Investigation of adherent-invasive *E. coli* in patients with Crohn's disease

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Abstract

**Background:** Crohn’s disease and Ulcerative colitis are known as inflammatory bowel disease with high morbidity which are as a result of increasing immune responses to intestinal microbiota in genetically susceptible individuals. The association of adherent invasive Escherichia coli with Crohn’s disease in human has been discussed for decades. The principal aim of this study was to assess the relationship between adherent invasive *Escherichia coli* in Iranian patients with Crohn’s disease.

**Methods:** The presence of adherent invasive *Escherichia coli* DNA and viable adherent invasive *Escherichia coli* cells were identified through PCR and conventional culture methods, respectively. All the specimens were subsequently cultured in Hi Chrome Agar medium.

**Results:** Using molecular assay, the invasive plasmid antigen H and invasion-association locus genes were detected from tissue samples confirming the presence of adherent-invasive *Escherichia coli*. The invasive plasmid antigen H was detected in 46.7% of CD and 13.3% of healthy peoples. The invasion-association locus gene was found in 36.7% of patients with Crohn’s disease and 10% in individuals without IBD.

**Conclusion:** This study demonstrated an increased frequency of adherent invasive *E. coli* with invasive plasmid antigen H and invasion-association locus genes in comparison to control individuals. Moreover, it was shown that adherent invasive *E. coli* with the invasive plasmid antigen H and invasion-association locus genes can act as a predisposing factor in the development of IBD.

**Keywords:** Crohn Disease, Inflammatory bowel disease, *Escherichia coli*, PCR

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Introduction

Inflammatory bowel disease (IBD) is a chronic inflammatory disorder divided into Ulcerative colitis (UC) and Crohn’s disease (CD) (1, 2). The rising trend of the disease has observed in Middle Eastern countries as well as in other parts of the world and statistics shows the incidence also is on the rises in North America and Europe as well as other parts of the world. Likewise, a recent study demonstrated that the prevalence of IBD is increasing dramatically in Iran (3).

The incidence and prevalence of ulcerative colitis and Crohn’s disease have been increased all over the world, especially among children and adults. It is believed that several factors such as immunology, genetic factors, stress, diet, being an alcoholic or a smoker, as well as bacteria such as the adherent-invasive strains of *Escherichia coli*, *Campylobacter spp.*, *Clostridium difficile*, *Mycobacterium avium* subspecies *Paratuberculosis*, and *Bacteroides fragilis* (4-7) may play a role in the development of IBD. Since gastrointestinal (GI) tract of healthy people is colonized by a wide variety of different microorganisms

†What is “already known” in this topic:
Inflammatory bowel disease (IBD) is comprised of Crohn’s disease (CD) and Ulcerative colitis (UC). The prevalence and incidence of IBD are continuously rising in Iran. No study has been conducted to investigate the role of adherent invasive *E. coli* in patients with Crohn's disease occurred in the country.

—What this article adds:
Due to the rising trend of IBD prevalence and incidence in Iran, and also the significant role of intestinal microbiota in the development of disease, further investigation into the possible causing factors is vitally imperative.
Investigation of adherent-invasive *E. coli* in patients with Crohn’s disease

hence, dysbiosis of the intestinal microbiota is likely cause of IBD (8).

It is known that intestinal bacteria can cause CEACAM6 expression through inducing inflammatory cytokines. The expression can then leads to production of *E. coli* with AIEC phenotype. The AIEC can attach to epithelial cells by a mechanism involving polymerization of microtubules. In fact, AIEC adheres to GP2 (glycoprotein 2) upon M cells by LPF (long polar fimbiae) and enter to Peyer’s patches and exacerbates inflammation in the intestine (9). Moreover, AIEC able to adhere epithelial cells and invade into the cytoplasmic eukaryotic infectious cells with type 1 fimbiae (*fimH*), invasive plasmid antigen H (*ipaH*) and invasion-association locus (*ial*) (10).

However, *E. coli* with adherent-invasive phenotype should be regarded as a separate issue of pathogenicity of *E. coli* causing inflammation in the human intestine.

The principal purpose of this study was to investigate of *E. coli* with adherent-invasive phenotype and their relation to Crohn’s disease.

### Methods

In the present study, sixty subjects including thirty patients with lesions of Crohn’s colitis and thirty people without IBD were collected during colonoscopy examinations. Samples with CD were obtained from lesions of colon, or terminal ileum. Moreover, the biopsy of control group was performed on normal areas. DNA was extracted from the tissue samples and PCR assay performed by confirming as AIEC by biochemical tests and PCR assay. The all isolated bacteria were confirmed as AIEC by biochemical tests and PCR assay. The.

The principal purpose of this study was to investigate of *E. coli* with adherent-invasive phenotype and their relation to Crohn’s disease.

### Microbial identification

Samples were immediately transferred into sterile vials containing either thioglycolate broth or saline (Sigma-Aldrich, Hi Media) and incubated for 18-24h at 35±2°C. The bacteria were stored in TSB broth containing 30% glycerol at a temperature of -70°C for further analysis.

### DNA Extraction

Tissue biopsies were crushed and DNA extracted through RTP® Mycobacteria kit (Berlin, Germany).

### PCR assay

All samples were tested for the presence of *ipaH* and *ial* genes using molecular PCR. The nucleotide sequence of primers (Macrogen, Pishgam) and production size (base pairs) for amplification of the *ipaH* and *ial* genes are shown in Table 1 (11, 12). PCR was performed in 12.5μL comprising 5μL master mix (Amplicon, Pishgam), 0.5 μL of each primer, 2 μL of the DNA template (50 ng) and 4.5μL of ddH2O. Subsequently, the thermal cycling status was used: 300 seconds at 94°C and 25 cycles of amplification consisting of 60 seconds at 95°C, 55 seconds at 58°C, and 60 seconds at 72°C, with 300 seconds at 72°C for the final extension. PCR products were investigated by electrophoresis on a 1% agarose gel in 1X TBE buffer [10.8 g Tris and 5.5 g Boric acid, 0.5 M Na2EDTA (pH 8.0)] (13).

<table>
<thead>
<tr>
<th>Genes</th>
<th>Nucleotide Sequences(5’-3’)</th>
<th>Size of product, bp</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>ipaH</em></td>
<td>F-GTTCCCTTGACCCCTTCCGATACGGTC</td>
<td>619</td>
</tr>
<tr>
<td></td>
<td>R-GCCGCTAGGCACCCTCTGAGAGTCAC</td>
<td></td>
</tr>
<tr>
<td><em>ial</em></td>
<td>F-CTGAGATGATGTATGGTGGAGG</td>
<td>320</td>
</tr>
<tr>
<td></td>
<td>R-GGAAGGCCAACAAATTATTTCC</td>
<td></td>
</tr>
</tbody>
</table>

### Statistical Analysis

Data were analyzed using Pearson Chi-Square test, and *P* value below 0.05 considered as statistically significant.

### Results

**Clinical information of patients and controls**

The average age of patients with IBD and controls were 38.8 and 52.8 years old respectively. The participants included 14 males and 16 female patients with CD, and 18 males and 12 females without IBD. In addition, the age range for patients with CD and without IBD was 18-64 and 25-76 years old respectively.

**Detection of adherent-invasive *E. coli* with *ipaH* and *ial* genes**

Of 60 tissue samples collected, *E. coli* were isolated from 20 (66.6%) patients with CD and 22 (73.3%) from healthy people (Table 2). All isolated bacteria were confirmed as AIEC by biochemical tests and PCR assay. The
ipaH, ial genes were amplified by utilizing particular primers and become visible as a band of approximately 619 and 320 kb on agarose gel respectively (Figs. 1 and 2). The difference between patients with Crohn’s disease and controls was not significant ($p=0.59$). Of 30 patients with CD, the positive and negative rate of ipaH gene was 46.7% (n=14) and 53.3% (n=16) respectively. The percentage of ipaH among 30 individuals without IBD was 13.3% (n=4) but 86.6% (n=26) was not detected (Table 3). Furthermore, the positivity of ial gene were 36.7% (n=11) and 10% (n=3) in patients with CD and healthy people respectively (Table 4). Moreover, the presence of ipaH and ial genes in adherent-invasive E. coli in patients with CD was more than control populations.

Due to its high sensitivity, PCR assay was more reliable than cultivation. The difference between the correlation of adherent-invasive E. coli with ipaH and ial in CD patients with control populations was statistically significant ($p<0.05$). All positive amplified fragments were sequenced and high percentage of adherent-invasive E. coli was identified.

Furthermore, a chi square test was performed and the correlation between adherent-invasive E. coli with ipaH and ial in patients with CD and UC found to be ($N=30$) =7.937, $p=.005$ and ($N=30$) =5.963, $p=.015$ respectively. Nonetheless all positive amplified fragments were sequenced and high percentage of adherent-invasive E. coli was detected.

**Discussion**

Crohn's disease is considered as a chronic inflammatory of GI disorder. Although the etiology of inflammatory bowel disease is not still known (14), but numerous studies demonstrated that the mortality rate of this disease is high (15). Furthermore, it is demonstrated that several factors may play role in induction of the disease. In a research by Sartor RB et al, the intestinal microbiota effect on epithelial cells, and inflammation of the intestinal mucosa have shown to trigger the pathogenesis of both CD and UC (16). Moreover, CD patients demonstrated an altered intestinal microbial community, with different kind of bacteria in colonic and ileal areas (17).

Previous studies showed that Enterobacteriaceae especially E. coli could contributed the onset of IBD. Nevertheless other bacteria can trigger the pathogenesis of in-

![Fig. 1. Amplification of the ipaH gene. Lanes: 1, DNA molecular size marker (100-bp ladder); 2-7, Crohn’s disease samples; 8, negative control (Water).](image)

![Fig. 2. Amplification of the ial gene. Lanes: 1, DNA molecular size marker (100-bp ladder); 2-7, Crohn’s disease samples; 8, negative control (Water).](image)

**Table 3.** PCR Analysis of the ipaH gene for CD and nIBD samples

<table>
<thead>
<tr>
<th>Group</th>
<th>Positive</th>
<th>Negative</th>
<th>$p$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crohn’s disease</td>
<td>14</td>
<td>16</td>
<td>.005*</td>
</tr>
<tr>
<td>Count</td>
<td>46.7</td>
<td>53.3</td>
<td></td>
</tr>
<tr>
<td>CD (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nIBD</td>
<td>4</td>
<td>26</td>
<td></td>
</tr>
<tr>
<td>nIBD (%)</td>
<td>13.3</td>
<td>86.7</td>
<td></td>
</tr>
<tr>
<td>$P$ value</td>
<td>0.24</td>
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<td></td>
</tr>
</tbody>
</table>

*Significant at alpha=0.05

**Table 4.** PCR Analysis of the ial gene from CD and nIBD samples

<table>
<thead>
<tr>
<th>Group</th>
<th>Positive</th>
<th>Negative</th>
<th>$p$ value</th>
</tr>
</thead>
<tbody>
<tr>
<td>Crohn’s disease</td>
<td>11</td>
<td>19</td>
<td></td>
</tr>
<tr>
<td>Count</td>
<td>36.7</td>
<td>63.3</td>
<td></td>
</tr>
<tr>
<td>CD (%)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>nIBD</td>
<td>3</td>
<td>27</td>
<td></td>
</tr>
<tr>
<td>nIBD (%)</td>
<td>10.0</td>
<td>90.0</td>
<td></td>
</tr>
<tr>
<td>$P$ value</td>
<td>0.34</td>
<td></td>
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</tr>
</tbody>
</table>
Investigation of adherent-invasive *E. coli* in patients with Crohn’s disease

flamatory bowel disease including Bacteroidales, Clostridiales, Pasteurellaceae (*Haemophilus* sp.), Veillonellaceae, Neisseriaceae, and Fusobacteriaceae (18). Significant information exists regarding the role of adherent invasive *E. coli* in the CD. Numerous studies reported that adherent invasive *E. coli* could be a candidate for the development of CD (19).

An emerging evidence indicated an association between adherent invasive *E. coli* with IBD and colorectal cancer (20, 21 and 22). The present study shows no difference in the incidence of *E. coli* positive culture between CD and control patients (Table 2). The lack of *E. coli* in some tissue sample was probably due to consumption of antibiotics which in turn can cause dysbiosis in the human gastrointestinal tract (23). In some studies, using the culture-based method demonstrated that *E. coli* bacteria were found in the intestinal mucosa as well as in ulcers of both CD and UC patients compared to controls (24). In comparison with nIBD, our finding shows that the abundance of adherent invasive *E. coli* harboring *ipaH* and *ial* genes was higher in CD individuals. Additionally, we found that 46.7% and 36.7% of CD specimens harbored *ipaH* and *ial*, an increased proportion of AIEC, compared to control individuals. In spite of interesting debate, Dogan et al conducted a similar prevalence of AIEC in the ileum of patients with CD (25). Several studies showed a high proportion of AIEC harboring *fimH*, *fimA* and *Cas* genes in CD (26, 27). According to the present study, in comparison with nIBD, PCR assay displayed a high abundance of *ipaH* and *ial* genes in CD patients with statistically significant difference. These data proposed that AIEC most likely harbored *ipaH* and *ial* genes which in turn could be effective in the initiation of the CD. Nonetheless, since other virulence factors for AIEC were not analyzed, so it may be taken into consideration in the future study.

**Conclusion**

Despite the role of several factors in the progression of IBD, the present study displays a high prevalence of AIEC with *ipaH* and *ial* genes from patients with CD. According to these findings, *E. coli* with AIEC phenotype could be a predisposing factor in the development of inflammatory bowel disease. In addition to AIEC, host immune response, genetics of patients and environmental factors play an important role in the initiation of IBD. Therefore the present study suggests that appropriate treatment against AIEC could be practically effective in patients with inflammatory bowel disease.

**Acknowledgments**

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**Funding/Support**

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**Conflict of Interests**

The authors declare that they have no competing interests.

References


7. Sartor RB. Genetics and environmental interactions shape the intestinal microbiome to promote inflammatory bowel disease versus mucosal homeostasis. *Gastroenterology*. 2010;139:1816-1819.


23. Small CL, Reid-Yu SA, McPhee JB, Coombes BK. Persistent infection with *Crohn’s disease-associated adherent-invasive*


