Detection of assemblages A and B of *Giardia duodenalis* in water and sewage from São Paulo state, Brazil

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**ABSTRACT**

*Giardia duodenalis* is a protozoan that parasitizes humans and other mammals and causes giardiasis. Although its isolates have been divided into seven assemblages, named A to G, only A and B have been detected in human faeces. Assemblage A isolates are commonly divided into two genotypes, AI and AII. Even though information about the presence of this protozoan in water and sewage is available in Brazil, it is important to verify the distribution of different assemblages that might be present, which can only be done by genotyping techniques. A total of 24 raw and treated sewage, surface and spring water samples were collected, concentrated and purified. DNA was extracted, and a nested PCR was used to amplify an 890 bp fragment of the *gdh* gene of *G. duodenalis*, which codes for glutamate dehydrogenase. Positive samples were cloned and sequenced. Ten out of 24 (41.6%) samples were confirmed to be positive for *G. duodenalis* by sequencing. Phylogenetic analysis grouped most sequences with *G. duodenalis* genotype AII from GenBank. Only two raw sewage samples presented sequences assigned to assemblage B. In one of these samples genotype AII was also detected. As these assemblages/genotypes are commonly associated to human giardiasis, the contact with these matrices represents risk for public health.

**Key words** | genotyping, *Giardia*, glutamate dehydrogenase, sewage, water

**INTRODUCTION**

*Giardia duodenalis* (syn. *lamblia* or *intestinalis*) is a flagellated protozoan that parasitizes the small intestine of humans and other mammals, causing giardiasis. Isolates of this species are morphologically similar, but have been divided into seven assemblages, named A to G, on the basis of genetic heterogeneity. To date only assemblages A and B have been found in humans (Thompson 2004; Monis et al. 2009).
In developed countries, the prevalence of human giardiasis varies from 2 to 5%. In Brazil, studies show that it ranges from 16 to 26% (Mascarini & Donalisio 2006; Silva et al. 2009; Tashima et al. 2009).

*G. duodenalis* is a waterborne pathogen. Cysts of the organism can survive for long periods in water and are resistant to some of the processes used by the water industry, such as filtration and disinfection. To protect public health, therefore, it is important to search for *Giardia* cysts in water and sewage samples (Faubert 2000; Slifko et al. 2000; Smith et al. 2006; Carmena et al. 2007).

Only molecular characterization techniques can be used to differentiate *G. duodenalis* assemblages. These techniques have been used to characterize *Giardia* isolates from environmental sources in a number of countries (Caccio et al. 2003; Sulaiman et al. 2004; Bertrand & Schwartzbrod 2007; Castro-Hermida et al. 2008; Plutzer et al. 2008).

In Brazil, this protozoan has been detected in water and sewage samples by immunofluorescence assay (Franco et al. 2001; Cantusio Neto & Franco 2004; Hachich et al. 2004; Heller et al. 2004; Cantusio Neto et al. 2006; Nishi et al. 2009; Razzolini et al. 2010); however, the molecular characterization of *Giardia* cysts from these sources has not yet been published. Thus, the significance of cysts in the environment for public health is not known in this country.

The objective of this study was to detect and characterize the genotypes of *Giardia* sp. in water and sewage samples from São Paulo state, Brazil, discussing the importance of findings for public health.

**MATERIALS AND METHODS**

**Water and sewage samples**

A total of 24 water and sewage samples were collected from May 2008 to March 2009 in São Paulo state, Brazil (18 in São Paulo Metropolitan Region and 6 in two small municipalities within the state: Piracicaba and São Lourenço da Serra).

Raw (6) and treated (6) sewage samples were collected at six different wastewater treatment plants that operate by stabilization ponds, activated sludge, anaerobic reactors or by a match of two of these systems. Effluent from these plants is discharged into water bodies and, in some cases, is directed to non-potable industrial uses. Two raw sewage samples were collected at different entrances of a lake that has been used as a water supply.

Surface water grab samples (11) were taken from a reservoir, close to the abstraction point supplying a drinking water treatment plant. The reservoir is also used as a recreational area. A spring water sample (1) was also collected. All samples were processed within 24 hours after collection.

**Sample concentration**

Samples (10 L) were concentrated by the modified membrane filtration technique (Araújo et al. 2010), which consists of filtration and centrifugation steps. Membranes with pores of 1 m and diameters of 14 cm (Millipore®, Brazil) were employed. Pre-filters were also required for treated sewage filtration.

Raw sewage samples (100 ml) were concentrated by centrifugation. Sewage was distributed into 50 ml conical tubes and centrifuged at 7428 × g for 15 minutes at 24°C. The sediments were resuspended and pooled into one tube and then washed with ultra-pure water (Milli Q®). The suspension was centrifuged (7.428 × g/15’/24°C) and supernatant was discharged.

**Sample purification**

Sediment obtained from the concentration step was purified by fluctuation in zinc sulfate solution (33%) according to Faust et al. (1938), with some modifications. Briefly, sediment was washed with ultra-pure water (Milli Q®). Supernatant was discharged after centrifugation (7428 × g/15’/24°C). Ten millilitres of zinc sulfate solution was added. After homogenization, tubes were centrifuged (3714 × g/5’/24°C). The pellet was removed with a 10 mL pipette. The supernatant left in the tube (2 ml) was washed twice with ultra-pure water (Milli Q®). The pellet was resuspended in ultra-pure water (Milli Q®).

**DNA extraction and amplification**

Genomic DNA was extracted using the phenol-chloroform-isoamilic alcohol protocol (Araújo et al. 2010), with small
modifications as follows: all concentrated sediment was submitted to DNA extraction and the incubation period at 65°C was reduced to 80 minutes.

The PCR mix consisted of 25 ng of DNA, 10 × buffer, 2 mM of MgCl₂, 1% of PVP, 300 μM of deoxynucleoside triphosphate mix, 0.5 μM of each primer, 1.25 U of Tth DNA polymerase (Biotools®, Madrid, Spain) and ultra-pure water (Milli Q®) to make up to a final volume of 25 μl. The same PCR mix, but without the PVP, was used for the second amplification. Amplification primers and conditions are described in Table 1.

The nested PCR product was resolved by electrophoresis using a 1.8% agarose gel prepared with 1 × TAE buffer and stained with ethidium bromide. A 100 bp DNA Ladder Plus (Fermentas) was included as a size marker. Gel images were obtained by UV transillumination and captured by a gel documentation system (Epi Chemi II Darkroom and Software Labworks – UVP).

Following successful PCR, the products were purified (Ilustratm GFXtm PCR DNA and Gel Band Purification Kit, GE Healthcare, UK). Molecular cloning and sequencing were done according to the methods of Ivanova et al. (2001). Analyses of 825 positions of the gdh gene sequences of the clones were compared with their closest relatives in the GenBank database by BLAST searches (http://blast.ncbi.nlm.nih.gov/Blast.cgi). Further phylogenetic and molecular evolutionary analyses were performed with the MEGA 4.1 program (Tamura et al. 2007).

### RESULTS AND DISCUSSION

PCR amplification of the 890 bp gdh gene fragment was detected in 14 (58.3%) out of 24 water and sewage samples analysed (Figure 1). Eleven of the positive samples were cloned and sequenced; ten (41.6%) were confirmed to be

### Table 1

<table>
<thead>
<tr>
<th>PCR reaction</th>
<th>Primer ID</th>
<th>Sequence*</th>
<th>ID</th>
<th>Cycles</th>
<th>D</th>
<th>A</th>
<th>E</th>
<th>FE</th>
<th>Band size</th>
</tr>
</thead>
<tbody>
<tr>
<td>1st</td>
<td>GdhR (F)</td>
<td>5’CGAGCGCGAGCGCCAAGT ATATCC5’</td>
<td>95°C, 7 min</td>
<td>40</td>
<td>95°C, 2 min</td>
<td>50°C</td>
<td>1 min</td>
<td>72°C</td>
<td>5 min</td>
</tr>
<tr>
<td></td>
<td>#579II (R)</td>
<td>5’GATGTTYGCRCCCATCTG RTAGTTCC5’</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>2nd</td>
<td>GDH-FI (F)</td>
<td>5’AAYGAGGTYATGCGCTT CTGCCA5’</td>
<td>94°C, 2 min</td>
<td>30</td>
<td>94°C, 35 s</td>
<td>56°C</td>
<td>35 s</td>
<td>72°C</td>
<td>1 min</td>
</tr>
<tr>
<td></td>
<td>#579II (R)</td>
<td>5’GATGTTYGCRCCCATCTG RTAGTTCC5’</td>
<td></td>
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</tr>
</tbody>
</table>

ID = Initial denaturation, D = Denaturation, A = Annealing, E = Extension, FE = Final Extension and * = position 659–1485 from the start of the gene.
positive by sequencing (Table 1). One to ten clones of each sample were sequenced, resulting in a total of 71 nucleotide sequences. Some samples had clones with identical sequences, therefore only 64 nucleotide sequences were submitted to GenBank (GenBank accession numbers: GQ503101–GQ503141, GQ503152–GQ503157 and GQ503159–GQ503174). Phylogenetic analyses grouped most of the 64 sequences with G. duodenalis genotype AII sequences from GenBank. Only two raw sewage samples contained sequences assigned to assemblage B. In one of these samples, both genotype AII and assemblage B were detected (Table 2, Figure 2).

The presence of Giardia in water and sewage is well documented worldwide (Karanis et al. 2006; Robertson et al. 2006; Anceno et al. 2007; Bertrand & Schwartzbrod 2007; Castro-Hermida et al. 2008; Plutzer et al. 2008). In Brazil, the detection of this protozoan has also been documented in some studies (Franco et al. 2001; Cantusio Neto & Franco 2004; Hachich et al. 2004; Heller et al. 2004; Cantusio Neto et al. 2006; Nishi et al. 2009; Razzolini et al. 2010).

Table 2 | PCR, sequencing and genotyping results of Giardia isolates detected in water and sewage samples from São Paulo, Brazil

<table>
<thead>
<tr>
<th>Sample origin</th>
<th>Sample number</th>
<th>PCR results</th>
<th>Number of sequenced clones</th>
<th>Sequencing results</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>Number of clones successfully sequenced/GenBank accession numbers</td>
</tr>
<tr>
<td></td>
<td></td>
<td></td>
<td></td>
<td>All</td>
</tr>
<tr>
<td>Raw sewage</td>
<td>1</td>
<td>P</td>
<td>5</td>
<td>5/GQ503101–GQ503104a</td>
</tr>
<tr>
<td></td>
<td>2</td>
<td>P</td>
<td>10</td>
<td>0/GQ503106–GQ503115</td>
</tr>
<tr>
<td></td>
<td>3</td>
<td>P</td>
<td>9</td>
<td>9/GQ503116–503120b</td>
</tr>
<tr>
<td></td>
<td>4</td>
<td>P</td>
<td>4</td>
<td>4/GQ503121–GQ503124</td>
</tr>
<tr>
<td></td>
<td>5</td>
<td>N</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>6</td>
<td>P</td>
<td>7</td>
<td>6/GQ503125–GQ503130</td>
</tr>
<tr>
<td>Treated sewage</td>
<td>7</td>
<td>N</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>8</td>
<td>P</td>
<td>–</td>
<td>–</td>
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<td>9</td>
<td>P</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>10</td>
<td>P</td>
<td>9</td>
<td>9/GQ503152–GQ503158c</td>
</tr>
<tr>
<td></td>
<td>11</td>
<td>P</td>
<td>1</td>
<td>–</td>
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<tr>
<td></td>
<td>12</td>
<td>N</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Surface water</td>
<td>13</td>
<td>P</td>
<td>8</td>
<td>1/GQ503105</td>
</tr>
<tr>
<td></td>
<td>14</td>
<td>N</td>
<td>–</td>
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<td>N</td>
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<td>18</td>
<td>N</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td></td>
<td>19</td>
<td>P</td>
<td>10</td>
<td>10/GQ503132–GQ503141</td>
</tr>
<tr>
<td></td>
<td>20</td>
<td>P</td>
<td>10</td>
<td>10/GQ503159–GQ503168</td>
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<td></td>
<td>21</td>
<td>P</td>
<td>6</td>
<td>6/GQ503169–GQ503174</td>
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<td>22</td>
<td>N</td>
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<td>23</td>
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<tr>
<td></td>
<td>24</td>
<td>N</td>
<td>–</td>
<td>–</td>
</tr>
<tr>
<td>Spring water</td>
<td></td>
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</tr>
</tbody>
</table>

P = positive sample
N = negative sample
a = 2 identical sequences (GQ503102)
b = 5 identical sequences (GQ503116)
c = 3 identical sequences (GQ503154)
In the present study, 10 out of 24 (41.6%) water and sewage samples analysed were found to be positive for *G. duodenalis*, corroborating previous reports that *G. duodenalis* is the only species of *Giardia* found in water sources.

Data on the genotypes of *Giardia* isolates found in Brazil are scarce and mainly derived from analysis of human and animal stool specimens (Rocha et al. 2003; Souza et al. 2007; Volotão et al. 2007, 2008). Although Paulino (2005) employed the technique of PCR to detect *G. duodenalis* in surface water samples, genotyping of the isolates was not performed.

The present study is the first to genotype *G. duodenalis* from environmental samples in Brazil and to demonstrate that assemblages A (genotype AII) and B of *G. duodenalis* are present in different water sources including surface water and raw and treated sewage. These findings are similar to those reported worldwide demonstrating the presence of assemblages A and B in environmental samples (Cacciò et al. 2003; Sulaiman et al. 2004; Robertson et al. 2006; Anceno et al. 2007; Bertrand & Schwartzbrod 2007; Castro-Hermida et al. 2008; Plutzer et al. 2008).

As observed in other studies, assemblage A of *G. duodenalis* was more frequently observed than assemblage B, which was detected in only two raw sewage samples (Cacciò et al. 2003; Sulaiman et al. 2004; Bertrand & Schwartzbrod 2007). In a study carried out in São Paulo, in 2007, Souza et al. (2007) demonstrated that genotype AII was observed in 29 out of 32 clinical samples analysed, and assemblage B in only eight samples. This finding indicates that, in the present study, genotype AII observed in sewage samples may represent the genotype circulating in the population.
An unexpected number of Single Nucleotide Polymorphisms (SNPs) was detected in the majority of sequences obtained in this work. Most sequences had from one to five SNPs. None of these SNPs was observed in sequences recovered from GenBank. Besides, most SNPs resulted in non-synonym substitutions. Once sequencing presented high-quality and very well-defined peaks, these substitutions were not considered to be real, but were assumed to have occurred due to nucleotide incorporation problems during PCR, possibly because 7th DNA polymerase, a low-fidelity enzyme, was used.

The presence of G. duodenalis genotypes associated to human giardiasis in raw sewage indicates that there is risk in the reuse of sub-products of the sewage treatment process as observed in Table 2. Detection of genotype AII and assemblage B in treated sewage reveals that more attention should be given to sewage treatment processes, since effluents of sewage treatment plants can be used for domestic, agricultural or industrial purposes. Furthermore, this matrix can be released in surface waters that are subjected to indirect reuse including drinking water treatment. Sewage sludge may contain $10^3$ to $10^6$ Giardia cysts/kg $^{-1}$ (Straub et al. 1993; Thiriat et al. 1997), and even though this matrix was not analysed in the present work it will be important to characterize G. duodenalis isolates recovered from this kind of sample, especially because of the lack of data (Rimhanen-Finne et al. 2001).

The detection of genotype AII in surface waters also represents risk for public health because this matrix is commonly used as recreation areas or as a source of water supply for humans.

**CONCLUSIONS**

The presence of genotype AII and assemblage B, commonly associated to human giardiasis, in water and sewage samples from São Paulo state indicates that contact with these matrices is a risk to public health. Therefore, more attention should be given to water and sewage treatment processes and to the uses of treated sewage and its discharges in watersheds, which should be protected against sources of contamination.

Studies of detection, quantification, infectivity and genotyping of G. duodenalis cysts from environmental samples should be encouraged in order to provide enough data for the decisions that need to be taken by public health authorities.

**ACKNOWLEDGEMENTS**

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