PDF hosted at the Radboud Repository of the Radboud University Nijmegen

The following full text is a publisher's version.

For additional information about this publication click this link.
http://hdl.handle.net/2066/206814

Please be advised that this information was generated on 2020-02-28 and may be subject to change.
Association between genotypes of rs34436714 of NLRP12 and serum tumor necrosis factor-alpha in inflammatory bowel disease

A case-control study

Erminia Dellaporta, MD, Lazaro-Dimitrios Lazaridis, MD, PhD, Vasileios Koussoulas, MD, PhD, Mihai G. Netea, MD, PhD, Evangelos J. Giamarellos-Bourboulis, MD, PhD, Konstantinos Triantafyllou, MD, PhD

Abstract

We aimed to investigate the impact of the single nucleotide polymorphisms of rs34436714 of the NOD-like receptor protein 12 gene on the production of tumor necrosis factor alpha (TNFα) in patients with inflammatory bowel disease (IBD).

In a matched case-control study 90 patients with IBD, 56 with Crohn disease (CD) and 34 with ulcerative colitis, were genotyped and compared to 98 healthy comparators matched for age and gender. Expression level of TNFα, interleukin (IL)-6, IL-12, and soluble triggering receptor expressed on myeloid cells were measured in patients’ sera. Peripheral blood mononuclear cells (PBMCs) were isolated and stimulated for TNFα production.

Serum TNFα was greater among carriers of GT/TT genotypes than GG genotypes of rs34436714. Stimulated TNFα production was also higher in carriers of GT/TT genotypes. The frequency of CD with fistulizing behavior and with CD involving the small intestine was greater among carriers of GT/TT genotypes than of the GG genotype. Distribution of the GG, GT, and TT genotypes of rs34436714 were in Hardy–Weinberg equilibrium in both groups. The genotype distribution was the same in both groups.

Carriage of minor frequency alleles of rs34436714 was accompanied by greater circulating levels of TNFα and by greater capacity for stimulated TNFα production by PBMCs. These alleles had an impact on the phenotype of patients with CD.

Abbreviations: CD = Crohn disease, IBD = inflammatory bowel disease, IL = interleukin, LPS = lipopolysaccharide, NLRP12 = NOD-like receptor protein 12, NOD = nucleotide binding domain, PBMCs = peripheral blood mononuclear cells, SNP = single nucleotide polymorphism, sTREM-1 = soluble triggering receptor expressed on myeloid cells-1, TNFα = tumor necrosis factor-alpha, UC = ulcerative colitis.

Keywords: inflammatory bowel disease, NLRP12, single nucleotide polymorphisms, TNFα

1. Introduction

The interaction of gut microbiota with tissue macrophages is more and more recognized as a key component in the pathogenesis of inflammatory bowel disease (IBD). This interaction is mediated by the recognition of pathogen-associated patterns of bacterial flora by the nucleotide binding domain (NOD)-like intracellular receptors of macrophages. Carriage of single nucleotide polymorphisms (SNPs) in any of these receptors may modulate the susceptibility of the host for the development of IBD.[1]

One well-recognized receptor is NOD-like receptor protein 12 (NLRP12). NLRP12 is associated with the protein adaptor ASC inducing the formation of an active IL-1β maturing inflammasome.[2] It also acts as a negative regulator of pro-inflammatory cytokine production via inhibition of non-canonical NF-κB...
activation. The NLRP12 has been shown to play a role in the maintenance of intestinal homeostasis and protection against tumorigenesis in animal models. Recent data revealed decreased expression of NLRP12 in patients with active ulcerative colitis (UC) as compared to healthy controls and patients with inactive UC. Since NLRP12 is a negative regulator of inflammation, it may be hypothesized that it also downregulates the production of tumor necrosis factor-alpha (TNFα). TNFα is recognized as a key molecule in the pathogenesis of IBD and factors affecting its production may participate in pathogenesis.

NLRP12 is located on chromosome 19. One common SNP of NLRP12 is rs34436714 where guanine is substituted by thymine leading to the missense substitution of glycine by valine. Taking into consideration the above described role of NLRP12 to downregulate inflammation in the gut and the lower NLRP12 expression among patients with IBD, we questioned if carriage of SNP alleles of rs34436714 may modulate the production of TNFα.

2. Patients and methods

2.1. Study design

This was a case-control study of patients with IBD and healthy comparators. The study was approved by the Ethics Committee of the ATTIKON University Hospital, in Athens, Greece.

Inclusion criteria for patients were:

1. Caucasian origin;
2. age equal to or above 18 years;
3. both genders;
4. written informed consent provided by the patients; and
5. diagnosis of IBD with clinical, endoscopic, and histological documentation.

Inclusion criteria for the comparators were to be of the same age and gender and to provide written informed consent as the patients and not to have any known chronic disorder. Exclusion criteria were:

1. age below 18 years;
2. denial to consent;
3. any other chronic inflammatory disorder;
4. infection by the human immunodeficiency virus;
5. chronic hepatitis B or C; and
6. any fungal infection.

Ten millilitres of peripheral blood was sampled from each patient or comparator after venipuncture of the forearm vein under aseptic conditions; 5 ml were collected into EDTA-coated tubes (Vacutainer, BD) to isolate genomic DNA by standard methods; another 5 ml were collected into sterile and clean tubes free of anticoagulant. After centrifugation, serum was stored at −80°C until assayed.

Genomic DNA was isolated from whole blood using standard procedures. The genotype for the NLRP12 polymorphism rs34436714 in the patients was screened by the TaqMan SNP assay C_25927410_10, on the 7300 ABI Real-Time polymerase chain reaction system (Applied Biosystems, CA).

In 1 out of 5 patients, another 20 ml of whole blood was sampled and collected into heparinized tubes. Peripheral blood mononuclear cells (PBMCs) were isolated after gradient centrifugation over Ficoll (Merck, Darmstadt, Germany). After 3 consecutive washings in ice-cold phosphate-buffered saline (pH: 7.2), PBMCs were counted in a Neubauer chamber with trypan blue exclusion of dead cells. Cells were distributed in duplicate in wells of 96-well plates and incubated at a density of 5 × 10⁶/ml without/with 10 ng/ml of lipopolysaccharide (LPS) of Escherichia coli O55:B5 (Sigma, St. Louis). The growth medium was RPMI1640 enriched with 5% glutamate (Merck). Plates were incubated for 24 hours at 37°C in 5% CO₂ atmosphere. At the end of the incubation plates were centrifuged and supernatants were collected and stored at −80°C until assayed for TNFα.

TNFα, interleukin (IL)-6, IL-12, and soluble triggering receptor expressed on myeloid cells-1 (sTREM-1) were measured in serum and supernatants of patients by an enzyme immunoassay assay according to the instructions of the manufacturer (R&D Inc, Minneapolis). The lower limit of detection was 5.6 pg/ml for TNFα and IL-6; 31.3 pg/ml for IL-12; and 15.1 pg/ml for sTREM-1.

The primary study endpoint was the impact of the genotype of rs34436714 on TNFα levels. Secondary study endpoints were:

1. the impact of the genotype of rs34436714 on the other measured serum cytokines;
2. the impact of the genotype of rs34436714 on the clinical characteristics of Crohn disease (CD); and
3. the difference in genotype distribution of rs34336714 between patients and comparators.

2.2. Study power

The study was powered for the primary endpoint. It was hypothesized that

1. 30% of patients would be carriers of at least 1 minor frequency allele and 70% of patients of major frequency alleles; and
2. the mean difference of serum TNFα would be 50 pg/ml and the standard deviation would vary by 70 pg/ml.

In order to demonstrate this difference at the 10% level of significance with 80% power at least 80 patients should be enrolled.

2.3. Statistical analysis

Cytokine concentrations were expressed as means±SE and compared by the Mann–Whitney U test. Genotype and allele distribution were expressed as frequencies and compared by the Fisher exact test. Any value of P below .05 was considered significant.

3. Results

A total of 90 patients with IBD, 34 with UC and 56 with CD, and 98 healthy comparators were enrolled. The study flow chart is shown in Figure 1. The demographics of patients and comparators are provided in Table 1.

The primary study endpoint was the modulation of TNFα by SNPs of rs34436714. As it can be seen in Figure 2A, circulating concentrations of TNFα were greater among patients carrying at least 1 T allele of rs34436714. In order to elaborate this further, we isolated PBMCs from 20 patients, 10 with UC and 10 with CD. After stimulation with bacterial LPS, PBMCs of patients carrying T alleles of rs34436714 produced more TNFα than PBMCs of patients carrying only the major frequency allele (Fig. 2B). However, it is suggested that treatment with chemical or biological
Disease response modifiers may modulate the ability of the host for TNFα production.\(^{[6]}\) To this end, circulating concentrations of TNFα were compared separately between patients carrying major and minor frequency alleles of rs34436714 in relation to treatment with at least 1 drug and with at least 2 or more drugs. Circulating TNFα was greater among patients under treatment with 2 or 3 drugs who were carriers of at least 1 minor frequency T allele of rs34436714 (Fig. 2C).

Expression levels of sTREM-1, IL-6, and IL-12 did not differ between carriers of at least 1 T allele of rs34436714 and carriers of only major frequency alleles (Fig. 3).

We hypothesized that carriage of minor frequency T alleles that was associated with greater production capacity for TNFα might also be associated with the clinical phenotypes of CD. Analysis showed that carriage of GT and TT genotypes was associated with greater frequency of CD with fistulizing behavior (Fig. 4A) and with CD located only at the small intestine (Fig. 4B).

Among the comparators, 66 (67.3%), 28 (29.5%), and 4 (4.1%) had GG, GT, and TT genotypes, respectively. Among IBD patients, 59 (65.6%), 28 (31.1%), and 3 (3.3%) had GG, GT, and TT genotypes, respectively. No deviation from Hardy–Weinberg equilibrium was detected in either comparators (HWE: 0.01; \(P = .976\)) or patients (HWE: 0.02; \(P = .884\)). No difference in the genotype distribution was found between patients and comparators (\(P = .907\)); 81.6% (n = 160) of comparators were carriers of major frequency G alleles and 18.4% (n = 36) were carriers of minor frequency T alleles; this distribution was 81.8% (n = 146) and 80.2% (n = 34), respectively among patients.

### 4. Discussion

Our study shows how patients suffering with IBD who are carrying minor frequency T alleles of rs34436714 of NLRP12 have greater circulating levels of TNFα and greater potential for the production of TNFα after PBMCs stimulation. It also shows how carriage of these alleles may have an impact on the phenotype of patients with CD.

<table>
<thead>
<tr>
<th>Table 1</th>
<th>Demographic and clinical characteristics of patients enrolled in the study.</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>Ulcerative colitis (n = 34)</td>
</tr>
<tr>
<td>Male gender (n, %)</td>
<td>18 (52.9)</td>
</tr>
<tr>
<td>Age, yr (mean ± SD)</td>
<td>49.5 ± 17.2</td>
</tr>
<tr>
<td>History of operation (n, %)</td>
<td>2 (5.9)</td>
</tr>
<tr>
<td>Extraintestinal manifestations (n, %)</td>
<td>2 (5.9)</td>
</tr>
<tr>
<td>Extent of GI involvement (n, %)</td>
<td></td>
</tr>
<tr>
<td>Up to sigmoid</td>
<td>4 (11.8)</td>
</tr>
<tr>
<td>Pancolitis</td>
<td>30 (88.2)</td>
</tr>
<tr>
<td>Colon and terminal ileum</td>
<td>9 (16.1)</td>
</tr>
<tr>
<td>Colon and small intestine</td>
<td>30 (88.2)</td>
</tr>
<tr>
<td>Terminal ileus only</td>
<td>0</td>
</tr>
<tr>
<td>Small intestine only</td>
<td>0</td>
</tr>
<tr>
<td>Behavior (n, %)</td>
<td></td>
</tr>
<tr>
<td>Inflammatory</td>
<td>0</td>
</tr>
<tr>
<td>Fibrostenotic</td>
<td>0</td>
</tr>
<tr>
<td>Fistulizing</td>
<td>0</td>
</tr>
<tr>
<td>Activity(^\ast) (n, %)</td>
<td></td>
</tr>
<tr>
<td>Nonactive</td>
<td>19 (55.9)</td>
</tr>
<tr>
<td>Mild</td>
<td>8 (23.5)</td>
</tr>
<tr>
<td>Moderate</td>
<td>4 (11.8)</td>
</tr>
<tr>
<td>Severe</td>
<td>3 (8.8)</td>
</tr>
<tr>
<td>Medications (n, %)</td>
<td></td>
</tr>
<tr>
<td>5-amino salicylate</td>
<td>28 (82.4)</td>
</tr>
<tr>
<td>Immunosuppressants(^\dagger)</td>
<td>9 (26.5)</td>
</tr>
<tr>
<td>Anti-TNF(^\ddagger)</td>
<td>0</td>
</tr>
<tr>
<td>Corticosteroids</td>
<td>2 (5.9)</td>
</tr>
</tbody>
</table>

\(\text{TNF} = \) tumor necrosis factor alpha, \(SD = \) standard deviation.

\(\ast\) Mayo score for ulcerative colitis and Harvey–Bradshaw score for Crohn disease.

\(\dagger\) Azathioprine or cyclosporine.

\(\ddagger\) Infliximab or adalimumab.
Figure 2. Impact of rs34436714 genotype of NLRP12 on TNFα. Results are provided for (A) serum TNFα; (B) production of TNFα by PBMCs of patients after stimulation with bacterial lipopolysaccharide; and (C) serum TNFα in relation to the intake of disease-modifying drugs (see Table 1). P values refer to the indicated statistical comparisons. Production of TNFα by PBMCs without stimulation was below the limit of detection. NLRP12 = NOD-like receptor protein 12, PBMCs = peripheral blood mononuclear cells, TNFα = tumor necrosis factor-alpha.

Figure 3. Serum concentrations of sTREM-1 and of IL-6 and -12 in relation to the rs34436714 genotype of NLRP12. P values refer to the indicated statistical comparisons. IL = interleukin, NLRP12 = NOD-like receptor protein 12, sTREM-1 = soluble triggering receptor expressed on myeloid cells-1.
A thorough literature search identified few studies on the impact of the function of NLRP12 gene for the pathogenesis of IBD. To our knowledge there is only clinical study trying to investigate the role of the expression of NLRP12 in IBD: in a paired comparison that involved 10 pairs of monozygotic UC twins, healthy twins, and 7 UC patients, gene-profiling showed reduced expression of NLRP12 in active UC.

However, the role of rs34436714 was not explored.

Our results point towards an impact of SNPs of rs34436714 on the production of TNFα. Indeed, IBD has been associated with increased expression of TNFα in intestinal tissues.[17, 18] The lack of measurements of TNFα in at the gut tissue level may, at first glance, appear as a limitation of our study. However, 2 points may be argued to strengthen the impact of the analyzed SNPs of rs34436714 on TNFα expression as performed in this study through the use of serum TNFα measurements:

1. Increased serum TNFα has been described by others in patients with IBD[8, 9]; and
2. Carriage of minor frequency T alleles of rs34436714 was associated with greater serum TNFα but not with other circulating cytokines.

This is in accordance with the current knowledge that IBD is a disease hallmarked by elevated TNFα[10] but not by elevated IL-6 and IL-12.

It has been shown that circulating monocytes of patients with CD produce more TNFα than healthy volunteers or patients with UC.[11] Although it is anticipated that greater production of TNFα may be associated with the behavior of CD and refractoriness to treatment, such data are not published. To this end, only indirect evidence is available. More precisely, it has been shown in patients with IBD that carriage of minor frequency A alleles at the -308 gene position increases by 6- to 7-fold the gene transcription of TNFα and the subsequent TNFα deposition at the tissue level. This influences the behavior of CD towards less steroid-dependent disease.[12–14] To this end, it was interesting to find that carriage of minor frequency T alleles of rs34436714 that are associated with elevated circulating TNFα and with high stimulated production of TNFα by PBMCs was also associated with the behavior of CD and with response to treatment. These carriers presented commonly with CD with fistulizing behavior involving the small intestine and necessitated 2 or 3 drugs.

Although this may be considered of importance from a pharmacogenomics perspective, a recent genome-wide association study of 359 patients using the Illumina immunochip and covering 196,524 SNPs did not report any association between durability of response to anti-TNFα and rs34436714.[15]

The production of TNFα in the gut is stimulated by microbiota where NLRP12 may function as a modulator. This is supported by studies describing NLRP12 as an antagonist of pro-inflammatory signals induced by Toll-like receptor ligands and Mycobacterium tuberculosis[16] and downregulation of TLR-dependent NFκB after gene silencing of NLRP12.[13] The diversity of gut microbiota is decreased when mice that are deficient for NLRP12 become obese after being fed high-fat diet; this is associated with greater systemic inflammation.[17] Similar findings were shown in mice subject to experimental colitis.[18]

The increased production of sTREM-1 that was found in the IBD patients of our study is in agreement with the findings of a previous study of our group that identified sTREM-1 as a mediator in IBD positively correlated with IBD activity.[18] Despite the elevation of sTREM-1 in CD, this was not affected by the carriage of minor frequency alleles of NLRP12. This outscores the importance of the pathway linking NLRP12 to TNFα and not to other pro-inflammatory mediators.

The small study population is also a limitation of our study. However, the primary endpoint, that is, the association of serum TNFα with the carriage of minor frequency T alleles of rs34436714 was shown even under that limitation.

Our findings showed that carriage of minor frequency alleles of rs34436714 of NLRP12 was accompanied by greater circulating levels of TNFα and by greater capacity for stimulated TNFα production by PBMCs. These alleles had an impact on the phenotype of patients with CD. Although our results pinpoint some significance of SNPs of rs34436714 in the pathogenesis of IBD, they cannot prove if they drive or not a direct modulation of the production of blood TNFα.

**Author contributions**

**Conceptualization:** Mihai G. Netea, Evangelos Giamarellos-Bourboulis, Konstantinos Triantafyllou.

**Data curation:** Erminia Dellaporta, Lazaros-Dimitrios Lazaridis, Vassilios Koussoulas.

**Formal analysis:** Evangelos Giamarellos-Bourboulis, Konstantinos Triantafyllou.

**Funding acquisition:** Evangelos Giamarellos-Bourboulis.

**Methodology:** Mihai G. Netea, Evangelos Giamarellos-Bourboulis.

**Software:** Erminia Dellaporta.
Supervision: Konstantinos Triantafyllou.
Writing – original draft: Evangelos Giamarellos-Bourboulis, Konstantinos Triantafyllou.
Writing – review and editing: Erminia Dellaporta, Lazaros-Dimitrios Lazaridis, Vasilieios Koussoulas, Mihai G. Netea, Evangelos Giamarellos-Bourboulis, Konstantinos Triantafyllou.

References


