obtained; of these, two matched A. cantonensis and Ancylostoma caninum, respectively, with $100 \%$ identity. Exact identities of the remaining twelve sequences could not be determined due to low percent similarities. Of the sequenced nematodes, A. cantonensis occurred with the highest frequency ( 139 out of 226). Most of these ( 131 out of 139) were collected in just one area in Quezon City. Nematode infection of A. fulica in this area and two others from Makati and another area in Quezon City, respectively, were highest, combining for $95 \%$ of the total infection. Ancylostoma caninum, on the other hand, was detected in four different sites. A. caninum is a canine parasite, and this is the first report of the nematode in A. fulica. These results cause public health concerns as both $A$. cantonensis and $A$. caninum are zoonotic to humans.


## INTRODUCTION

Angiostrongyliasis is a condition characterized by acute headache, visual disturbances, photophobia, neck stiffness, neck pain, hyperesthesias and paresthesias (Weller \& Liu, 1993; Tsai et al., 2003; Tomanakan et al., 2008). This is caused by infection of the rat lungworm, Angiostrongylus cantonensis (family Angiostrongylidae) in humans (Cowie \& Robinson, 2003; Li et al., 2008). Rats are normally the final hosts of $A$. cantonensis (Anderson, 2000; Graeff-Teixeira et al., 2009), while snails and slugs are used as intermediates (Lee \& Yen, 2005). Humans, however, may be accidentally infected by consuming the intermediate host. Such infection is the most common cause of human
eosinophilic meningitis. Cases of $A$. cantonensis infection have become prevalent throughout the Pacific, Southeast Asia, Africa, Australia and North, Central and South America (Kliks \& Palumbo, 1992).

It has been proposed that $A$. cantonensis was introduced in Asia and the Pacific region during World War II, when its intermediate host, the giant African land snail, Achatina fulica (family Achatinidae), was used as an alternative food source by the Japanese (Alicata, 1966; Latonio, 1971). Once introduced, A. fulica can easily establish and spread in the area (Raut \& Barker, 2002; Cowie \& Robinson, 2003; Thiengo et al., 2007). On average, an infected snail carries about 20 parasites. Highly infected ones, however, may harbor 500-2000 juveniles (Caldeira et al., 2007). The ability of A. fulica
to carry large numbers of A. cantonensis and its dispersal by human means contribute to the spread and zoonosis of $A$. cantonensis not only to its natural hosts but also to accidental hosts, including humans (Cowie \& Robinson, 2003; Li et al., 2008). Cases of A. cantonensis infection in rodents and mollusks have been documented in the Philippines. Much of these studies detected A. cantonensis in several provinces in Luzon (Salazar \& Cabrera, 1969; Westerlund \& Chamberlain, 1969; Garcia, 1979; Antolin et al., 2006;) and one area in the Visayas (Guerrero \& Guerrero, 1972). Less studies, however, has been done to detect $A$. cantonensis in Metro Manila, which is inhabited by more than 11 million people.

Identification of nematodes in the environment is important to assess their potential risks to humans. Most nematodes present in intermediate hosts, however, are juveniles. In such stages, species are difficult to differentiate based on morphology. As an alternative, a small section of a DNA sequence from a standardized region of the genome can be used to identify species (Dasmahapatra \& Mallet, 2006). The 5' end of the small subunit ribosomal RNA gene (SSU rDNA) has been used to differentiate soil nematodes including Angiostrongylus species (Floyd et al., 2002; Fontanilla \& Wade, 2008). It was proposed that two sequences belong to the same species if they are $99.5 \%-100 \%$ identical for the 450 bp of
the 5' end of the SSU rDNA (Floyd et al., 2002). Thus the identity of the species can be determined by matching the sequence to an accessible sequence database such as GenBank. Evaluating the role of A. fulica in the spread of $A$. cantonensis and potentially other nematodes is important in the Philippines, especially in the densely populated area of Metro Manila. This would allow proper assessment of the epidemiology of the diseases that they cause. The objectives of this study were to (1) detect the presence of the human-infective third-stage juveniles of $A$. cantonensis in A. fulica populations in Metropolitan Manila using the SSU rDNA as a genetic marker; and (2) to determine the prevalence of this nematode in these ubiquitous snails.

## MATERIALS AND METHODS

Achatina fulica specimens were collected from 12 sites in Metro Manila (Table 1; Figure 1). These were cut into small pieces and digested overnight in Ash's digestive fluid (Ash, 1970). Nematodes were collected and stored at $-20^{\circ} \mathrm{C}$ prior to use. The following procedure adapted from Floyd et al. (2002) was performed to extract genomic DNA. Nematodes were incubated in $20 \mu \mathrm{l} 0.25 \mathrm{M}$ NaOH for five hours. After incubation, the tubes were heated for three minutes at $95^{\circ} \mathrm{C}$, cooled at room temperature and centrifuged.

Table 1. Areas sampled in this study

| Site | City | District | Area type |
| :--- | :--- | :--- | :--- |
| CAL | Caloocan City | Camarin | Residential area |
| LPI | Las Pinas City | Moonwalk | Church grounds |
| MKT | Makati City | Santa Cruz | Public cemetery |
| MB1 | Malabon City | Potrero | Residential area |
| MB2 | Malabon City | San Agustin | Church grounds |
| MNL | Manila | Ermita | Hospital grounds |
| MRK | Marikina City | Tumana | Residential area |
| PAS | Pasay City | Baclaran | Public cemetery |
| QC1 | Quezon City | Fairview | Residential area |
| QC2 | Quezon City | Novaliches | Park area |
| QC3 | Quezon City | Batasan Hills | Residential area |
| QC4 | Quezon City | Diliman | School grounds |



Figure 1. Location of sampling areas. CAL, Barangay Camarin, Caloocan City; LPI, Moonwalk Village, Las Pinas City; MKT, Santa Cruz, Makati City; MB1, Barangay Potrero, Malabon City; MB2, San Agustin, Malabon City; MNL, Ermita, Manila; MRK, Barangay Tumana, Marikina City; PAS, Baclaran, Pasay City; QC1, Barangay Fairview, Quezon City; QC2, Novaliches, Quezon City; QC3, Barangay Batasan Hills, Quezon City; QC4, Diliman, Quezon City

The following reagents were then added: $4 \mu \mathrm{l}$ $1.0 \mathrm{M} \mathrm{HCl} ; 10 \mu \mathrm{l} 0.5 \mathrm{M}$ Tris-HCl; and $5 \mu \mathrm{l} 2 \%$ Triton X-100. This was followed by another round of centrifugation, heating for three minutes at $95^{\circ} \mathrm{C}$, and cooling at room temperature. The DNA extracts were stored at $-20^{\circ} \mathrm{C}$ prior to use.

The first 480-bp from the 5 ' end of the SSU rDNA was amplified from the extracts (Fontanilla \& Wade, 2008). The primers used were as follows: SSU_F_07 (sense) 5'- AAAGATTAAGCCATGCATG-3' and SSU_R_09 (anti-sense) 5'- AGCTGGAATTA CCGCGGCTG-3' (Blaxter et al., 1998). The final volume was $50 \mu \mathrm{l}$ containing $5 \mu \mathrm{~L}$ PCR buffer with 1.5 mM MgCl2-, $1.0 \mu \mathrm{~L} 10 \mathrm{mM}$
$\mathrm{dNTPs}, 2.5 \mu \mathrm{~L} 10 \mu \mathrm{M}$ for each of the primers, $10 \mu \mathrm{~L}$ Q buffer (Qiagen ${ }^{\mathrm{TM}}, \mathrm{USA}$ ), $0.25 \mu \mathrm{~L} 1.25 \mathrm{U}$ Taq DNA polymerase (Roche, USA) and $4 \mu \mathrm{l}$ (5-20 ng/ $\mu \mathrm{L}$ ) DNA sample. The PCR running conditions were as follows: $94^{\circ} \mathrm{C}$ for 3 min and 43 cycles at $94^{\circ} \mathrm{C}$ for $30 \mathrm{~s}, 45^{\circ} \mathrm{C}$ for 30 s and $65^{\circ} \mathrm{C}$ for 1 min , and final extension at $72^{\circ} \mathrm{C}$ for 5 min . PCR products were visualized in $1 \%$ agarose gels with ethidium bromide. The PCR products were extracted from the gel using a Qiagen ${ }^{\text {TM }}$ Gel Extraction Kit (Qiagen ${ }^{\mathrm{TM}}$, USA). The eluted PCR products were sent to First BASE Laboratories (Selangor, Malaysia) for sequencing of the anti-sense strand.

DNA sequences were assembled using the STADEN package version 1.5.3 (Staden et al., 1994) and aligned using the BioEdit Sequence Alignment Editor (BioEdit v. 5.0.5; Hall, 1999) and subjected to Basic Local Alignment Search Tool on Genbank to determine if they matched A. cantonensis or any other nematode (Altschul et al., 1990).

The prevalence of nematode infection for each site was computed by taking the percentage of snails infected with nematodes (Roberts \& Janovy, 2005). The parasite load (number of nematodes present in infected snails) range of A. fulica for each site was also determined. Multiple infections of different parasites were likewise reported.

## RESULTS

## Nematode infection of A. fulica populations

A total of 365 snails were collected from the twelve sites surveyed. Nematode infection of $A$. fulica was observed in all of the sites and details of the infection rate and parasite load of snails per population are summarized in Table 2. Of the 365 snails sampled, 61 snails were infected with nematodes. The A. fulica population in QC2 had the highest infection rate with 19 out of 30 snails (63.3\%) infected. The remaining populations did not exceed an infection rate of $23.3 \%$. Achatina fulica in PAS and LPI had the lowest infection rate (only one snail in 30 or $3.3 \%$ ) among the 12 populations sampled. A total of 965 nematodes were collected from the 61

Table 2. Percent infection and parasite load per site sampled for $A$. fulica. N , number of A. fulica specimens collected per site

| Site | N | Infected Snails <br> (\% Infection) | Total Nematode Count <br> (Parasite Load Range) |
| :--- | :---: | :---: | :---: |
| CAL | 30 | $2(6.7 \%)$ | $3(1-2)$ |
| LPI | 30 | $1(3.3 \%)$ | $1(1)$ |
| MKT | 30 | $7(23.3 \%)$ | $202(1-179)$ |
| MB1 | 30 | $4(13.3 \%)$ | $5(1-2)$ |
| MB2 | 30 | $2(6.7 \%)$ | $6(2-4)$ |
| MNL | 30 | $3(10.0 \%)$ | $5(1-3)$ |
| MRK | 30 | $7(23.3 \%)$ | $8(1-2)$ |
| PAS | 30 | $1(3.3 \%)$ | $1(1)$ |
| QC1 | 30 | $7(23.3 \%)$ | $640(3-340)$ |
| QC2 | 30 | $19(63.3 \%)$ | $70(1-10)$ |
| QC3 | 50 | $7(14.0 \%)$ | $18(1-11)$ |
| QC4 | 15 | $1(6.7 \%)$ | $6(1-5)$ |
| Total | 365 | $61(16.7 \%)$ | $965(1-340)$ |

Table 3. Nematode sequences obtained in this study and their closest match in GenBank. Each Metro Manila Sequence (MMS) refers to a unique sequence

| Sequence | Closest match | Identity | Frequency |
| :--- | :--- | :---: | :---: |
| MMS 1 (GB JX512217) | Ancylostoma caninum | $100 \%$ | $11(4.9 \%)$ |
| MMS 2 (GB JX512218) | Angiostrongylus cantonensis | $100 \%$ | $139(61.5 \%)$ |
| MMS 3 (GB JX512219) | Oslerus rostratus | $99.5-99.7 \%$ | $2(0.9 \%)$ |
| MMS 4 (GB JX512215) | Rhabditis sp. | $100 \%$ | $11(4.9 \%)$ |
| MMS 5 (GB JX512220) | A. caninum | $99.3 \%$ | $1(0.4 \%)$ |
| MMS 6 (GB JX512221) | Aphelenchoides sp. | $89.1 \%$ | $1(0.4 \%)$ |
| MMS 7 (GB JX512216) | Caenorhabditis briggsae | $98.1 \%$ | $1(0.4 \%)$ |
| MMS 8 (GB JX512214) | Oslerus rostratus | $98.2 \%$ | $1(0.4 \%)$ |
| MMS 9 (GB JX512222) | Oslerus osleri | $99.1 \%$ | $17(7.5 \%)$ |
| MMS 10-14 (GB JX512209- JX512213) | Cephaloboides nidrosiensis | $89.9-96.4 \%$ | $42(18.6 \%)$ |

infected snails. Most of the infected snails carried a small number (1-11) of nematodes. Less than 20 nematodes were collected in each population, with the exception of the $A$. fulica populations in QC2 (70 nematodes), MKT (202), and QC1 (640). Three snails were heavily infected, two of which were from QC1 (212 and 340 nematodes, respectively) and another one from MKT (179 nematodes).

## Distinct SSU rDNAsequences identified

Of the nematodes isolated, 226 individuals were subjected to DNA extraction, PCR
amplification and sequencing. BLAST results for the SSU rDNA sequences obtained from the nematodes are summarized in Table 3, showing 14 distinct Metro Manila sequences (MMS).

MMS 1 from CAL, QC3, MKT, and MB1 matched the nematode, Ancylostoma caninum (GB AJ920347), with 100\% percent identity. MMS 2 from QC1, QC4, and MKT matched A. cantonensis (GB GQ181114) with 100\% identity. MMS3 from MKT matched Oslerus rostratus (GB GU946678) with 99.5\% and $99.7 \%$ identity, respectively. A $100 \%$
match for Rhabditis sp. (GB EU196004) was also detected from MMS4 from QC3. For the other sequences that did not have exact match (below $100 \%$ ), the closest similarity based on BLAST was noted (Table 3). Some of the MMS have slightly different sequences but have the same closest match in GenBank, thus different identity scores were observed (see MMS 10-14; Table 3).

Of the 14 unique MMS detected, MMS 2 (A. cantonensis) occurred with the highest frequency. Out of the 226 nematode sequences, 139 (61.5\%) matched $A$. cantonensis. The parasite was found in QC1, QC4 and MKT. The most diverse
population of nematodes was found in MKT, where six distinct MMS were observed. Three distinct MMS were found in QC3, and only one MMS each in CAL, MB1, QC1 and QC4. MMS 10-14 from MRK and QC2 had Cephaloboides nidrosiensis (GB EU196020) as the closest match (Table 4).

## Occurrence of infection by multiple nematode species

There were five cases observed wherein an individual snail is infected by more than one nematode species. A summary of these cases is shown in Table 5.

Table 4. Nematode infection for each site. Values are numbers of nematodes for each area exhibiting each of the MMS

| Area | MMS1 | MMS2 | MMS3 | MMS4 | MMS5 | MMS6 | MMS7 | MMS8 | MMS9 | MMS10 -14 | TOTAL |
| :--- | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: | :---: |
| CAL | 3 | - | - | - | - | - | - | - | - | - | 3 |
| LPI | - | - | - | - | - | - | - | - | - | - | 0 |
| MKT | 1 | 2 | 2 | - | - | 1 | - | 1 | 13 | - | 20 |
| MB1 | 1 | - | - | - | - | - | - | - | - | - | 1 |
| MB2 | - | - | - | - | - | - | - | - | - | - | 0 |
| MNL | - | - | - | - | 1 | - | - | - | - | - | 1 |
| MRK | - | - | - | - | - | - | - | - | - | 2 | 2 |
| PAS | - | - | - | - | - | - | - | - | - | - | 0 |
| QC1 | - | 131 | - | - | - | - | - | - | - | - | 131 |
| QC2 | - | - | - | - | - | - | - | - | 4 | 40 | 44 |
| QC3 | 6 | - | - | 11 | - | - | 1 | - | - | - | 18 |
| QC4 | - | 6 | - | - | - | - | - | - | - | - | 6 |

Table 5. Individuals infected by more than one nematode species

| Site | Species identified | Frequency |
| :--- | :--- | :---: |
| MKT (1) | MMS $1(100 \%$ Ancylostoma caninum $)$ | $1 / 2(50.0 \%)$ |
|  | MMS $8(98.2 \%$ Oslerus rostratus) | $1 / 2(50.0 \%)$ |
| MKT (2) | MMS $9(99.1 \%$ Oslerus osleri) | $12 / 14(85.7 \%)$ |
|  | MMS $4(100 \%$ Oslerus rostratus $)$ | $2 / 14(14.3 \%)$ |
| QC2 | MMS 11 (91.1\% Cephaloboides nidrosiensis) | $1 / 5(20.0 \%)$ |
|  | MMS 9 (99.1\% Oslerus osleri) | $4 / 5(80.0 \%)$ |
| QC3 (1) | MMS $1(100 \%$ Ancylostoma caninum $)$ | $1 / 3(33.3 \%)$ |
|  | MMS 7 (98.1\% Caenorhabditis briggsae $)$ | $2 / 3(66.7 \%)$ |
| QC3 (2) | MMS 1 (100\% Ancylostoma caninum) | $1 / 2(50.0 \%)$ |
|  | MMS 7 (98.1\% Caenorhabditis briggsae) | $1 / 2(50.0 \%)$ |

## DISCUSSION

## The SSU rDNA detected $A$. cantonensis and other nematodes in A. fulica from Metro Manila

Based on Floyd et al.'s threshold of 99.5\%$100 \%$ identity among sequences belonging to the same species, only $A$. cantonensis and A. caninum could be identified with certainty to species level based on GenBank BLAST results. Sequences that matched Rhabditis sp. were only assigned to that genus. Although two sequences from MKT matched Oslerus rostratus within the desired threshold, they could not be assigned to the said taxon with absolute certainty as less than 450 bases were available due to the poor quality of the sequences. For the remaining sequences, their exact identification could not be determined as of this time. A match below $99.5 \%$ is not uncommon because many nematodes are not yet barcoded; the sequences in GenBank are thus far from complete (Floyd et al., 2002).

Angiostrongylus cantonensis were found in Quezon City and Makati City populations
Of the 12 sites sampled, only three areas showed a high infection rate. Approximately $95 \%$ of the nematodes collected in this study were found in QC1, QC2, and MKT. These three varied in terms of habitat type (Table 1). The area types of the nine other sites also varied, showing no observable trend in parasite or even host preference.

Although A. cantonensis infection was shown to have the highest frequency in this study, this was concentrated in QC1, a residential area in Fairview, Quezon City, where 131 individuals of $A$. cantonensis was identified. Apart from that, only six were identified from QC3, two from MKT, and none from the rest of the areas studied. The abundance of $A$. cantonensis in only one area may be due to the uneven distribution of both the parasite and snail host. For instance, Biseru (1971) observed high variation in infection rates of $A$. cantonensis in A. fulica even within a small geographic area in West Malaysia, with even two populations exhibiting no infection. Further, the
prevalence of the parasite is subject to the availability of the hosts, both definitive and intermediate, in order for the parasite to complete its life cycle. Thus, the distribution of rodents as definitive hosts may have had an effect on the observed distribution of $A$. cantonensis, but this was not determined in this study. Nonetheless, the high incidence of the nematode observed in certain areas is still a cause for concern.

## Ancylostoma caninum was detected in four different Metro Manila areas

This study demonstrates for the first time the presence of the hookworm Anclylostoma caninum in A. fulica. This nematode utilizes dogs as definitive hosts while its larval stages are free-living in the soil. The larvae infect the definitive host via skin penetration or ingestion (Hotez et al., 1990; Roberts \& Janovy, 2005; Franke et al., 2011). These are most likely the same routes by which A. fulica is infected. It is alarming that $A$. caninum was detected in four areas of Metro Manila (namely, CAL, MKT, MB1, and QC3), and this finding is significant from an epidemiological perspective because $A$. caninum is also zoonotic to humans via skin penetration or oral ingestion (Hotez et al., 1990). Ancylostoma caninum is a facultative skin penetrator, being able to degrade human fibronectin (Hotez et al., 1990), which can cause cutaneous diseases (Croese et al., 1994). Accidental ingestion, on the other hand, may lead to eosinophilic enteritis as manifested by a non-severe form of abdominal pain as A. caninum adapts poorly to the human host (Croese et al., 1994).

Ancylostoma caninum infection in humans has been cited in Australia, United States, South America, Israel and even in the Philippines (Roberts \& Janovy, 2005; Croese et al., 1994). Such infections are usually associated with interaction with infected pets or contact with contaminated soil. This study presents another route via handling of contaminated snails.

## Other nematodes were also recovered from Achatina fulica

All MMS were most similar with species that belong to the order Rhabditida, a
taxonomic group that includes free-living and parasitic species (Smyth, 1994). Of these, only $A$. cantonensis and $O$. rostratus (feline lungworm), both under suborder Strongylida, are known to use A. fulica as an intermediate host (Grewal et al., 2003). Two other members of the Strongylida, A. caninum and O. osleri, are nematode parasites of dogs (Hotez et al., 1990).

Two sequences from this study, MMS 4 and MMS 7, were most similar to two taxa from the family Rhabditidae, Rhabditis sp. and Caenorhabditis briggsae, respectively, and were collected from QC3. Different species of the genus Rhabditis use snails as hosts (Grewal et al., 2003). Caenorhabditis briggsae, on the other hand, is a free-living soil nematode. As stated previously, it is unlikely that these nematode sequences are actually what they closely match due to the low percent identities (89.9-96.4\%). Some nematodes become available in the soil and thus associate with invertebrate hosts upon entering the dauer stage. The nematode in this stage undergoes changes leading to developmental arrest for survival and dispersal in unfavorable conditions (Inoue et al., 2007; Tissenbaum et al., 2000). This may be true for those that matched Cephaloboides nidrosiensis. Members of the family Cephalobidae are usually free-living, and the recovery in A. fulica of taxa possibly related to cephalobids may be attributed to the dauer larval stage (Anderson et al., 2009). Furthermore, some parasitic nematodes undergo this stage when the infective larval stages are deposited to the environment. The availability of the host triggers the exit of the larvae in the dauer stage (Tissenbaum et al., 2000). Ancylostoma caninum is known to pass through this stage, making itself available in the soil and thus possibly accidentally infecting A. fulica.

In conclusion, A. cantonensis was detected in A. fulica populations in Metro Manila using the SSU rDNA; another nematode species, $A$. caninum, was also identified. Both species are able to infect humans and may pose a threat to public health. This study showed that A. fulica populations in Metro Manila are infected with nematodes zoonotic to humans. Their ability
to spread and their close association with humans increases the risk of spreading the parasites they harbor and passing them on to humans. The results of this study necessitate an increase in public awareness, particularly in handling these snails. A. fulica populations in Quezon City and Makati may be further sampled since it is in these populations where the highest parasite load and highest nematode diversity were observed. Other regions of the Philippines should also be evaluated, particularly Mindanao, where no data is currently available.

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