ORIGINAL ARTICLE



Prevalence of *Giardia intestinalis* with other co-infecting parasites in Barak Valley, Assam, India: a molecular approach

Madhumita Roy^{1,2} · Baby Singha¹ · Debadatta Dhar³ · Shubhadeep Roychoudhury²

Received: 1 December 2018/Accepted: 26 March 2019/Published online: 9 April 2019 © Indian Society for Parasitology 2019

Abstract Giardia intestinalis was included in the World Health Organization's Neglected Disease Initiative in 2004 as it may range from asymptomatic to chronic or severe diarrhoea and chronic disorders post-infection. The present study aimed to find out the rate of sole infection of G. intestinalis and co-infection of this with other protozoan parasites among the inhabitants of Barak Valley region of Southern Assam by conventional and molecular detection. A total of 1168 samples were collected from different groups of individuals, all the collected samples were subjected to microscopy after specific staining by Lugol's iodine solution, Trichrome staining and modified ZN staining procedures. Microscopically positive samples were further confirmed by PCR using specific primer sets. Of the total no. of samples, 267 (22.85%) were positive by PCR for G. intestinalis with a little higher rate of infection in female (24.06%) (OR = 1.2192, CI = 0.9262 to 1.6049) than male (21.27%). The rate of infection is comparatively higher (25.93%) in the age group of 0-5 years (OR = 1.9149, CI = 1.2558 to 2.9200). In 196 samples G. intestinalis co-existence was observed and detected by PCR with some other protozoan parasites like Entamoeba spp., Cryptosporidium spp. and Blastocystis spp. The rate of infection was higher (31.96%) among the participants

 Baby Singha babysingha@gmail.com
 Madhumita Roy madhumitaroy1133@gmail.com

- ¹ Department of Zoology, Gurucharan College, Silchar, Assam, India
- ² Department of Life Science and Bioinformatics, Assam University, Silchar, Assam, India
- ³ Silchar Medical College and Hospital, Silchar, Assam, India

who collected water from river. Least of the participants showed diarrhoeal symptoms (18.18%) but majority (28.45%) complained for having abdominal cramps (OR = 1.3402, CI = 0.8815 to 1.7855). Among the human infective assemblages, assemblage specific molecular detection revealed the rate of infection of assemblage B was comparatively higher (60.30%) than assemblage A.

Keywords Giardiasis · Gastrointestinal · Prevalence · Assemblages · Epidemiology

Introduction

Giardia intestinalis is one of the most common protozoan parasites that causes diarrhoea and other gastrointestinal problems in developing country as well as in the industrial country. The disease caused by G. intestinalis is considered as a zoonotic disease indicating transmission between human and animal. Six Giardia species have been distinguished based on both morphological and molecular traits. Among which G. intestinalis causes giardiasis to human and other mammals. Thus giardiasis is considered as zoonotic disease (Fang and Xiao 2011). By molecular analysis, till to date eight different assemblages are recognized within the G. intestinalis species complex which include assemblage A-H (Lasek-nesselquist et al. 2009) where assemblage A and B infect a large array of mammals including humans (Monis 1998; Easow et al. 2005; Lebbad et al. 2008). There are two distinct stages in the life cycle of G. intestinalis. These stages are cyst and trophozoite. The cyst is the infective stage which can persist in the environment up to several months. The size of the cyst is $10 \ \mu m \times 8 \ \mu m$ with four nuclei, four median bodies and four axonema (Ford 2005). Upon excystation, each cyst produces two trophozoite that is pear-shaped, bilaterally symmetrical and with four flagellum and two nucleus of $10-12 \mu m$ length and 5–7 μm width. The cyst enters in the human body with contaminated food, water or surface (Dutta 1965).

Intestinal parasitic infections have been an important public health problem in the tropical countries, particularly in the developing countries like India. The prevalence varies between 2% and 5% in industrialized countries and may exceed 30% in developing countries. In 1988, the World Health Organization (WHO) estimated that around 280 million people are annually infected with *Giardia* spp. in Asia, Africa and Latin America (Molina et al. 2007).

The prevalence of this parasite is increasing day by day due to lack of knowledge of the molecular mechanism of this disease (Sethi et al. 1999). The disease is usually selflimiting and asymptomatic infections are common (Flanagan 1992). The potential health risk to humans from gastrointestinal parasites remains a significant problem throughout the world (Schantz et al. 1994). Although in recent years molecular investigation on Giardia has increased, no data are available from North East India in this regard with the single exception of work of Rebecca Justin Traub, 2003 (Ph.D. work) from Phulbari and Addabari tea estate in Assam. Whereas, there are several cases that indicate to the infection of different GI parasites in the local hospital or in community level. This study is significant because there is no report indicating the prevalence of this parasite in this study area. The report should be of interest to readers in the areas of Barak Valley zone of Assam. Hence, hospital-based, community-based and referral center based thorough study is needed to determine the molecular prevalence and diagnostic yield of human fecal samples irrespective of all ages.

Despite being detected in a large proportion of patients through recent molecular-based studies, the possible sources of gastrointestinal pathogens still remain unclear in this region of North East India. However, this thorough study aiming at simultaneous detection of gastrointestinal protozoan parasites through PCR will help to overcome problems in specific detection of protozoan diarrhoeal diseases, so as to cater to the health problems with specific drugs in this region for the benefit of people and public health welfare. In this study investigation on the co-existence of Cryptosporidium spp., Giardia spp., Entamoeba spp., and Blastocystis spp., in samples obtained from clinical patients and community level participants will help to elucidate possible routes of transmission of these emerging pathogens to human as understanding the spread of diarrhoeal pathogens and its transmission from environmental sources to human is essential for disease control and prevention.

Materials and methods

Study design

Through a cross-sectional study, a total no. of 1168 samples were collected from the month of September, 2013 to December, 2016.

The sample size is 1168, calculated by using the formula for cross sectional study (Charan and Biswas 2013; Lwanga et al. 1991) which is as follows:

 $n = z^2 p q/d^2$

where q = 1 - p.

Since there are no previous available studies on this topic, 50% of prevalence has been considered i.e., p = 0.5 (this would provide the maximum sample size), d = absolute precision i.e. = 0.028 (< 3% error), which may be decided by the researcher, z = 1.96 at 95% CI, p = proportion of + ve individuals, Therefore, n = 1168.

The study was carried out in the southern Assam, Barak Valley comprising of three districts (Cachar, Hailakandi and Karimganj). Samples were collected on the basis of sex, age group, drinking water sources and symptoms of diarrhoea. Our target population comprised children without and with diarrhoea of the age between 0 and 12 years and above, age 12–18 years and adults those who have been referred to Medicine Department and Paediatric Department of Silchar Medical College, Assam were also included. Samples were also collected from tea garden inhabitants of Cachar, Karimganj and Hailakandi districts covering entire Barak Valley, Southern Assam. Study was also carried out at community level including the rural and urban areas of the above-mentioned areas under study (Fig. 1).

Consent and ethical consideration

With the consent of each subject all the samples were collected on the basis of questionnaires. In case of minor or infant participants, consents were provided by the guardian/parents. Before commencement of the study, all the protocols were reviewed by Institutional Ethical Committee of Gurucharan College, Silchar, Assam and Silchar Medical College and Hospital, Silchar, Assam.

Collection of stool samples

All the samples were collected in a plastic disposable container. The samples were collected on the following day within 2–3 h of defecation and delivered to the laboratory and divided into two aliquots. One aliquot of each of the fecal samples was used immediately for direct microscopy and serological test for the qualitative identification of



Fig. 1 Map of sample collection sites

Giardia spp. (RIDASCREEN[®] Cryptosporidium/Giardia Combi) and the second aliquot was stored at -20 °C for PCR assay. Samples from distant areas were collected in duplicate. One aliquot was preserved in 10% aqueous formalin for microscopy upon arrival in the laboratory and the rests were brought to the laboratory in unpreserved condition by maintaining temperature of approximately 4 °C.

Microscopy

As shown in Fig. 2, for the detection of cyst and trophozoite of *G. intestinalis*, all the samples were concentrated by sedimentation technique and were examined in Lugol'sstained wet mounts (Fig. 3). At the same time, all samples were screened in the same slides stained in Lugol's iodine for the presence of *Entamoeba*, *Blastocystis* etc. (Fig. 4) and were observed at $40 \times$ and then confirmed in oil immersion at $100 \times$ magnification under a phase contrast microscope (CX31, Japan). For stained preparation, Trichrome stain was used for morphological identification (Fig. 5). For the detection of *Cryptosporidium* spp. modified ZN staining (Potters and Van Esbroeck 2010) was used (Fig. 6).

Serological test

The *G. intestinalis* antigen in the sample was distinguished by microwell ELISA kit according to the manufacturer's instruction (RIDASCREEN[®] *Cryptosporidium/G. intestinalis* Combi, Article No.: C1121) (Fig. 7).

Extraction of DNA

DNA was extracted from cysts using Nucleo-pore Stool DNA Mini Kit (Genetics Biotech Asia Pvt. Ltd) according





Fig. 3 a, b Cysts of *Giardia* spp. in Lugol's Iodine solution. Microscopy $(40 \times \text{ and } 100 \times)$ in oil immersion showing nucleus and cyst wall; c, d Trophozoite of *Giardia* spp. in Lugol's Iodine solution showing flagellum and nucleus



to the manufacturer's instruction. The eluted DNAs were quantified by spectrophotometer (BioPhotometer plus, Eppendorf) and stored at -20 °C for further use.

PCR assay for *Giardia* and co-infecting parasite detection

All the microscopically positive samples as well as positive by immune assay were further confirmed by single and nested PCR using specific primer as mentioned in Table 1. All the PCR amplifications were performed in a final volume of 20 μ l with approximately 100 mg of template DNA, 1 μ M of each primer, 1X PCR buffer with 2.5 mM MgCl2, 1X BSA, 0.2 mM dNTPs, and 1U of Taq DNA Polymerase (Thermo scientific, Wattham, USA) in the thermal cycler (Bio-Rad Laboratories, Hercules, CA). Further the amplicons from PCR were confirmed by their expected amplicon size (Table 1) through gel electrophoresis.

Fig. 4 e, f *Entamoeba* spp. in Lugol's Iodine solution in oil immersion $(100\times)$, F also shows the co-existence of *Entamoeba* spp. and) Cysts of *Giardia* spp. in same field; g, h *Blastocystis* spp. in Lugol's iodine solution. Both the microscopic image is in oil



Fig. 5 i, j Cysts of *Giardia* spp. in Trichrome stain in oil immersion $(100 \times)$



i



Fig. 6 k, **l** Oocysts of *Cryptosporidium* spp. in modified ZN stain



Purification of PCR product

The expected DNA band was purified using commercial purification kit for further downstream process. Purification helps to remove some inhibitors that may cause problem in PCR or in DNA sequencing. A single uniformly visualized band was purified using a QIAquick Gel Extraction kit (Qiagen, Germany) according to the manufacturer's instructions.



Fig. 7 m, n image of ELISA kit, detecting the Giardia intestinalis positive samples

DNA sequencing

The positive amplicons of *Giardia* were sequenced directly using their respective primers in ABI 3500 Genetic analyzer (Applied Biosystems Inc., CA, USA). For further validation, all the obtained sequences were subjected to search homology using nucleotide Blast (Blastn) available in National Centre For Biotechnological Information (http://www.ncbi. nlm.nih.gov). Sequences were submitted in GenBank.

Statistical analysis

All the collected data were statistically analyzed using statistical software SPSS version 16.0 (SPSS, Chicago, IL, USA). By univariate logistic regression analysis odds ratio (OD) and confidence interval (CI) were computed.

Phylogenetic analysis

The evolutionary history was inferred using the Neighbor-Joining method using kimura -2 parameter in the software MEGA-4. The *gdh* loci is used for phylogenetic analysis.

Result

Microscopy

Wet mounts preparation (Lugol's iodine)

All samples were screened by wet mount using Lugol's iodine solution in which 258 samples were found to be positive for *G. intestinalis* (Table 2). By this staining procedure, some other protozoan parasites like *Entamoeba*

spp., *Blastocystis* spp. etc.were also initially screened out (Table 8). The cysts of *G. intestinalis* measured about $10-12 \mu m$ in length and $4-6 \mu m$ in width.

Serological detection (ELISA)

The screening of total 1168 no of samples by ELISA were demonstrated about the total no of *Giardia* positive samples were 264 which were comparatively higher than that of the result of microscopic screening.

Molecular detection (PCR)

By the molecular detection based on PCR, using specific primer sets, total no of 267 samples were confirmed for the sole infection of *G. intestinalis*. The molecular screening of this organism was performed on the basis of particular molecular marker loci or genes. Three molecular markers or genes were selected for the genotypic characterization of *G. intestinalis* which are 18s rRNA, *gdh* and *tpi*.

Amplification-based on 18s rRNA generated a product of 350 bp (Fig. 8). The product size were respectively 605 bp and 503 bp bassed on *tpi* external and internal primer (Fig. 9 q and r). Amplification based on *gdh* loci generated 458 bp product (Fig. 9 s and t, whereas amplification based on assemblage specific primers generated 326 bp and 347 bp sized products respectively for assemblage A and assemblage B (Fig. 11).

Sensitivity and specificity of the diagnostic tests

Microscopic study results slightly differed from the results of serological detection and molecular detection (Table 3). In serological detection technique, 264 samples were found

Table 1 List of the primer used in this study

Giardia intestinalis 18s rRNA 350 67 Rai et al. (2005) F:AGCCGGACACCGCTGGCAACC R: CGGCTGCTGGCACCAGACCTT Giardia intestinalis tpi 605 50 Sulaiman et al. (2003) External F: AAATIATGCCTGCTCGTCG R: CAAACCTTTTCCGGAAACC Giardia intestinalis tpi 503 50 Sulaiman et al. (2003) Internal F: CACTTCATCGGIGGTAACTT R: GTGGCCACCACICCGTGCC Giardia intestinalis gath 458 56 Feng and Xiao (2011) F: TCAACGTCAACCGGGCTTCCGT R: GTGGCCACCACICCGTCCGT R: GTGGCCACCACICCGGTCCGT R: GTGGCCACACCCGGCTTCCG Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTCTGGCGGCTGCAA R: CAGGTAGCAGAGACACGT R: CAGGTAGCAGGAGACACCT R: GTGGCCACCGTGACACCTCCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: AGCTGTGCCGTGAGCAGTAACCT R: GTGGCCACGGGGTGCGAGT E: TAGCTGCGCGTGGAGGCGAA R: GTACAAGGGGAGGGAAA R: GTACAAGGGGAGGGAGAA R: GTACAAGGGGCAGGGAGGAA R: GTACAAGGGGCAGGGGAGGAA R: GTACAAGGGGAGGGAGAA R: GTACAAGGGGCAGGGGCGAA R: AGA GG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F: TCAGAGGCAATACATGCG- R: CCCTAATCCTTCGGAACAGGA- Internal- F: TTCTAGAGGTAATACATGCG- R: CCCTAATCCTTCGAACAGGA- Internal- F: TTCTAGAGCTAATACATGCG- R: CCCTAATCCTTCGA- R: CCCTAATCCT	Primer name and sequence	Amplicon size (bp)	Annealing temperature (°C)	References
F:AGCCGGACACCGCTGGCAACC R: CGGCTGCTGCCACCAGACCT Giardia intestinalis tpi	Giardia intestinalis 18s rRNA	350	67	Rai et al. (2005)
R: CGGCTGCTGGCACCAGACCTT Giardia intestinalis tpi 605 50 Sulaiman et al. (2003) External F: AAATTATGCCTGCTCGTCG R: CAAACCTTITCCGCAAACC Giardia intestinalis tpi 503 50 Sulaiman et al. (2003) Internal F: CCCTTCATCGGIGGTAACTT R: GTGGCCACCACICCCGTGCC Giardia intestinalis gdh 458 56 Feng and Xiao (2011) F:TCAACGTCAACCGCGGCTTCCGT R: GTGTCCTTGCACACTCTC R: GTGTCCTTGCACACTCTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGGCACTGCA R: CAGGTAGCAAGAAATCCCTCG Giardia intestinalis Assemblage B specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGGCCATGCA R: CAGGTAGCAAGAAATCCCTCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: TGCTTCGGGGGCCATGCA R: GTGACTGTGCAGTGAGCAGT R: GTGACAGGGAGGGACGTA R: GTACAAGGGCAGGGACGTA F: TAAGGTGTCAGGGGAGCGAA R: GTACAAGGGCAGGGACGTA Internal:- F: TAAGATGCACGAGAGCGGAACA R: GAG GT TAAC CGA AAT TAG Cyptosporidium spp. 825 55 Xiao et al. (1999) External:- F: TTTCTGAGAGCTAATCACTGCG- R: CCCTAATCCTTGGAACAGGA.	F:AGCCGGACACCGCTGGCAACC			
Giardia intestinalis tpi60550Sulaiman et al. (2003)ExternalF. AAATIATGCCTGCTGGTGGF: AAATIATGCCTGCTGGTGGSulaiman et al. (2003)Internal50350F: CCTTCATCGGIGGTAACTTSulaiman et al. (2003)InternalF. CCCTTCATCGGIGGTAACTTR: GTGGCCACCACICCGGCGCGiardia intestinalis gh458Giardia intestinalis gh45856F: CACGTCAACCGCGGGCTTCCGTF. GTTGTCCTTGCACATCTCCR: GTGGTCCTGCACATCTCCGiardia intestinalis Assemblage A specific326R: CAGGTAGCAGGAGACCCCTGGSami et al. (2012)F: TGCTTCGGGGCGCATGCAF. CAGGTAGCAGGAAACCCTCGGiardia intestinalis Assemblage B specific34758Vanni et al. (2012)F. ATGTGTCAGTGTGACAGTAACGTR: CAGGTGTGCCAGGAGACAGGAACGGTStatemal:F: TAAGATGCACGGGGAGCGAAS5Parija and Khairnar (2007)External:-F. TAAGATGCACGGGAGGGAAGAF: TAAGATGCACGAGAGGGAAGAGGGAAAS5Viao et al. (1999)External:-F. AAG CAT TGTTCTAGATCTGAGF: AAG AGG TCT AAC CGA AAT TAGCryptosporidium spp.Staternal:-S5Xiao et al. (1999)External:-F. AAG CAT TGTTCTGGAGAC-F: AAG AGG TCT AAC CGG AAT TAGF. CACCTATACCATGCG-F: AAG AGG TCT AAC CGA AAT TAGF. CACCTATACATGCG-F: TAGAGGTAATACATGCG-F. TTCTGAGAGCTAATACATGCG-F: TACAAAGGGCAAACAGGA-F. TTCTGAGAGCTAATACATGCG-F: TACAATACATGCGAACAGGA-F. TAGAGTATACATGCG-F: TACTTCTGGAACAGGA-F. TAGAGTATACATGCG-F: TAGAG	R: CGGCTGCTGGCACCAGACCTT			
External F: AAATIATGCCTGCTGCTGGTGG Giardia intestinalis tpi 503 50 Sulaiman et al. (2003) Internal F: CCCTTCATCGGIGGTAACTT R: GTGGCCACCACICCCGTGCC Giardia intestinalis gdh 458 56 Feng and Xiao (2011) F: TCAACGGGGCTTCCGT R: GTTGTCCTGCACACTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTCGGGGCAGTACCTG R: CAGGTAGCAGGACATCCCG Giardia intestinalis Assemblage B specific 347 S8 CAGGTAGCAGAGAATCCCTGG R: GTGGCCAGTGCAGT R: GTGGCCAGTGCAGT R: GTGGCCAGTGCAGT C Entamoeba histolytica 439 55 Parija and Khairnar (2007) External: F: TAAGATGCACGAGAGGGAAA R: GTACAAAGGGCAGGGAA R: GTACAAAGGGCAGGAA R: GTACAAAGGGCAGGGAA R: GTACAACGGAACAGGA- F: TAGGTAGTAGCGGAAG R: AAG AGG TCT AAC CGA AAT TAG C: Cyptosporidum spp. 825 55 Xiao et al. (1999) External:- F: TTCTAGAGGCAACAGGA- F: GCCTAATCCTGGAG- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGG- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGG- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCCTAATCCTGGA- F: GCCTAATCCTGGA- F: GCCTAATCCT	Giardia intestinalis tpi	605	50	Sulaiman et al. (2003)
F: AAATIATGCCTGCTGGTGGR: CAAACCTTTTCCGCAAACCGiardia intestinalis tpi50350Sulaiman et al. (2003)InternalF: CCTTCATCGGIGGTAACTTR: GTGGCCACCACICCCGTGCCGiardia intestinalis gdh45856Feng and Xiao (2011)F: TCAACGTCAACGCGGGCTTCGTR: GTGTCCTTGCAACGCGGCTTCGTR: GTTGTCCTTGCACATCTCGiardia intestinalis Assemblage A specific32658Vanni et al. (2012)F: TGCTTCGGGGCCCATGCAR: CAGGTAGCAGAGAAAACCCTCGGiardia intestinalis Assemblage B specific34758Vanni et al. (2012)F: AGTGTCCAGTGGACAGTAACGTR: GTGACTGTGACGGTGACGCAGTB: GTGACTGTGACGGTGAGCAGTF: TAAGATGCACGGAGGAGCGAAAR: GTACAAAGGGCAGGGAACGTAF: TAAGATGCACGAGAGCGAAAAR: GTACAAAGGGCAGGGAACGAAR: GTACAAAGGGCAGGGAACGAAR: AGG GAT TGTTTCTAGATCTGAGR: AAG AGG TCT AAC CGA AAT TAGCryptosporidium spp.82555Xiao et al. (1999)External:-F: TTCTAGAGCTAATACATGCG-F: TTCTAGAGCTCTTGGAACAGGA-Iternal:-F: TTCTAGAGCTAATACATGCG-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTGCAAACAGGA-Iternal:-F: TTCTAGAGCAAACAGGA-F: TTCTAGAGCAACAGGA-Iternal:-F: TTCTAGAGCTAATACATGCG-R: AGT TGTTCTGAAACAGGA-Iternal:-F: TTCTAGAGCAACAGGA-Iternal:-F: TTCTAGAGCAACAGGA-Iternal:-F: TTCTAGAGCAACAGGA-Iternal:- <td< td=""><td>External</td><td></td><td></td><td></td></td<>	External			
R: CAAACCTTITCCGCAAACC Giardia intestinalis tpi 503 50 Sulaiman et al. (2003) Internal F: CCCTTCATCGGIGGTAACTT F: CCCTTCATCGGIGGTAACTT F: CCCTTCATCGGGGCACACTCCC Giardia intestinalis gdh 458 56 Feng and Xiao (2011) F:TCAACGTCAACCGCGGCTTCCGT R: GTTGTCCTTGGACATCTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGGCGCATGCA R: CAGGTAGCAGAGAGAATCCCTCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: AGGTGCAGTGACGGGAGACGAGA R: CAGGTAGCAGGAGGCAGAT F: TAAGATGCACGGAGGAGCGAAA R: GTACAAAGGGCAGGAGCGAAA R: GTACAAAGGGCAGGGAGCGAAA R: GTACAAAGGGCAGGGAGCGAA R: AGA GG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F: TTCTAGAGCTAATACATGCG- R: CCCTAATCCTGAGACAGGA- Iternal:- F: TTCTAGAGGCTAATACATGCG- R: CCCTAATCCTGAGACAACAGG- Iternal:-	F: AAATIATGCCTGCTCGTCG			
Giardia intestinalis tpi50350Sulaiman et al. (2003)Internal	R: CAAACCTTITCCGCAAACC			
Internal F: CCCTTCATCGGIGGTAACTT R: GTGGCCACCACICCCGTGCC Giardia intestinalis gdh 458 56 Feng and Xiao (2011) F:TCAACGTCAACGCGGCTTCCGT R: GTGTCCTTGCACATCTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGCGCATGCA R: CAGGTAGCAGAGAATCCCTCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: ATGTGTCAGTGTGACAGTAACGT R: GTGACTGTGCCGTTGAGGCAGT R: GTGACTGTGCCGTTGAGGCAGT F: TAAGATGCAGAGAGCGAAA R: GTACAAAGGGCAGGAAC R: GTACAAAGGGCAGGAAC R: GTACAAAGGGCAGGAAC R: GTACAAAGGGCAGGAAC R: GTACAAAGGGCAGGACGGAA R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External: F: TAGGAGTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	Giardia intestinalis tpi	503	50	Sulaiman et al. (2003)
F: CCCTTCATCGGIGGTAACTT R: GTGGCCACCACICCCGTGCC Giardia intestinalis gdh 458 56 F: GACGCAACCGCGGCTTCCGT R: GTGTCCTTGCACATCTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGCGCATGCA Finder Turburg 1.2012) 1.2012) F: GCTTCGGGGCGCATGCA Turburg 2.2012) 1.2012) F: GCTGCAGTGGAGAAATCCCTCG Turburg 2.2012) 1.2012) F: AAGGTGCAGTAGCAGTAACGT Turburg 2.2012) 1.2012) F: ATGTGTCAGTGTGACAGTAACGT Turburg 2.2012) 1.2012) F: ATGGTCAGTGGCAGGAAACGT Turburg 2.2012) 1.2012) F: TAGGATGCACGAGAGGGAAGTA Turburg 2.2012) 1.2012) External:- F: TAAGATGCACGAGAGCGAAA Turburg 2.2012) F: AAG CAT TGTTTCTAGATCTGAG Turburg 2.2012) 2.2012) F: AAG CAT GTTTCTAGATCTGAG Turburg 2.2012) 2.2012) F: AAG AGG TCT AAC CGA AAT TAG Turburg 2.2012) 2.2012) External: F: TTCTAGAGCTAATACATGCG- Turburg 2.2012) 2.20	Internal			
R: GTGGCCACCACICCCGTGCCGiardia intestinalis gdh45856F:TCAACGTCAACCGCGGCTTCCGTR: GTGGCCAACCGCGGCGCTCCCGTR: GTGGCCTTGCACACTCCCGiardia intestinalis Assemblage A specific32658Vanni et al. (2012)F: TGCTTCGGGGCGCATGCAR: CAGGTAGCAGGAGAATCCCTCGGiardia intestinalis Assemblage B specific34758Vanni et al. (2012)F: ATGGTGCAGTGGACAGTR: GTGACTGTGCACGTGACAGTR: GTGACTGTGCACGTGACAGTEntamoeba histolytica43955Parija and Khairnar (2007)External:-F: AAG AGG CAGGAGAGCGAAR: GTACAAAGGGCAGGGAAGGGAAGR: AAG AGG TCT AAC CGA AAT TAGCryptosporidium spp.82555Xiao et al. (1999)External:-F: TTCTAGAGCTAATACATGCG-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-Internal:-I: TTCTAGAGCTAATACATGCG-R: CCTAATCCTTCGAACAGGA-I: I: I: I: I: I: I:	F: CCCTTCATCGGIGGTAACTT			
Giardia intestinalis gdh45856Feng and Xiao (2011)F:TCAACGTCAACCGCGGGTTCCGT	R: GTGGCCACCACICCCGTGCC			
F:TCAACGTCAACCGCGGCTTCCGTR: GTTGTCCTTGCACATCTCCGiardia intestinalis Assemblage A specific32658Vanni et al. (2012)F: TGCTTCGGGGCGCATGCAR: CAGGTAGCAGAGAATCCCTCGGiardia intestinalis Assemblage B specific34758Vanni et al. (2012)F: ATGTGTCAGTGTGACAGTAACGTR: GTGACTGTGCCGTTGAGGCAGTEntamoeba histolytica43955Parija and Khairnar (2007)External:-F: TAAGATGCACGAGAGGGAAAR: GTACAAAGGGCAGGGACGTAInternal:-F: AAG CAT TGTTTCTAGATCTGAGR: AAG AGG TCT AAC CGA AAT TAGCryptosporidium spp.82555Xiao et al. (1999)External:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACATGCG-R: CCCTAATCCTTCGAAACAGGA-Internal:-F: TTCTAGAGCTAATACAGGG-Internal:-F: TTCTAGAGCTAATACAGGG-Internal:-F: TTCTAGAGCTAATACAGGA-	Giardia intestinalis gdh	458	56	Feng and Xiao (2011)
R: GTTGTCCTTGCACATCTCC Giardia intestinalis Assemblage A specific 326 58 Vanni et al. (2012) F: TGCTTCGGGGGCGATGCA R: CAGGTAGCAGAGAATCCCTCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: ATGTGTCAGTGTGACAGTAACGT R: GTGACTGTGCCGTTGAGGCAGT Entamoeba histolytica 439 55 Parija and Khairnar (2007) External:- F: TAAGATGCACGAGAGCGAAA R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F: TTCTAGAGCTAATACATGCG- R: CCCTAATCCTTCGAAACAGGA- Internal:-	F:TCAACGTCAACCGCGGCTTCCGT			
Giardia intestinalis Assemblage A specific32658Vanni et al. (2012)F: TGCTTCGGGGCGCATGCA	R: GTTGTCCTTGCACATCTCC			
F: TGCTTCGGGGCGCATGCA R: CAGGTAGCAGAGAATCCCTCG Giardia intestinalis Assemblage B specific 347 58 Vanni et al. (2012) F: ATGTGTCAGTGTGACAGTAACGT T F F R: GTGACTGTGCCGTTGAGGCAGT T F F Entamoeba histolytica 439 55 Parija and Khairnar (2007) External:- F TAAGATGCACGAGAGGGAAAA T F: TAAGATGCACGAGGGGAGGGAA T F T R: GTACAAAGGGCAGGGAAGGGAA T T F F: TAAGATGCACGAGGGAAGGGAAGGA T T F F: AAG AGGGCAGGGAAGGGAAGGA T T F F: AAG AGG TCT AAC CGA AAT TAG T T T Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F T T F F: TTCTAGAGCTAATACATGCG- T T T R: CCCTAATCCTTCGAAACAGGA- T T T Internal:- T T T T F: TTCTAGAGCTAATACATGCG- T T T T Internal:- <td>Giardia intestinalis Assemblage A specific</td> <td>326</td> <td>58</td> <td>Vanni et al. (2012)</td>	Giardia intestinalis Assemblage A specific	326	58	Vanni et al. (2012)
R: CAGGTAGCAGAGAATCCCTCG34758Vanni et al. (2012)Giardia intestinalis Assemblage B specific34758Vanni et al. (2012)F: ATGTGTCAGTGTGACAGTAACGT </td <td>F: TGCTTCGGGGCGCATGCA</td> <td></td> <td></td> <td></td>	F: TGCTTCGGGGCGCATGCA			
Giardia intestinalisAssemblageB specific34758Vanni et al. (2012)F: ATGTGTCAGTGTGACAGTAACGT	R: CAGGTAGCAGAGAATCCCTCG			
F: ATGTGTCAGTGTGACAGTAACGT R: GTGACTGTGCCGTTGAGGCAGT <i>Entamoeba histolytica</i> 439 55 Parija and Khairnar (2007) External:- F: TAAGATGCACGAGAGCGAAA R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG <i>Cryptosporidium</i> spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	Giardia intestinalis Assemblage B specific	347	58	Vanni et al. (2012)
R: GTGACTGTGCCGTTGAGGCAGT Entamoeba histolytica 439 55 Parija and Khairnar (2007) External:- F: TAAGATGCACGAGAGCGAAA R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R: CCCTAATCCTTCGAAACAGGA- Internal:-	F: ATGTGTCAGTGTGACAGTAACGT			
Entamoeba histolytica43955Parija and Khairnar (2007)External:-F: TAAGATGCACGAGAGCGAAAF: TAAGATGCACGAGGGACGTAInternal:-F: AAG CAT TGTTTCTAGATCTGAGF: AAG AGG TCT AAC CGA AAT TAGCryptosporidium spp.82555Xiao et al. (1999)External: </td <td>R: GTGACTGTGCCGTTGAGGCAGT</td> <td></td> <td></td> <td></td>	R: GTGACTGTGCCGTTGAGGCAGT			
External:- F: TAAGATGCACGAGAGCGAAA R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG <i>Cryptosporidium</i> spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	Entamoeba histolytica	439	55	Parija and Khairnar (2007)
F: TAAGATGCACGAGAGCGAAA R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCTAATCCTTCGAAACAGGA- Internal:-	External:-			
R: GTACAAAGGGCAGGGACGTA Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG <i>Cryptosporidium</i> spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	F: TAAGATGCACGAGAGCGAAA			
Internal:- F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG <i>Cryptosporidium</i> spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	R: GTACAAAGGGCAGGGACGTA			
F: AAG CAT TGTTTCTAGATCTGAG R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	Internal:-			
R: AAG AGG TCT AAC CGA AAT TAG Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	F: AAG CAT TGTTTCTAGATCTGAG			
Cryptosporidium spp. 825 55 Xiao et al. (1999) External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	R: AAG AGG TCT AAC CGA AAT TAG			
External:- F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	Cryptosporidium spp.	825	55	Xiao et al. (1999)
F:TTCTAGAGCTAATACATGCG- R:CCCTAATCCTTCGAAACAGGA- Internal:-	External:-			
R:CCCTAATCCTTCGAAACAGGA- Internal:-	F:TTCTAGAGCTAATACATGCG-			
Internal:-	R:CCCTAATCCTTCGAAACAGGA-			
	Internal:-			
F:GAAGGGTTGTATTTATTAGATAAAG	F:GAAGGGTTGTATTTATTAGATAAAG			
R:AAGGAGTAAGGAACAACCTCCA	R:AAGGAGTAAGGAACAACCTCCA			
Blastocystis spp. 462 55 Yoshikawa et al. (2000)	Blastocystis spp.	462	55	Yoshikawa et al. (2000)
F:TCTTGCTTCATCGGAGTC	F:TCTTGCTTCATCGGAGTC			
R:CCTTCTCGCAGTTCTTTATC	R:CCTTCTCGCAGTTCTTTATC			

Table 2 Result of comparison of positive samples of two different staining techniques

Total no of specimen	Positive in Lugol's iodine solution	Positive in Trichrome stain
1168	258	258

to be positive among the total collected samples, whereas, molecular detection technique indicated 267 samples as

positive for G. intestinalis (Table 4). Sensitivity and specificity analysis indicated with the 100.00% positive

Table 3 Result of microscopic, serological and PCR analysis

Study group		Total no. of specimen	Serologically positive specimen	PCR positive specimen	Microscopic positive specimen
Sex	Male	503	106	107	102
	Female	665	158	160	156
Age	0-5 years	318	97	98	94
	5-12 years	311	67	66	63
	12-18 years	331	65	67	66
	Adults	208	35	36	35
Source of drinking water	Municipality supply water	501	87	89	85
	Tube well	207	33	31	29
	River	460	146	147	144
Symptoms	Diarrheal	363	65	66	63
	Abdominal pain	383	108	109	103
	Asymptomatic	422	93	92	92

Table 4 Sensitivity and specificity of Diagnostic techniques

		Microscopy		Total number
		Positive	Negative	
ELISA (reference method)	Positive	258 (TP)	06 (FN)	264 TInfected
	Negative	00 (FP)	904 (TN)	904 TUninfected
	Total Number	258 TTest Positive	910 TTest Negative	1168 Total Number
Sensitivity (%) [95% CI]		97.73%		
		95.12-99.16%		
Specificity (%) [95% CI]		100.00% (99.59-100.00	%)	
Negative predictive value (%) [95% CI]	99.34% 98.56-99.70%		
Positive predictive value (%) [9	5% CI]			
		100.00%		

TP positive in both microscopy and ELISA; FP positive in microscopy but not in ELISA; FN negative in microscopy but positive in ELISA; TN negative in both ELISA and microscopy

predictive value and 99.67% negative predictive value showing the sensitivity and specificity respectively 98.88% and 100.00%.

Socio-demographic analysis of the studied population

Of the total collected samples, 665 samples were collected from female individuals and 503 samples were collected from male individuals. Among the female participants, 160 samples were confirmed as positive for *G. intestinalis* infection by PCR (Figs. 8, 9) showing the prevalence rate of 24.06% (p = 0.1575) on the other hand 107 samples were found to be positive in males showing the prevalence of 21.27% with the odds ratio (OR) = 1.2192 at 95% CI (0.9262 to 1.6049).

Samples were collected considering four age groups. A total no of 318 samples were collected from the children within the age groups of 0-5 years of which 98 samples were found positive showing the prevalence rate of 27.22% (OR = 1.9149, CI = 1.2558 to 2.9200). 311 samples were collected from the age groups of 5-12 years and 66 (21.22%) were found to be positive by PCR with the OR = 1.5915 (CI = 1.0175 to 2.4893). 331 samples were collected from the children within the age groups of 12–18 years and 67 (20.24%, OR = 1.4381, CI = 0.9222 to 2.2427) and the rest 240 samples were collected from adult individuals, i.e. within the age groups of > 18 where the rate of infection was about 17.80% (36). Among the subjects of different age groups, the age groups between 0 and 5 years, 5–12 years and 12–18 years had the comparatively higher rate of infection than the adults (Fig. 10i).

Fig. 8 o, p Representative gel image of positive samples using18 s rRNA specific primer set. M stands for marker lane and NTC indicates the lane with negative control. Lane 1, 3, 5, 6 (o) and lane 3 (p) indicates positive samples



Collected samples were also categorized separately on the basis of drinking water sources of the subjects. It was observed that the inhabitants of the particular study sites use three different sources to collect their drinking water which were-municipality supply water, tube well and river. 501 sample providers use municipality supplied water in which 17.76% (89) were found to be positive by PCR for Giardial infection (OR = 2.1741, CI = 1.6082 to 2.9391). Whereas, 207 subjects were dependent on tube well water having the infection rate of 14.97% (OR = 2.174 & CI = 1.7360 to 4.0954) (Fig. 10ii). 460 individuals collect their drinking water from the Barak river and showing the higher rate of infection than other two groups (31.96%) as shown in Table 5.

Considering the symptomology, 363 samples were collected from diarrhoeal patients of which in 66 cases (18.18%) were PCR positive for G. intestinalis. But the percentage of positive samples collected from the patients having abdominal cramps was about 28.45% and the rests were asymptomatic for any type of intestinal problem (Fig. 10iii).

The human intestinal parasite G. intestinalis though found to be prevalent throughout the year but during this course of study, it was little higher in pre-monsoon, monsoon and post-monsoon season especially from the month of May to October (Table 6). During the first year of study, the sampling began from the month of September, i.e. in the post monsoon season which little differed from the data obtained from the consecutive years. Whereas, in next course of study, the occurrences were almost nil in the winter season (Fig. 10iv).

Molecular analysis revealed the distribution and prevalence of this protozoan parasite in three different districts under the Barak Valley region. The prevalence rate of

Hailakandi district was relatively higher (24.28%) than the prevalence rate of Cachar (21.03%) and Karimganj district (23.91%) with the odd ratios 1.1368 and 1.1546 and p = 0.4235 and 0.3962 respectively (Table 7).

With the infection of G. intestinalis, there were several cases where co-existence of this parasite was also found with the other gastrointestinal protozoan parasites. A close association was observed with Entamoeba spp., Cryptosporidium spp., and Blastocystis spp.

The co-existing organisms were also confirmed by molecular analysis using amplification of genes which were genus-specific for the particular parasite Blastocystis spp. Of the total positive G. intestinalis, 196 samples were confirmed as having mixed infection of G. intestinalis with Entamoeba spp., Cryptosporidium spp., and Blastocystis spp. (Figs. 4, 6).

Of the total 196 mixed infected samples, 11.73% (23) cases indicated about the co-existence of G. intestinalis with Entamoeba spp. by molecular detection (Fig. 11). The highest cases of co-existence of G. intestinalis were found with Cryptosporidium spp. which was about 17.35% (34) of the total co-infected samples. Whereas, association rate was about 10.71% (21) of G. intestinalis and Blastocystis spp. (Table 8).

The result of molecular analysis also indicated, among the total positive samples, 92 samples were positive for assemblage A with the prevalence rate of 34.45%. Total 143 samples were found to be positive for assemblage B showing the prevalence rate of 53.56%. Whereas, in 32 samples both the assemblages. i.e. assemblage A and assemblage B were found to be present showing the rate of mixed infection as 11.98% (Table 9).

Of the G. intestinalis positive samples in different sexes, 27.10% (29) samples were positive for assemblage A in the



Fig. 9 q, r Representative PCR amplification using *Giardia intestinalis* using *tpi* primer pairs. s, t Representative PCR amplification using *Giardia intestinalis* using *gdh* primer pairs

males. Among the 160 positive samples of females, assemblage A was found to be present in 20.63% (33). Assemblage B was found to be present in 61.68% in male and the rest 11.21% were detected as mixed infection of assemblage A & B. In females assemblage B was found in 116 (72.50%) cases and mixed assemblages were detected in 6.86% (11) (Table 10).

Among the three different districts, Cachar district, showed higher prevalence of assemblage B than the assemblage A. Assemblage A was detected in 26.53%,

whereas, assemblage B was found to be present in 60.20% and in 13.26% cases, mixed assemblages were detected (Fig. 12). The prevalence rate was almost similar in Karimganj district where the prevalence were 33.33%, 55.91% and 10.75% respectively for assemblage A, B and mixed assemblages. But the result differed greatly in Hailakandi district. In Hailakandi, assemblage A was 23.68% prevalent, the prevalence rate was about 69.74% of assemblage B and mixed assemblage was found in 6.58% cases (Table 11) (Fig. 13).



(iii)

Table 5 Logistic regression analysis of socio demographic factors associated with Giardia intestinalis among the inhabitants of Barak Valley inhabitants

Study group	s	Microscopy and PCR results					ODDS	Confidence	P value	Total no.
		Only microscopic positive	Serological test positive	Only PCR positive	Rate of infection of PCR positive (%)	No. of negatives by PCR	RATIO (OR)	interval (CI 95%)		of specimen
Sex	Male	102	106	107	21.27	446	1	0.9262-1.6049	0.1575	503
	Female	156	158	160	24.06	547	1.2192			665
Age	0-5 years	94	97	98	27.22	290	1.9149	1.2558-2.9200	0.0025	318
	5-12 years	63	67	66	21.22	235	1.5915	1.0175-2.4893	0.0417	311
	12-18 years	66	65	67	20.24	264	1.4381	0.9222-2.2427	0.1090	331
	Adults	35	35	36	17.80	204	1			208
Source of Drinking water	Municipality supply water	85	87	89	17.76	412	2.1741	1.6082–2.9391	< 0.0001	501
	Tube well	29	33	31	14.97	176	2.6664	1.7360-4.0954	< 0.0001	207
	River	144	146	147	31.96	313	1			460
Symptoms	Diarrhoeal	63	65	66	18.18	297	1		0.0932	363
	Abdominal pain	103	108	109	28.45	366	1.3402	0.9521–1.8864		383
	Asymptomatic	92	93	92	21.80	330	1.2545	0.8815-1.7855	0.2079	422

117 sequences obtained under this study represent the diversity of G. intestinalis under this area. All the obtained sequences were manually edited to obtain a high level of sequence homology with the help of Clustal W by adjusting the alignment at the 50 ends.

The sequence analysis process began by comparing the unknown sequences to a database of DNA sequence

Table 6 Seasonal positive cases in four consecutive years of s	tudy
--	------

Name of months	No. of positive cases in different month of the studied years							
	2013	2014	2015	2016				
January	_	03	00	01				
February	_	05	04	03				
March	_	02	03	01				
April	-	05	04	05				
May	-	08	09	07				
June	-	09	11	17				
July	-	11	10	12				
August	-	08	11	11				
September	04	10	13	11				
October	06	09	08	10				
November	05	10	06	04				
December	01	03	02	05				

Table 7 Prevalence of Giardia intestinalis in three Districts of Barak Valley zone

Region	No. of screened samples	No. of positive samples	Prevalence	Odds ratio (OR)	Confidence interval (CI 95%) (%)	P value
Cachar	466	98	21.03	1	0.8304-1.5563	0.4235
Karimganj	389	93	23.91	1.1368		
Hailakandi	313	76	24.28	1.1546	0.8284-1.6093	0.3962



Fig. 11 u, v, w Representative PCR assays of Cryptosporidium spp., Entamoeba spp. and Blastocystis spp. respectively

Table 8 Rate of mixed infection of Giardia intestinalis with other parasites

Name of Parasite	Total no. of infection	Total % of infection	Total no. of mixed infection	
Giardia intestinalis + Entamoeba spp.	23	11.73	196	
Giardia intestinalis + Cryptosporidium spp.	34	17.35		
Giardia intestinalis + Blastocystis spp.	21	10.71		

Table 9	Overall	prevalence of	of Gi	ardia	intestinalis	and	prevalence	of	different	assemblages
---------	---------	---------------	-------	-------	--------------	-----	------------	----	-----------	-------------

Total no. of collected samples	1168
Total no. of Giardia positive samples by PCR	267
Over all prevalence rate	22.85%
Total no.of positive samples having assemblage A infection	92
Percentage of positive samples having assemblage A infection	34.45%
Total no. of positive samples having assemblage B infection	143
Percentage of positive samples having assemblage B infection	53.56%
Total no. of positive samples having mixed infection of assemblage A and assemblage B	32
Percentage of positive samples having mixed infection of assemblage A and assemblage B	11.98%

Table 10 Overall prevalence of Giardia intestinalis and prevalence of different assemblages among different sex

Study group	Total no of sample	PCR positive samples	Assemblage a positive (% of prevalence)	Assemblage b positive (% of prevalence)	No. of mixed assemblages (% of prevalence)
Male	503	107	29 (27.10%)	66 (61.68%)	12 (11.21%)
Female	665	160	33 (20.63%)	116 (72.50%)	11 (6.86%)

available on the public databases of NCBI using BLAST (Table 12).

The Phylogenetic tree was constructed using 23 taxa. Of those 3 were the sample sequences. Those representative sequences were aligned with a set of similar sequences from GenBank and were subjected to analysis using the software MEGA4. The optimal tree with the sum of branch length = 0.24838034 is shown. The evolutionary distances were computed using the Kimura 2-parameter method and were in the units of the number of base substitutions per site. Condon positions included were 1st + 2nd + 3rd + Noncoding. All positions containing gaps and missing data were eliminated from the dataset (Complete deletion option). There were a total of 529 positions in the final dataset.

Discussion

This study revealed the existence as well as the prevalence of one of the most common gastrointestinal parasites across the world, *G. intestinalis* among the inhabitants of Barak Valley, Assam, NE India. It was detected as the most prevalent gastrointestinal parasitic organism in the particular study area but a majority of the infected individuals were unaware because of lacking knowledge and proper detection techniques or diagnosis.

Detection technique selection was another important aspect in this type of study as an error in detection may lead to misinterpretation. During this study, three diagnostic techniques were applied to overcome the chance of misdiagnosis. Microscopic analysis is the most primitive and cost-effective reliable method of diagnosis which depends on the morphological structure of an organism. But there is a chance of confusion or error. As sometimes if the severity remains very less in an individual, then the causative agent may not be detected in that particular slide kept under the microscope. In the second stage of detection, ELISA was used for further confirmation of the positive and negative samples. Lastly, molecular detection technique was employed as it has a high sensitivity and specificity amongst different techniques. As per literature available and by statistical analysis, PCR detection technique was considered as gold standard detection technique and in this present study, the result of PCR positive was considered as true positives.

In this present study, the prevalence rate was calculated as 22.85% which is the first report from the North-East region of India. This prevalence rate is similar to that found in other regions of India. The possible cause of infection in this study site is not yet so clear and requires further investigations.

Most of the studies suggested that the incidence and severity of Giardial infection depend on location and period of time. Some of the studies carried out in India indicate the severity of infection during the month of July, August and September that are considered as rainy season (Kaur et al. 2002). In our course of study, it was observed the rate of infection was relatively higher in the pre and post monsoon season. This seasonal outbreak is the result of the scarcity of water during pre-monsoon season which leads to unhygienic practices and promotes waterborne



Fig. 12 x, y Representative PCR assay of *Giardia intestinalis* using Assemblage A Primer set; z, z1 Representative PCR assay of *Giardia intestinalis* using Assemblage B primer set. Expected amplicon sizes

are indicated on the left side. M indicates the marker lane. The numbers in the upper lane indicated the lane number and NTC indicates negative control DNA

Table 11 Overall prevalence of Giardia intestinalis and prevalence of different assemblages among different Districts

Districts	Total no of sample	PCR positive samples	Assemblage a positive (% of prevalence)	Assemblage b positive (% of prevalence)	No. of mixed assemblages (% of prevalence)
Cachar	466	98	26 (26.53%)	59 (60.20%)	13 (13.26%)
Karimganj	389	93	31 (33.33%)	52 (55.91%)	10 (10.75%)
Hailakandi	313	76	18 (23.68%)	53 (69.74%)	05 (6.58%)

diseases. Besides this, during the rainy season, there is a regular occurrence of a flood that promotes contamination of drinking water or crop fields. The Economic condition of most of the individuals found to be positive was not that good and mostly depended on river water for their daily consumption. The majority of them did not even filter or purify water for drinking which provided a huge scope of infection. Improper washing of raw fruits and vegetables before consumption may also be a cause of transmission of gastrointestinal protozoan parasites which further causes chronic disease. In tropical developing countries children are found to be highly susceptible to protozoal infection due to environmental contamination and poor hygiene practices (Rai et al. 2005). The current study also supports this statement as among the infected individuals, the number of the children within the age range of 0-12 years is bit higher than other groups. Infants are more vulnerable due to lack of immune competency to fight against external pathogens. Besides this, children of this age range are mostly school going and having a



Fig. 13 Phylogenetic relationship among Giardia intestinalis of the studied area

Table 12 Diversity of Giardia intestinalis and genotypes identified from Barak Valley, Assam, India

Sl no.	Species	Accession number	Reference sequence at GenBank	Identities (%)
1	Giardia intestinalis	KY654094	EU272168	100
2	Giardia intestinalis	KY654095	KM190773	100
3	Giardia intestinalis	KY659046	HG792784	100

tendency to play with soil and water which expose them to various contaminated diseases while playing and after handling pets such as cats or dogs.

Considering the sex, the higher prevalence of G. *intestinalis* in the females has been observed. This may be

due to females are mostly busy with household activities like washing of utensils, clothes etc. thus getting exposed to contaminated water. Though males are also associated with household and agricultural activities but such a number of individuals participated in the present study is relatively less.

The role of G. intestinalis in causing diarrhoea is still controversial whereas, malnutrition, loss of weight are some of the common symptoms found in case of infection (Celliksoz et al. 2005). Most of the hosts, who shed infectious cysts and act as transmission vehicle may be found as asymptomatic but various cases also reported with chronic or severe diarrhoea (Ish-horowicz et al. 1989). In healthy adults, G. intestinalis infection is considered to be self-limiting and previously infected individuals are less likely to develop symptoms. It has been observed that some of the affected individuals do not have any symptoms of diarrhoea, however, most of them complained about having an abdominal cramp. Besides this, some participants also agree to have the problem with indigestion or acidity problems. Most of the children, positive for G. intestinalis were found to be suffering from malnutrition and retarded growth.

Sources of water used for drinking, washing clothes and utensils, taking bath etc. play an important role in such spread of disease. It has been observed that most of the families who reside nearby the river had a higher rate of infection. This may be due to using river water without proper filtration which may be contaminated with various parasites. A significant association has been found of G. intestinalis with other protozoan parasites like Entamoeba spp., Cryptosporidium spp. and Blastocystis spp. Among the protozoan parasites, co-infection rate of G. intestinalis with Cryptosporidium spp. is quite higher as described in other literature. Besides this, there are also cases of coexistence of G. intestinalis with Entamoeba spp. followed by Blastocystis spp. The co-existence of the parasites is whether coincidental or either have any close association, that is yet to be confirmed and requires further analysis.

Considering the human-specific assemblages, this study indicated about the higher rate of assemblage B in comparison assemblage A as reported earlier (Lebbad et al. 2008). A good percentage also indicates having mixed infection of both assemblage A and B.

Analysis of homology of the sequences showed that the sequences are within the assemblage A and B and there is no separate cluster for any of the isolates. It can also be said that the taxon position variation is an example of mixed assemblage as reported frequently in case of dogs. However, in detected mixed genotypes, the reason may be mixed infection or genetic recombination. The zoonotic relationship is not clear in this study as only the assemblages reported as human assemblages were found, thus does not provide the evidence of zoonotic transmission.

Acknowledgements The authors want to acknowledge Department of Medicine and Department of Microbiology of Silchar Medical College for providing samples. Authors also greatly acknowledge The Molecular Parasitology Laboratory of Gurucharan College Silchar funded by DBT, DST and UGC for helping in molecular analysis under this study. We are grateful to Prof. Jaishree Paul, School of Life Sciences, JNU, New Delhi for providing all the positive controls used in this study as a kind gift to us. We would also like to convey our sincere gratitude to Prof. Sankar Kumar Ghosh, Vice Chancellor, Kalyani University, West Bengal for helping in the sequencing part in his previous laboratory of Dept. of Biotechnology, Assam University, Silchar. This research did not receive any specific grant from funding agencies in the public, commercial, or not-for-profit sectors.

Author's contribution The study design, aim and methodology were prepared by Dr. Baby Singha and Dr. Shubhadeep Roychoudhury. All the clinical samples along with patient details were provided by Dr. Debadatta Dhar. The experimentation, data analysis, statistical analysis were done by Dr. Madhumita Roy. The manuscript was prepared primarily by Dr. Madhumita Roy and further checked and modified by all the co-authors.

Funding The research leading to these results has received funding from UGC, DBT and DST grants given to the Molecular Parasitology Laboratory, Department of Zoology, G. C. College, Silchar, Assam.

Compliance with ethical standards

Conflict of interest All the authors declare that they have no conflict of interest.

Ethics approval The protocol of the study was reviewed and approved by the Institutional Ethical Committee (Ref. No. GCC/9440) of Gurucharan College, Silchar, Assam, before the commencement of the Study and Silchar Medical College and Hospital, Silchar, Assam.

Informed consent For the present study all stool samples were collected with the consent of each patient/subject, in the form of questionnaires. All study participants had given written consent before enrolment into the study. On behalf of all the infant participants consent had given by the parents/guardians.

References

- Çelİksöz A, Aciöz M, DeĞerlİ S, Çinar Z, Elaldi N, Erandaç M (2005) Effects of giardiasis on school success, weight and height indices of primary school children in Turkey. Pediatr Int 47:567–571
- Charan J, Biswas T (2013) How to calculate sample size for different study designs in medical research? Indian J Psychol Med 35(2):121
- Dutta G (1965) Cytochemistry and fluorescence microscopy of *Giardia intestinalis*. Proc Natl Acad Sci India 31:151–165
- Easow JM, Mukhopadhyay C, Wilson G, Guha S, Jalan BY, Shivananda PG (2005) Emerging opportunistic protozoa and intestinal pathogenic protozoal infestation profile in children of western Nepal. Nepal Med Coll J 7:134–137
- Feng Y, Xiao L (2011) Zoonotic potential and molecular epidemiology of Giardia species and giardiasis. Clin Microbiol Rev 24:110–140
- Flanagan P (1992) Giardia–diagnosis, clinical course and epidemiology. A review. Epidemiol Infect 109:1
- Ford BJ (2005) The discovery of Giardia. Microsc Chicago 53:161–167

- Ish-horowicz M, Korman SH, Shapiro M, Har-even U, Tamir I, Strauss N, Deckelbaum RJ (1989) Asymptomatic giardiasis in children. Pediatr Infect Dis J 8:773–779
- Kaur R, Rawat D, Kakkar M, Uppal B, Sharma V (2002) Intestinal parasites in children with diarrhea in Delhi, India. Southeast Asian J Trop Med Public Health 33:725
- Lasek-Nesselquist E, Welch D, Thompson RCA, Steuart RF, Sogin ML (2009) Genetic exchange within and between assemblages of Giardia duodenalis. J Eukaryot Microbiol 56:504–518
- Lebbad M, Ankarklev J, Tellez A, Leiva B, Andersson JO, Svärd S (2008) Dominance of Giardia assemblage B in Leon, Nicaragua. Acta Trop 106:44–53
- Lwanga SK, Lemeshow S, World Health Organization (1991) Sample size determination in health studies: a practical manual. World Health Organization, Geneva
- Molina N, Polverino D, Minvielle M, Basualdo J (2007) PCR amplification of triosephosphate isomerase gene of Giardia lamblia in formalin-fixed feces. Rev Latinoam Microbiol 49:6–11
- Monis PT (1998) Molecular epidemiology: assumptions and limitations of commonly applied methods. Int J Parasitol 28:981–987
- Parija SC, Khairnar K (2007) Detection of excretory Entamoeba histolytica DNA in the urine, and detection of *E. histolytica* DNA and lectin antigen in the liver abscess pus for the diagnosis of amoebic liver abscess. BMC Microbiol 7:41
- Potters I, Van Esbroeck M (2010) Negative staining technique of Heine for the detection of Cryptosporidium spp.: a fast and simple screening technique. Open Parasitol J 4:1–4

- Rai K, Sherchand JB, Bhatta DR, Bhattarai NR (2005) Status of *Giardia intestinalis* infection among the children attending Kanti children hospital, Nepal. Sci. World 3:102–105
- Schantz P, Sarti E, Plancarte A, Wilson M, Criales J, Roberts J, Flisser A (1994) Community-based epidemiological investigations of cysticercosis due to Taenia solium: comparison of serological screening tests and clinical findings in two populations in Mexico. Clin Infect Dis 18:879–885
- Sethi S, Sehgal R, Malla N, Mahajan R (1999) Cryptosporidiosis in a tertiary care hospital. Natl Med J India 12:207–209
- Sulaiman IM, Fayer R, Bern C, Gilman RH, Trout JM, Schantz PM, Das P, Lal AA, Xiao L (2003) Triosephosphate isomerase gene characterization and potential zoonotic transmission of Giardia duodenalis. Emerg Infect Dis 9:1444
- Vanni I, Cacciò SM, van Lith L, Lebbad M, Svärd SG, Pozio E, Tosini F (2012) Detection of Giardia duodenalis assemblages A and B in human feces by simple, assemblage-specific PCR assays. PLoS Neglect Trop Dis 6:e1776
- Xiao L, Morgan UM, Limor J, Escalante A, Arrowood M, Shulaw W, Thompson R, Fayer R, Lal AA (1999) Genetic diversity within Cryptosporidium parvum and related Cryptosporidium species. Appl Environ Microbiol 65:3386–3391
- Yoshikawa H, Abe N, Iwasawa M, Kitano S, Nagano I, Wu Z, Takahashi Y (2000) Genomic analysis of Blastocystis hominisStrains isolated from two long-term health care facilities. J Clin Microbiol 38:1324–1330

Publisher's Note Springer Nature remains neutral with regard to jurisdictional claims in published maps and institutional affiliations.