

Correlation of *Giardia duodenalis* assemblages with clinical and epidemiological data in Turkish children

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25 th ECCMID Copenhagen, Denmark

Objectives

Giardia duodenalis (*G. duodenalis*) highly prevalent intestinal parasite in Turkish children. To date, eight main assemblages of *G. duodenalis* have been described, but only A and B genetic groups are known to infect humans. The purpose of this study was to determine the prevalence of different *G. duodenalis* assemblages among children with giardiasis, and investigate associations with clinical and epidemiological data collected from children.

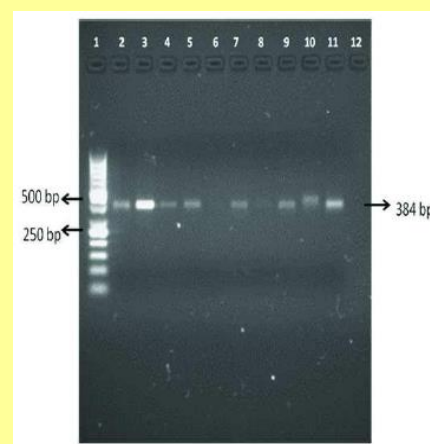


Figure 1. A representative 2% agarose gel to visualize PCR amplified fragment of the β -giardin gene. Lane 1, 50 bp marker; lane 2, positive control; lane 12, mixture control; other lines, clinical samples.

Methods

In the present study, 987 fecal samples from children were collected from Kocaeli University Hospital during 2012-2013 to search for the presence of *Giardia* by microscopy. To the microscopically positive samples, PCR was used to generate a 384 bp fragment for β -giardin. The PCR products were sequenced and the sequences were subjected to phylogenetic analysis by using PHYLIP.

Table 1 BLAST search results of the isolated β -giardin sequences.

Sample Number	Assemblages	% coverage of the query	E-value	% Identity
9	B	%96	4e-175	%99
2	B	%96	1e-180	%99
3	B	%96	3e-177	%98
29	A	%100	1e-176	%99
22	A	%100	1e-169	%99
7	A	%100	1e-188	%99
33	A	%100	1e-180	%99
38	A	%100	1e-103	%99
45	A	%99	1e-103	%99
42	A	%100	1e-175	%99
10	A	%100	1e-175	%99
13	A	%99	1e-180	%99
16	A	%99	1e-175	%99
14	A	%99	1e-176	%99
18	AB	%99	1e-150	%99
21	AB	%100	1e-152	%99
19	B	%97	1e-162	%98
11	AB	%55	8e-103	%100
20	AB	%55	8e-103	%100
36	B	%97	1e-180	%98
5	B	%100	1e-175	%99
40	B	%97	1e-165	%99

Results

Of 987 stool samples examined, 85 were positive to *G. duodenalis* by microscopy. DNA from 68 of 85 (80%) samples was successfully amplified by PCR for β -giardin (Fig. 1). Based on the phylogenetic analysis of the sequences, assemblage A, B and mixed (AB) were determined (Fig. 2). Of 68 isolates, 45 were identified to be assemblage A (66%), 16 were assemblage B (24%) and 7 were assemblage AB (10%) (Table 1). No association between epidemiologic data and assemblages was detected (Table 2).

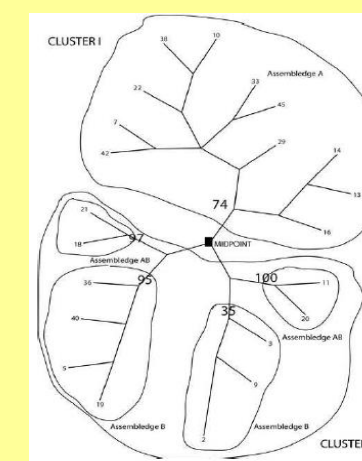


Figure 2. Phylogenetic analysis of *G. duodenalis* assemblages

Nevertheless, assemblage A was more frequently encountered in children with diarrhea, flatulence or abdominal pain than assemblages B and AB ($P > 0.01$).

Table 2 Association between *G. duodenalis* assemblages and the epidemiological data analyzed in studied children.

Characteristic	Assemblage A (n=11)		Assemblage B (n= 7)		Mixed assemblages A+B (n=4)		P
	n	%	n	%	n	%	
Symptomatic group	8	72,7	2	28,6	3	75	0,163 ^a
Asymptomatic group	3	27,3	5	71,4	1	25	
Sex							0,854 ^a
Male	7	63,6	5	71,4	2	50	
Female	4	36,4	2	28,6	2	50	
Residing area							0,602 ^a
Urban	3	27,3	3	42,9	2	50	
Rural	8	72,7	4	57,1	2	50	
Age							0,002 ^b
Mean value (±SD)	3,82 (±1,72)		8,14 (±2,73)		6,5 (±1,91)		
Median	3		7		7		
Interval	2-7		5-13		4-8		

^aMonte Carlo Chi-Square test
^bOne-way ANOVA

Conclusion

Since assemblage A is more prevalent compared to assemblage B, it might be responsible for common *Giardia* infections in Turkey. Further molecular epidemiological studies are needed to be done in other regions to identify the prevalence of the species to develop novel strategies in the control and prevention of *G. duodenalis* infection in Turkey.

