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Title:

PHARMACOGENETIC BIOMARKERS OF RESPONSE IN CROHN'S DISEASE

RUNNING TITLE:

GENETIC PREDICTORS OF RESPONSE IN CROHN'S DISEASE

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The authors declare that there is not conflict of interest that could be perceived as prejudicing the impartiality of the research reported and there is not any competing financial interest in relation to the work described in this article.
ABSTRACT

Crohn’s disease (CD) is a chronic condition which affects to the immune system. It can affect to any part of the digestive tract and be associated with external manifestations. The causes of the disease remain unknown, although it seems to be the result of a combination of factors, such as genetic predisposition, environment, lifestyle and the composition of the microbiota, among others. The treatment protocol begins with a change in eating and smoking habits, and is continued with different lines of treatment, including corticosteroids, immunomodulators, and biologic therapy (infliximab and adalimumab), which have shown differences in response among patients, especially with biologic treatment. Several studies have considered the possibility that these differences in response are caused by the genetic variability of patients. Many genes have been investigated as potential predictors of response to biological drugs such as ADAM17, ATG16L1, EMSY, CASP9, CCNY, FASLG, FCGR, NOD2, PTGER4, IL13, IL1B, IL27, IL11, IL17F, TNF, and TNFR genes. In this review, we will gather the information on influence of gene polymorphisms investigated to date on response to biological drugs in CD patients.

INTRODUCTION

Crohn’s disease (CD) is a chronic condition which affects to the immune system. It can affect to any part of the digestive tract and be associated with external manifestations. Fistulas and/or stenosis are commonly developed, which are explained by the transmural nature and tendency to fibrosis of the disease. It is also characterized by cycles of active disease and remission periods (1).

According to a recent study, the incidence is higher in developed industrialized countries, such those in Europe and North America, where it reaches values of 12.7 to 20.2/100,000 (2). The prevalence is also increased in these countries, reaching values of 322-319/100,000 (2).

The causes of the disease remain unknown, although it seems to be the result of a combination of factors, such as genetic predisposition (mainly abnormalities in genes of the immune system), environment and lifestyle (hygiene, diet, sleep, stress, smoking habits...), medication (particularly non-steroidal anti-inflammatory drugs), and the composition of the microbiota, among others (3,4). Smoking is one of the risk factors associated with CD (OR:1.76; CI95%:1.4-2.22) (5); even passive smokers have shown increased risk develop this disease (6). Individuals from large families who have been breastfed and also exposed to farm animals from an early age have shown decreased CD risk, which is directly related to the composition of their microbiota (7). Patients with greater diversity in their microbiota are less predisposed to inflammatory bowel disease (IBD) and especially to CD. Many other factors such as hygiene, infections, antibiotic use have also been associated to CD (8-11). Appendectomy is another factor that has been associated with the onset of the disease after 20 years (12). In relation to diet, several studies corroborate that a fibre-rich, fat-low diet decreases the risk of CD, whereas fat-rich, vitamin D deficient diets are related to the appearance of IBD (13,14). CD family antecedents are present in 2-14% of CD patients; furthermore, the risk of IBD after the thirties increases in 1 out of 3 individuals when both parents are affected, showing a strong genetic influence (8). Among the genetic factors, there are DNA regions related to the immune system which have shown a high association with CD (9). A recent study in 75000 patients has identified 163 risk genes for CD (10). Some of the genes included in these regions are NOD2 (also known as CARD15), associated with a 20-40 fold increased risk in homozygous patients, and a 2-4 fold increase in heterozygotes (11,12); HLA, ATG16L1, IRGM and SLC11A1 (9,13). Other genes involved with the immune response which are associated with the onset of the disease are the NF-kB gene (14), interleukin genes IL1, IL6, IL23R (15), and CARD9 (13). Some, but not all of these genes have been investigated as potential biomarkers of outcomes in biological therapy for CD.

In this article, we will review the research studies conducted to date focused on the influence of gene polymorphisms on response to biological drugs in CD patients.
2.1 PHARMACOTHERAPY OF CROHN’S DISEASE

The severity of the disease needs to be assessed to define the treatment. The Crohn’s disease activity index (CDAI) quantifies the inflammatory activity and measures 8 variables, including 7 clinical and one analytical parameter (16). A greater CDAI score indicates higher severity of the disease. When CDAI>220 and CRP levels>10 mg/l are reached, it is considered as active disease. Remission is established when CDAI is less than 150, and response when CDAI decreases 100 points from baseline (17). Response to treatment is usually complemented with a questionnaire to the patient, the Inflammatory Bowel Disease Questionnaire (IBDQ), to assess their quality of life (18). The Harvey-Bradshaw Index (HBI) is a simple index of Crohn’s disease activity also used to quantify the symptoms of CD (19).

The CD treatment guidelines start from changing eating and smoking habits, as they have proven to be a factor for the occurrence and recurrence of the disease (15). The treatment protocol is then continued with corticosteroids such as prednisone, prednisolone and budesonide, or aminosalicylic acid (17). Complementation with immunomodulators (azathioprine and mercaptopurine), which are never used as monotherapy, is used when symptoms persist. Methotrexate is recommended when there is no response to the above treatments or they are contraindicated. When the disease becomes serious, the patient is switched to biological therapy with tumour necrosis factor inhibitors (anti-TNF), mainly adalimumab (ADA) and infliximab (IFX). And finally, when the disease is recurrent despite treatments, surgery is recommended (17). More recently, studies are also being carried out with other biological drugs, like cytokine inhibitors such as natalizumab, vedolizumab (20) and ustekinumab (21) for CD treatment. Other drugs have also been tested for CD therapy, but with less success, such as tofacitinib and abatacept (22,23). The pharmacogenetics of none of the latter has been studied.

2.1.1 Anti-TNF DRUGS

The anti-TNF drugs are recombinant human IgG1 antibody proteins, with similar functions but differently obtained. ADA is a protein obtained from recombinant DNA in mammalian cells(24), whereas IFX is a chimeric protein derived from mice(25).

2.1.2 Cytokine inhibitors

Several cytokine inhibitors have been tests in CD patients:

- Natalizumab: recombinant humanized anti-α4-integrin antibody produced on a murine cellular line by recombinant DNA technology (26).
- Vedolizumab: Humanized monoclonal antibody IgG type that binds to human α4β7 integrin and is produced in hamster ovary cell (27).
- Ustekinumab: monoclonal IgGκ anti-interleukin 12/23 human antibody, produced in a mouse myeloma cell line using recombinant DNA technology (28).

3 PHARMACOGENETICS

Pharmacogenetics studies the influence of variations in the DNA sequence on drug response (29). The use of biological drugs (ADA, IFX) as one of the lines of treatment for CD has greatly improved the outcomes, but has also showed a great variability in response among patients. Several studies have considered the possibility that these differences in response are caused by genetic variability of patients (30–33). In this regard, different lines of research carried out in recent years have tried to associate variants of ADAM17, ATG16L1, EMSY, CASP9, CCNY, CNTN5, Fas Ligand, FCGR, NOD2, NR1I2, PTGER4, IL13, IL1B, IL27, IL11, IL17F, TNF, TRAF3IP2 and TNFR genes with the response to treatment with biologics in CD. Some of them, like ATG16L1, NOD2...
have also been associated with CD and that prompted the interest in exploring their potential role in CD outcomes to biological therapies.

3.1.1 ADAM17

ADAM17 is a gene whose transcriptomic product leads to a protein that binds to the membrane and displays functions related to cell-cell biological processes and cell-matrix interactions. It is also involved in processes of muscle development, neurogenesis and fertilization. Furthermore, the proteins of the ADAM family are structurally related to snake venom disintegrins (34,35).

Several variants in ADAM17 gene (rs2001658, rs12469362, rs883399, rs1048610, rs2276338, rs1056204, rs10929587, rs1880439, rs10495565, rs4464248, rs11684747, rs10929590) were investigated in 222 Caucasian patients treated with IFX, including luminal and fistulizing cases (33). Remission was considered if CDAI was below 150 at week 4 for patients with luminal CD. For patients with fistulizing CD, remission was considered if they had complete absence of fistula drainage at week 10. A decrease of 70 points in CDAI from baseline at week 4 was considered response in luminal patients, while in fistulizing patients the definition of response was a decrease of 50% of the fistula drainage at two consecutive visits at week 10. Changes in CRP levels were evaluated at weeks 0, 4, 8 and 12. No association of the different haplotypes with remission or response to IFX was shown. However, the rs2001658TT, rs12469362CC, rs883399GG, rs1048610CC, rs2276338CC, rs10929587TT, rs10495565GG, rs4464248AA, rs11684747AA haplotype was significantly less frequent in the clinical non-responders (p=0.0027) (Table 1). Interestingly, all homozygous patients for this haplotype (n=16) presented clinical response according to a CDAI and also biological response according to CRP (40% relative reduction). The haplotype composed by rs12469362C, rs1056204C, rs10495565G and rs4464248A in homozygosis was significantly associated with response to IFX (nonadjusted P<0.002).

3.1.2 ATG16L1

The ATG16L1 gene is located on chromosome 2 and encodes a protein related to autophagy processes. It has been observed that defects in this gene can cause susceptibility to inflammatory bowel disease (36).

In order to investigate the influence on response to ADA of different single gene polymorphisms (SNP) associated to CD risk, 33 SNP in 31 genes were sequenced in 102 Slovak patients with CD (37). NOD2, IL23R, SLC22A5, SLC22A4, CTLA4, PTGER4, CASP9, IL27, EMSY, CCNY, IL13, NR1I2 were among the genes studied. Response was measured using the IBDQ and CRP levels at 4, 12, 20 and 30 weeks. The T-allele of the rs10210302 variant of the ATG16L1 gene showed the strongest association with response at 12 weeks (OR: 9.44, CI95%: 2.49-35.83, pc=0.027, p=8.11·10^-4), and was maintained after 20 weeks (p=4.5·10^-3) (Table 1 and 2). Patients carrying the T-allele also showed higher variation in CRP levels after 12 weeks (pc=0.059, p=1.79·10^-3) and 20 weeks (p=7.6·10^-4). Furthermore, patients with the TT genotype maintained the good response to ADA, according to IBDQ after 20 (p=4.61·10^-2) and 30 weeks of treatment (p=4.93·10^-2) (Tabla 2).

3.1.3 EMSY

This gene is also known as C11orf30, is located on chromosome 11 and its N-terminal domain is related to the BRCA2 protein, silencing the gene activation (38).

The CC genotype of the rs7927894 variant was associated with lower levels of CPR and a better IBDQ score in 102 Slovak patients with CD (37). In particular, the difference between the ADA response in CC patients was even greater at week 20, compared with those carrying the T allele (p=5.83·10^-3, pc=0.192) (Table 2).
3.1.4 CASP9

CASP9 gene, located on chromosome 1, encodes the caspase 9 protein, involved in the apoptosis signalling pathway. It belongs to the family of cysteine-aspartic proteases. CASP9 protein can be proteolysed and activated by the action of the apoptosisome (39,40).

The influence of several apoptosis-related genes (FASLG, FAS, TNFRSF10A, CASP3, CASP9, BAD, BCL2, BIRC5, MMP1, MMP3) on response to treatment was investigated in 287 CD patients (204 luminal/83 fistulizing) treated with IFX complemented with immunomodulators (azathioprine/mercaptopurine) (31). Total response was considered when CDAI reached a score of 150 or a decline of 70 points compared to initial CDAI; luminal CD response was measured after 4 weeks and fistulizing CD at week 10. The rs4645983 variant in CASP9 was associated to response only in patients with luminal CD (Table 1). Specifically, the TT genotype was associated with a better response (OR: 1.50, CI95%: 1.34-1.68, p=0.044). The good effect of the TT genotype on response to anti-TNF drugs was also recently shown in 102 CD Slovak patients treated with ADA (Table 2) (37). In fact, all responders at week 12 presented the TT genotype. However, this effect became non-significant after Bonferroni correction.

3.1.5 CCNY

This gene is known as cyclin Y and encodes a protein which regulates cell cycle and different transcription factors. One of their main functions is to activate the promoter of v-myc avian myelocytomatosis viral oncogene homolog (MYC) proto-oncogene, which promotes cell cycle progression and takes part in apoptosis and cellular transformation (41).

A recent study showed better response in patients carrying the CC-genotype of the rs12777960 variant of the CCNY gene in 102 Slovak CD patients treated with ADA for 4 weeks (OR:3.26, CI95%: 1.27-8.38, p=1.56·10-02, pc=0.515). An improvement in CRP levels was also showed after 12 and 20 weeks (p=6.78·10-3, pc=0.224) (Table 2) (37).

3.1.6 CNTN5

The CNTN5 gene is located on chromosome 11 and encodes a cell adhesion molecule (contactin 5), a member of the immunoglobulin superfamily, which mediates cell surface interactions during nervous system development. Alternative names for this gene are NB-2 and HNB-2s (42).

Gene polymorphisms rs1568885, rs1813443, and rs4411591 in CNTN5 have been recently investigated in a cohort of 126 Greek CD patients treated with IFX (43). Remission was established according to HBI, CRP levels and ileocolonoscopy at weeks 0, 12 and 20. The T-allele of rs1568885 variant was associated to lower response rate (TT: OR_{non-responder/good} 8.14, CI95%: 1.35-49.05, p=0.024; AT: OR:2.71, CI95%: 1.11-6.64, p=0.035; TT: OR_{non-responder/good} 21.37, CI95%: 2.73-167.2, p=0.007/ AT: OR: 4.75, CI95%: 1.26-17.9, p=0.032) (Table 1). The CC-genotype of the rs1813443 polymorphism was associated to poor response (OR_{non-responder/good} 6.13, CI95%: 1.74-21.63, p=0.005) and to non-response to IFX (OR_{non-responder/good}11.5, CI95%: 2.5-52.84, p=0.002). The rs4411591 variant did not showed association to drug response.

3.1.7 FASLG

FASLG, located on chromosome 1, encodes the Fas ligand, a transmembrane protein which binds the FAS receptor to induce apoptosis. Its function is closely related to the regulation of the immune system (44,45).

Twenty-one gene polymorphisms in several genes involved in the apoptotic process (FASLG, FAS, TNFRSF10A, CASP3, CASP9, BAD, BCLXI, API4, MMP1, MMP3) were investigated in a cohort of 287 CD patients treated with IFX (204 refractory luminal and 83 fistulizing) (31). Total response was considered for patients with CDAI score of 150 or a decrease of 70 units from the baseline value, and was evaluated at 4 weeks for luminal patients and at 10 weeks for fistulising cases. Remission in fistulising patients was defined as disappearance of open fistulas, and moderate
response when open fistules drainage had reduced less than 50%. The C-allele of the rs763110 variant of the FASLG gene was associated to better response to IFX in both luminal and fistulising patients (luminal: OR:0.11, CI95%:0.08-0.56, p=0.002; fistulising: OR:1.66, CI95%: 1.21-2.29, p=0.02) (Table 1). However, the C-allele has also been associated to a higher risk of hypersensitivity reactions to IFX in 126 CD patients (OR: 4.0, CI95%: 1.1-22.4, p=0.041) (46). This study also investigated the effect of rs75622480 and rs5030772 polymorphisms in FASLG, failing to find any association to response to IFX.

3.1.8 **FCGR3A**

*FCGR3A* gene, also known as *FCγRIIIA*, encodes a protein related to the immune system, specifically with the antibody dependent response (47). It is located on chromosome 1 and has different variants. Specifically, the T>G substitution at rs396991 (F158V) gene polymorphism corresponds to the change of the aminoacid phenylalanine (F) by valine (V) at position 175 of the protein. F presents low affinity for IgG, whereas V shows high affinity (48).

The high affinity variant (VV) of the F158V polymorphism was associated with a better response to IFX in a cohort of 344 CD patients (Table 1) (49). Patients with baseline CRP values within the two highest quartiles (n=156) carrying the VV genotype showed a trend toward a greater relative change in CRP at week 6 (p=0.085, one-tailed p=0.043). This effect of the VV genotype on CRP improvement was further confirmed in a cohort of 102 Japanese CD patients (Table 1) (50). Response was evaluated according to CDAI and CPR levels at 8 and 30 weeks. The VV genotype was associated to CPR improvement at week 8 (p=0.044), but the effect was not significant after 30 weeks. This study also investigated the potential influence of other polymorphisms in FCGR3A gene (FCGR3A-159, FCGR3A-160), but no associations were found (50).

Other studies with smaller samples (106 and 189 patients) have failed to find an effect of F158V variant on response to IFX in CD patients (51,52).

3.1.9 **NOD2**

The *NOD2* gene encodes the caspase recruitment domain-containing protein 15 (CARD15) or inflammatory bowel disease protein 1 (IBD1). Its main function is to activate NFKB protein in bacterial infections, by recognizing the muramyl dipeptide moiety (53,54). It has also been related to CD susceptibility (55).

The association of *NOD2* variants (rs2066844 or R702W, rs2066845 or G908R and rs2066847 L1007Profs) with relapse after IFX treatment was investigated in 14 CD patients, with no effect observed (56). In consonance with this, these variants did not influence response to ADA either in 102 Slovak CD patients treated (according to IBDQ and CRP levels measured at 4, 12, 20 and 30 weeks) (37) or 16 CD patients (evaluated by CDAI after 52 weeks) (57). Remission after IFX treatment was not associated either to NOD2 polymorphisms (G881R, G908R, R675W, R702W, 980fs, 3020insC) in 534 patients with active CD (Table 1 and 2) (58).

3.1.10 **NR1I2**

The *NR1I2* gene is located in chromosome 3 and encodes a protein which belongs to the superfamily of nuclear receptors, whose main function is to bind response elements, as receptor X retinone (RXR), to regulate CYP3A4 transcription (59,60). The GG genotype in rs3814057 polymorphism of NR1I2 gene showed a trend to good long-term response to ADA (p=9.64·10⁻³, pcorr=0.318) in 102 Slovak CD patients, but the statistical significance was lost after multiple comparison correction (Table 2) (37).

3.1.11 **PTGER4**

*PTGER4* gene, located in chromosome 5, encodes a prostaglandin receptor which belongs to the G-protein coupled receptor family and is one of four receptors identified for prostaglandin E2. It acts by activating signalling factors of T cells (61).
The GG genotype of the PTGER4 rs10512734 variant has showed a trend to short-term response in 102 Slovak CD patients (week 12: p=4.62·10^{-3}, pcorr=0.152) (Table 2) (37).

3.1.12 TRAF3IP2

Located in the chromosome 6, the protein encoded by this gene is involved in the process of regulating the immune system in response to pathogens, inflammatory and stress signals. Specifically, it regulates cytokine response to Rel/NF-kappaB transcription factors (62,63).

The association of several variants of this gene (rs10872070, rs6941014, rs1883136, rs1040383, rs9374263, rs2075966) with response to IFX was studied in 113 Japanese CD patients. Only the rs1883136 polymorphism was associated with response to IFX after 1 year of treatment, showing a lower frequency of the AA genotype (recessive model) in responders (OR_{AA}: 0.213, CI95%: 0.053-0.860, p=0.041)(Table 1)(64).

3.1.13 IL11

The protein encoding this gene is interleukin 11, whose main function is to stimulate the development of T cell dependent immunoglobulin produced by B lymphocytes. It belongs to the gp130 family of cytokines, with the role of assembling the receptors subunits contained in the IL6ST transmembrane signalling molecule (gp130) (65).

The influence of rs116760 and rs1042506 polymorphisms in IL11 gene on response to IFX were investigated in 350 patients (Table 3) (66). Response criteria were established as HBI<4 for luminal CD and 100% fistulae healing for fistulising CD patients; partial responders were defined as HBI<3 and >50% reduction in fistulae, respectively. The rs1126760_C y rs1042506_T haplotype was associated with better response to IFX (OR: 1.72, 95%CI: 0.91-3.21, p=0.068) (66).

3.1.14 IL13

IL13 gene is located in chromosome 5, and encodes a cytokine mainly involved in immune processes. Its transcription is activated by Th2 cells, and leads to the activation of IgG4 and IgE synthesis in B cells (67).

The AA genotype of the rs1295686 variant of IL13 gene was associated to long-term response (over week 20) to ADA (Table 2), according to IBDQ values in 102 Slovak CD patients (p=6.07·10^{-1}, pc=0.2) (37). Patients with AA genotype improved IBDQ at week 30 compared to patients with the G allele (p=1.84·10^{-2}, pc=0.607).

3.1.15 IL27

The IL27 gene is located on chromosome 16 and encodes one of the subunits of a heterodimeric cytokine which participates in protection against virus, by promoting proliferation of naive CD4+ T cells (68).

The rs8049439 variant of IL27 gene was found to be associated with response to ADA after 4 weeks, according to IBDQ and CRP in 102 CD patients. The T-allele was more frequent among responders, compared with the CC genotype (OR: 9.67, CI95%: 1.65, 56.22, p=9.71·10^{-3}, pc=0.320); increased CRP was higher in patients with TT genotype compared to CC patients (p=1.61·10^{-3}, pc=0.531). Regarding IBDQ, the T-allele also presented a trend to better response (p=2.96·10^{-2}, pc=0.977) (Table 2) (37).

3.1.16 IL17F

IL17F gene is located on chromosome 6, and its protein product is involved in the defence against pathogens, since it is expressed in the mucosa and epithelial barrier. It is also expressed in CD4+ T lymphocytes and monocytes activated, and works as a recruiter of leukocytes (neutrophils), promoting granulopoiesis and inducing inflammation by activating cytokines like IL6, IL8, IL2 and GSF2/GM-CSF (69,70).
The association of different variants of this gene (rs763780, rs766748, rs12201582, rs9382084, rs722323, rs1266828, rs2294934) with response was studied in 113 Japanese CD patients treated with IFX (Table 3). Response was defined as decrease in CDAI less than 150, while no changes in CDAI or exacerbation of disease activity was categorized as non-response. Among the different polymorphisms studied, only rs766748 was associated with response after a year of treatment. In particular, the dominant model for the A-allele was less frequent among responders (OR:0.203, p=0.019) (64). This study also included different polymorphisms of genes related to IL17 as were IL17A (rs4711998, rs8193036, rs3819024, rs2275913, rs3819025), IL17RA (rs2270241, rs2241042, rs5748863, rs5748864, rs2241049, rs2229151, rs2895332), IL17R (rs7627880, rs279545). None of these polymorphisms showed association with response to IFX.

3.1.17 TNF/TNFR

The main function of the tumour necrosis factor (TNF) gene is to promote immune response and processes involved in inflammation, differentiation, proliferation, apoptosis and coagulation. It is located in chromosome 6. The superfamily of TNF receptors (TNFRSF10A, TNFR1, TNFR2 and TNFRSF1B), important for the proper functioning of the immune system, are also related with this gene (71). Mutations in these genes are strongly related with autoimmune diseases (32,72,73).

The extensive study of TNF gene has yielded many polymorphisms potentially associated to response to biological therapy in CD patients, among them rs1799724, rs1799964, rs1800629, and rs361520 (Table 4).

3.1.17.1 TNF-238

The variant in position -238 of the promoter region of the TNF gene (rs361525) did not show influence on response to IFX in 106 Greek CD patients after 20 weeks (51). Song et al. recently investigated the influence of several TNF gene polymorphisms on response to biological therapy, especially anti-TNF, in patients with different autoimmune diseases (psoriasis, ankylosing spondylitis and CD) in a meta-analysis which included 16 studies (including 7 in CD patients) and 983 (452 with CD) patients (72). The G variant was associated to good response to treatment in the overall population (OR:2.208, CI95%:1.197-4.074, p=0.011), particularly for Caucasian patients (OR:2.196, CI95%:1.161-4.154). However, the stratification by disease did not show association of this polymorphism with response.

3.1.17.2 TNF-308

A study with 23 CD patients treated with IFX showed a high number of A carriers of the TNF-308 (rs1800629) variant in the nonresponding group (74). The influence of this SNP on response to anti-TNF was also investigated in the recent meta-analysis by Song et al., showing the rs1800629G variant was associated to response in the overall population with different autoimmune diseases (OR:1.388, CI95%:1.388-2.150, p=0.000012) and in Caucasians (OR:2.005, CI95%:1.417-2.38, p=0.000086), but not Asians. This effect was also evident in the 496 CD patients (OR:1.508, CI95%:0.973-2.338, p=0.066) from 8 studies and in spondylitis patients (72).

3.1.17.3 TNF-857

The -857 variant (rs1799724), located in the promoter region of TNF gene, was also investigated in the recent meta-analysis by Song et al. (72). The C-allele was associated with good response to anti-TNF in the overall population (OR:1.889, CI95%:1.245-2.866, p=0.003), particularly in Caucasian patients (OR:1.779, CI95%:1.319-3.790, p=0.03). The stratification by disease failed to confirm this association individually.
3.1.17.4 TNFRSF1A

The TNFRSF1A, also known as TNFR1, located in chromosome 12, encodes the 1A member from the TNF superfamily of receptors. It is activated after NF-κB binding, promoting apoptosis (75,76).

A recent study has investigated the role of two polymorphisms in TNFRSF1A (rs767455 and rs4149570) on response to IFX in 80 CD patients, according to HBI index (32). The rs4149570 polymorphism did not show any influence on response to IFX, but patients carrying the G-allele of rs767455 variant experienced reduced effectiveness of IFX, compared to AA patients (OR:0.37, CI95%: 0.11-0.82), and this association remained after adjust by clinical and sociodemographic variables, such as age, sex, disease location and life-style (OR:0.26, CI95%: 0.08-0.9). In consonance with this, a recent meta-analysis in autoimmune diseases (including 2 studies compiling 377 CD patients) has found a trend of the A-allele to better response to anti-TNF therapy (Table 4)(73).

The G-allele of the A36G (Pro12Pro) variant has been associated with lower response to IFX in 344 CD patients, defined as CDAI decrease to 70 points or normalized CDAI in 150 points (OR: 0.47, CI95%:0.234-0.946, p=0.0343), although biological response (CRP) was not associated (Table 4) (77).

Other polymorphisms in TNFRSF1A (rs4149584, rs4149570, and rs4149569) have showed no effect on response or adverse reactions in 126 CD patients treated with IFX (Table 4) (46).

3.1.17.5 TNFRSF1B

The TNFRSF1B, also known as TNFR2, is located in chromosome 1, encodes the 1b member from the TNF superfamily of receptors, whose function is to recruit anti-apoptotic proteins c-IAP1 and c-IAP2 (75).

The rs1061624A/rs3397T haplotype has been associated with worse response to IFX, according to HBI index, in 297 Spanish CD patients (OR:1.78, CI95%: 1.09-2.9, p=0.015)(78) and 80 Japanese CD patients (p=0.01) (32). In the Spanish study, the rs1061624A variant was also more frequent in non-responders (OR:1.63, CI95%:1.05-2.51, p=0.02), and the CC-genotype of the rs3397 variant was associated with better response rates (OR:3.19, CI95%:0.95-16.78, p=0.05) (Table 4) (78).

The effect of three variants in TNFRSF1B gene (rs976881, rs1061622, rs652625) on response to IFX after 12 weeks, measured according to HBI index, was evaluated in 126 CD patients (46). The T-allele of the rs652625 variant was related to a decreased risk of adverse reactions to IFX (OR:0.2, p=0.043), whereas the GG genotype of rs976881 variant and the G-allele of rs1061622 polymorphism were associated to better response (OR:3.3, CI95%:1.2-9.1, p=0.014; OR:5.5, CI95%:1.5-25.5, p=0.007, respectively) (46). Although other studies have not found the rs1061622 variant associated with response (32), the good effect of rs1061622G allele of TNFRSF1B gene has been recently confirmed in a meta-analysis including 1062 patients (377 with CD) from 8 studies in different autoimmune diseases (psoriasis, rheumatoid arthritis and CD), showing the T-allele associated to no response in the overall population (OR:0.72, CI95%: 0.57-0.93, p=0.087) (73). The stratification by disease only confirmed the effect on rheumatoid arthritis and psoriasis, but not in CD, probably due only 2 studies were included. The rs1061624 polymorphism was associated with worse/absence of response in the heterozygote (AG vs GG: OR: 2.54, CI95%:1.30-4.96, p=0.007) and dominant models (AA/AG vs GG: OR: 2.07, CI95%: 1.10-3.93, p=0.025) in the meta-analysis (73). The rs3397 was also associated with non-response in the heterozygote model (OR_{tt} vs TT: 1.17, CI95%:0.68-2.02, p=0.026). These associations were lost after stratification by disease. The rs1061622 (T587G) polymorphism in the TNFRSF1B gene did not show any influence on response to IFX in 344 CD patients, according to CDAI improvement and CPR levels (Table 4) (77).
3.1.17.6 TNFAIP6

The TNFAIP6 gene encodes a protein involved in the stability of the extracellular matrix and cell migration. Proteins which develop this type of function are characterized by secreting properties and present a hyaluron binding domain (79–81).

The association of different variants of this gene (rs11677200, rs2342910, rs3755480, rs10432475) with response to IFX was studied in 350 CD patients (66). The rs11677200_C/rs2342910_A/rs3755480A/rs10432475A haplotype showed a trend to better response to IFX (OR: 0.71; 95%CI: 0.46-1.09; p=0.10) (Table 4).

3.1.18 Other genes

During the last decade, the influence of other genes on response to biological therapy in patients with CD has also been investigated, although with poor results. Some of these genes are CD14, TLRA, MDR1, ABCG2, LTA, CRP, mainly related to the immune response or the onset of the disease. Genes related with calcium canals like S100A9, S100A12, S100A8, and surviving promoters have also been investigated. No influence of any of these genes was found with response to treatment in CD.

In some studies, the small sample size may have provoked the lack of association. CD14 (rs2569190) and TLRA (rs4986790) polymorphisms showed no effect on response to IFX or ADA in 24 Spanish CD patients after 52 weeks (57). ABCB1 (rs2032582 and rs1045642) and ABCG2 (rs2231137 and rs1131142) polymorphisms were investigated in 47 CD patients treated with IFX, but no significant associations with response were observed. The IBD5 locus includes the IGR variants IGR2060a_1G>C (rs20522057) and IGR3081a_1T>G (82), whose potential association with remission (CDAI<150) vs relapses after IFX discontinuation was investigated in 14 CD patients (56). Relapse after treatment was defined as loss of IFX-induced remission (CDAI>220), or evidence of active CD in patients who discontinued IFX. No association was found, probably due to the small size of the sample. The predictive value of the IL1B rs1143634 variant in IFX response was investigated in 29 CD and 18 ulcerative colitis patients. CRP and ESR levels were estimated after 3, 6 and 12 months. Response was considered when the improvement in CDAI was over 70 points, compared to baseline (Table 3) (83). In this case, despite of the small size sample, the C-allele was associated to poorer clinical remission after 14 weeks of treatment (p=0.027) and also showed a trend to worse response (p=0.051).

Several LTA gene polymorphisms (rs909253, rs2857713, rs875327, rs1041981, rs746868, 3093543) were investigated in a group of 264 patients with CD treated with IFX for 12 weeks (84). No association with response to IFX was found, not even after considering the potential influence of combined haplotypes.

Like in the above examples, the association of different polymorphisms in CRP gene (-717G/A, +1444C/T, 4A/G) with the response to treatment IFX (CDAI, CRP) could not be demonstrated in 189 CD patients (52).

Several variants in genes related to calcium channels, like S100A9 (rs11205276, rs30141866), S100A12 (rs724781), S100A8 (rs3006488) were investigated as possible predictors of response to IFX in 350 CD patients (66). The S100A9 (rs11205276_G, rs3014866_C) and S100A8 (rs724781_C, rs3006488_A) haplotypes were associated with non-response (OR: 1.54, 95%CI: 0.97, 2.43; p=0.05). The same study also explored the influence of polymorphisms in the GOS2 gene (rs4844486, rs2342910, rs3755480, rs10432475), which showed a trend to worse response in patients carrying the rs4844486_A/rs14733683_T haplotype (OR: 0.15; 95%CI: 0.45,15.23; p=0.15) (66).

Polymorphisms in surviving promoters (-625 G/C, -241 T/C, -31 C/T) have been investigated in a cohort of 97 Greek CD patients, but no influence on IFX was observed (85).
Other genes involved in apoptosis (BAD, BCLXI, API4, MMP1, MMP3) were investigated in 287 CD patients treated with IFX, but none of them showed association with response (86).

4 CONCLUSIONS

In the past decades, a great effort has been done to find pharmacogenetic biomarkers capable to predict the response to biologic therapy in CD patients. Many genes have been explored, and despite some polymorphisms emerged with a great potential, particularly in members of the TNF family, the overall results are poor and no good predictive biomarkers for IFX or ADA response have been established. Although some of these biomarkers have showed influence on response to biologic therapy in other inflammatory diseases, their effect in CD patients is not clearly demonstrated. The cause of this lack of association may be the small size of the studies undertaken, even the meta-analyses, and the few studies available for each gene. Therefore, a more thorough investigation of the pharmacogenetics of CD therapy is still needed, employing more comprehensive sets of genes or even large-scale unbiased studies, in large cohorts of patients, as a better approach to identify better biomarkers for CD pharmacotherapy.

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6 REFERENCES


