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## **4.2. ESTUDIO 2**

### **ANTICUERPOS ANTICITOPLASMA DE NEUTROFILO EN FAMILIARES DE PACIENTES CON ENFERMEDAD INFLAMATORIA INTESTINAL.**

# Antineutrophil Cytoplasmic Antibodies in Relatives of Patients with Inflammatory Bowel Disease

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**Background:** The occurrence of antineutrophil cytoplasmic antibodies (ANCA) has been reported more frequently than expected in healthy first-degree relatives of patients with ulcerative colitis, suggesting that these antibodies may represent a subclinical marker of genetic disease susceptibility. **Aim:** To determine the prevalence of ANCA in unaffected first-degree relatives of inflammatory bowel disease patients in a Spanish population. **Methods:** Three hundred and seventy sera obtained from 80 patients with inflammatory bowel disease (55 ulcerative colitis, 25 Crohn's disease), 217 unaffected first-degree relatives (157 from ulcerative colitis and 60 from Crohn's disease patients), 62 healthy controls, and 11 celiac disease patients were tested using an indirect immunofluorescence assay. **Results:** Antibodies were detected in 64% of patients with ulcerative colitis but in only 12.5% of patients with Crohn's disease. ANCA were seldom present in their unaffected first-degree relatives (4.6%), control subjects (1.6%), and celiac disease patients (0%). **Conclusions:** In the Spanish population studied, antineutrophil cytoplasmic antibodies occur more commonly in ulcerative colitis than in Crohn's disease, as reported in other Caucasian populations. Moreover, their presence is not increased in their first-degree relatives. These findings indicate that ANCA are not a subclinical marker of genetic susceptibility to inflammatory bowel disease in this population.

## INTRODUCTION

The etiopathogenesis of the chronic inflammatory bowel diseases (IBD), ulcerative colitis (UC) and Crohn's disease (CD), remains poorly understood. The most comprehensive theory proposed is that the disease occurs in a genetically susceptible subject, as a result of the interaction between environmental agents and host immunological responses (1).

Evidence for genetic predisposition is strongly supported by epidemiological and genetic studies showing ethnic differences in disease frequency, familial aggregation, increased monozygotic twin concordance, and different HLA associations for UC and CD (2).

Antineutrophil cytoplasmic antibodies (ANCA) directed against the cytoplasmic components of neutrophil granules were first described as an important marker in patients with Wegener's granulomatosis and other forms of vasculitis (3–5). Their clinical relevance has been well established in the diagnosis and management of the vasculitic syndromes (6). More recently, the occurrence of a subset of ANCA has been recognized in the sera of patients with IBD. The reported frequency of ANCA in patients with UC varies from 23 to 88%. In CD, ANCA have been detected much less frequently, with a prevalence of 0–25% and usually in low titers (7–15). In contrast to the vasculitides, however, the potential clinical significance of ANCA in IBD is still unclear. Currently available evidence indicates that they are not directly involved in its pathogenesis. On the other hand, their high degree of specificity for ulcerative colitis in comparison with other colitides, lack of correlation with disease extent and severity, and persistence after colectomy, suggests that they are not simply an epiphénomène related to active colonic inflammation. Rather, they may reflect an underlying immunoregulatory disturbance in a subgroup of UC patients.

For the last few years, a higher frequency of ANCA has been reported in unaffected family members of patients with UC than in control subjects (16, 17). These findings raised the question of whether such antibodies may represent a subclinical marker of genetic susceptibility to UC. This increased prevalence, however, has not been confirmed by other studies (18–21). The discrepancy between the various reports may reflect population and ethnic differences in the patients studied. In the present study we have evaluated the frequency of ANCA in first-degree family members of patients with IBD in a well-defined Spanish population.

Received Dec. 21, 1995; accepted Mar. 19, 1996.

### Study population

Serum samples obtained from patients with IBD, their first-degree relatives, and controls were coded and stored at -70°C until assayed.

All patients, family members, and controls analyzed in the present report are Caucasians, and were born and live in the same geographic area (province of Tarragona, Catalonia).

### IBD patients

Eighty patients with IBD attending the Gastroenterology Section and the Department of Internal Medicine of two participating medical centers were included in the study. All patients were well known to the investigators, their diagnosis having been established based on conventional clinicopathological criteria according to those described by Lennard-Jones (22). There were 55 patients with UC (25 men, 30 women; 40 yr mean age) and 25 patients with CD (8 men, 17 women; 31 yr mean age). The main clinical features of the patients studied are shown in Table 1.

### First-degree relatives of patients with IBD

One hundred fifty-seven first-degree relatives of patients with UC ranging in age from 13 to 78 yr (mean 39.5) were tested for ANCA. There were 51 parents (30 women and 21 men), 19 brothers, 39 sisters, and 48 children (27 daughters and 21 sons). The group of first-degree relatives of patients with CD consisted of 60 subjects ranging in age from 15 to 73 (mean 42). There were 10 fathers, 19 mothers, 10 brothers, 13 sisters, 7 sons, and 1 daughter.

At the time of the blood collection, relatives were interviewed and a detailed medical history was obtained to yield information concerning any significant gastrointestinal symptom or extraintestinal manifestation that may relate to as-yet-undiagnosed IBD. Five relatives were found to have IBD and were not included in the study population.

### Control subjects

As controls, we examined sera from 40 healthy blood donors (25 men, 15 women, 35 yr mean age) without any history of gastrointestinal disease, nor family members affected with IBD. We also investigated 22 healthy spouses of patients with IBD (20 UC, 2 CD; 14 men, 8 women; 45 yr mean age) as environmental controls, and 11 patients with celiac disease.

### Indirect immunofluorescence assay

A standard indirect immunofluorescence (IIF) method was used for detection of ANCA (23). Sera were diluted 1:20 in phosphate-buffered saline (PBS), and approximately 35 µL of the diluted sera was placed onto test wells on glass slides containing ethanol-fixed neutrophils as antigen sub-

TABLE I  
*Clinical Characteristics of Patients with Inflammatory Bowel Disease at the Time of Serum Sampling*

| Features             | Ulcerative Colitis | Crohn's Disease |
|----------------------|--------------------|-----------------|
| Number               | 55                 | 25              |
| Gender (Male/Female) | 25/30              | 8/17            |
| Mean age, yr (range) | 40 (18-76)         | 31 (17-61)      |
| Disease location     |                    |                 |
| Proctitis            | 6 (10.9%)          | —               |
| Proctosigmoiditis    | 16 (29.1%)         | —               |
| Left-sided colitis   | 14 (25.4%)         | —               |
| Extensive colitis    | 4 (7.3%)           | —               |
| Total colitis        | 10 (18%)           | —               |
| Small bowel          | —                  | 6 (24%)         |
| Ileocolic            | —                  | 6 (24%)         |
| Colonic              | —                  | 10 (40%)        |
| Postresection        | 5 <sup>a</sup>     | 3 <sup>b</sup>  |
| Disease activity     |                    |                 |
| Activity             | 19 (38%)           | 8 (36%)         |
| Remission            | 31 (62%)           | 14 (64%)        |
| Medication           |                    |                 |
| Steroids             | 10                 | 7               |
| Azathioprine         | 3                  | 4               |

<sup>a</sup> 3 ileostomy, 2 ileoanal anastomosis.

<sup>b</sup> 3 ileocolic anastomosis.

state (INOVA Diagnostics, San Diego, CA). All incubations were performed in humidified boxes at room temperature for 30 min. The slides were then washed with three changes of PBS for 5 min each. After a 30-min incubation period with anti-human IgG conjugated to fluorescein with Evans blue counterstain (INOVA Diagnostics), they were washed again as above, mounted under a coverslip with PBS-glycerin, and finally examined with a fluorescent microscope. Positive and negative controls were included for all assays. The slides were analyzed in a blinded fashion, and perinuclear or cytoplasmic immunofluorescence staining pattern was regarded as positive. All positive results and 20 negative results randomly selected were retested in another laboratory (Laboratory of Nephrology, Hospital Clinic i Provincial of Barcelona) following the same IIF test procedure by another investigator. Only sera with positive test results in both laboratories were regarded as positive in the final results. Sera with different results between the two laboratories were excluded from the final analysis.

Sera that produced a nuclear or equivocal perinuclear ANCA staining pattern in neutrophils were tested for the presence of antinuclear antibodies (ANA) using commercially prepared slides with fixed HEp2 cells as substrate (INOVA Diagnostics).

### Statistical analysis

Statistical comparisons of prevalence of ANCA in the study groups were performed by the chi-square test. To measure the correlation of tests performed in the two different laboratories, Cohen's kappa coefficient was used.

| Diagnosis                             | n   | ANCA Positive (n) (%) |
|---------------------------------------|-----|-----------------------|
| Ulcerative colitis                    | 53  | 34 (64)*              |
| Crohn's disease                       | 24  | 3 (12.5)              |
| First-degree relatives of UC patients | 155 | 6 (3.9)**             |
| First-degree relatives of CD patients | 60  | 4 (6.7)**             |
| Healthy controls                      | 40  | 1 (2.5)               |
| Spouses of IBD patients               | 22  | 0                     |
| Celiac disease                        | 11  | 0                     |

\* p < 0.0001 vs all other groups.

\*\* p NS vs healthy controls.

## RESULTS

### Interlaboratory correlation of the immunofluorescence test

Results of the sera (n = 72) tested in the two laboratories were as follows. Forty-seven sera tested ANCA positive and 20 tested ANCA negative in both laboratories. Only five sera tested different results. Thus, a high degree of correlation was found between the two laboratories (kappa score = 0.84; p < 0.001).

### Prevalence of ANCA in IBD patients

Thirty-four of 53 (64%) UC patients showed the presence of circulating ANCA. Perinuclear staining around neutrophil nuclei was the predominant IIF pattern observed (76.5%), similar to the proportion described in previous reports. In addition, a homogeneous cytoplasmic staining was given by eight sera. There was no correlation between ANCA positivity and duration, course, extent, and activity of the disease (data not shown). In CD, ANCA were detected in 3 of 24 patients (12.5%). Two patients had the disease confined to the colon and the other to the ileum.

### Prevalence of ANCA in first-degree relatives

Of the unaffected first-degree relatives of patients with UC studied, only 6 sera of 155 (3.9%) tested ANCA positive. Four of the 60 (6.7%) relatives of patients with CD were ANCA positive. All of these 10 positive ANCA relatives belonged to different families. Among them, one had seropositive rheumatoid arthritis and another ankylosing spondylitis, conditions known to exhibit ANCA. Table 2 summarizes the results.

### Control subjects

Only one of the 40 healthy controls tested ANCA positive. ANCA were not detected in any of the 22 spouses of patients with IBD, nor in the 11 patients with celiac disease.

### Antinuclear antibodies

Three patients with UC and one patient with CD had an equivocal ANCA or diffuse nuclear immunofluorescence staining of all leukocyte nuclei in ethanol-fixed human

neutrophils. In all cases they were found to be positive for ANA when tested on HEp2 cells. A total of 9 sera among 11 of family members assessed were positive for ANA.

## DISCUSSION

In recent years it has been firmly established that ANCA are often present in patients with UC but not in other IBDs, including CD (7–15). The results from the present study are within the limits of most previous reports. Thirty-four of 53 UC patients (64%) were ANCA positive compared with only 3 of 24 patients with CD (12.5%). Additionally, we did not detect an increased prevalence of ANCA in the unaffected first-degree relatives of IBD patients compared with healthy controls.

A familial predisposition to IBD is now widely recognized; the risk of developing the disease in family members is increased approximately 10-fold (24). At the present time, however, no subclinical markers are available to identify those at risk of developing the disease; studies of lymphocytotoxic antibodies, antibodies to colonic epithelial cells, colonic mucins, mucosal immunoglobulins, intestinal permeability, and complement system have not shown any consistent pattern (2). The role of ANCA as a potential subclinical marker of genetic predisposition to UC was first suggested by the finding of an increased prevalence of ANCA in the unaffected family members of patients with UC from two North American patient populations. The authors reported the presence of ANCA in 14 of 93 (15%) first-degree relatives to 38 UC patients in Los Angeles and in 9 of 43 (21%) first-degree relatives to 22 UC patients in Calgary, Canada (16). This observation was strengthened by a German study in which ANCA were detected in 30% of 142 first-degree relatives of patients with UC (17). In contrast to the American and German reports, however, four other studies from France, Italy, and England failed to detect a higher frequency of ANCA in the sera of relatives of IBD patients (18–21). In addition, Yang *et al.* have recently reported that ANCA were not significantly increased in healthy monozygotic twin siblings to twins with UC, thus arguing against the hypothesis of ANCA as a subclinical marker of genetic susceptibility to UC (25).

It is uncertain why our results are in agreement with the latter studies but differ from those of the North American and German ones. It has been suggested that the different methods used for the detection of ANCA may explain in part these substantial differences. The whole cell ELISA method used by Shanahan *et al.* (16) has provided in most studies a higher sensitivity but lower specificity than the IIF test. Thus, the ELISA test might detect antineutrophil cytoplasmic antibodies other than those responsible for ANCA in UC. On the other hand, although subjective in interpretation, IIF results are more reproducible and correlate well in independent laboratories as shown by Oudkerk Pool *et al.* (12, 13) and our own study. Of note, the American investigators used IIF to verify every positive ELISA result, and

ISBN Seibold et al. (17) applied the same IIF method performed in the other European studies. Thus, these differences are unlikely to be entirely caused by technical variations. So far, the nature of the antigen(s) to which ANCA react in UC remain unknown. It seems likely that their identification will allow the development of more specific assays to overcome these methodological problems.

Another explanation for the divergent results among unaffected relatives may be related to variability in different populations and ethnic groups. In fact, the reported frequency of positivity of ANCA in UC patients varies widely in several different study populations. Positivity is more than 70% in North America (7, 8), 70% in Germany (10), but only 50% in France (9), 50% in England (11), and 40% in Australia (15). Here again, differences could be caused by the use of different detection methods as alluded to earlier. Nevertheless, studies performing simultaneous analysis of samples from distinct populations in different laboratories have confirmed significant regional differences, thus suggesting genetic differences between these populations (13, 17). Similarly, such variability may occur not only in probands, but also in relatives in different geographic areas.

In summary, we have not found an increased prevalence of ANCA among the unaffected first-degree relatives of patients with IBD compared with healthy controls. Therefore, our results indicate that, at least in our population, ANCA do not represent a subclinical marker of genetic susceptibility to IBD.

#### ACKNOWLEDGMENTS

We thank Ms. Marta Targa and Ms. Montse Gandul for their great collaboration in the performance of this study.

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### **4.3. ESTUDIO 3**

**HETEROGENEIDAD GENETICA EN LA COLITIS  
ULCEROZA DETERMINADA POR UN POLIMORFISMO  
GENETICO DEL ANTAGONISTA DEL RECEPTOR DE LA  
INTERLEUCINA 1 Y ANTICUERPOS ANTICITOPLASMA  
DE NEUTROFILO.**

# Genetic heterogeneity within ulcerative colitis determined by an interleukin-1 receptor antagonist gene polymorphism and antineutrophil cytoplasmic antibodies

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**Background** Although there is strong evidence implicating genetic predisposition in the pathogenesis of the chronic inflammatory bowel diseases, the number and identity of susceptibility genes remain uncertain. Cytokine genes are tentative candidate loci, but data regarding association studies in different populations are conflicting.

**Aims** To determine potential associations of interleukin-1 receptor antagonist (IL-1ra), tumour necrosis factor  $\alpha$  (TNF $\alpha$ ), and tumour necrosis factor  $\beta$  (TNF $\beta$ ) gene polymorphisms with ulcerative colitis or subsets of ulcerative colitis in a Spanish population.

**Methods** Genotyping for IL-1ra, TNF $\alpha$  and TNF $\beta$  gene polymorphisms was performed by the polymerase chain reaction in 95 patients with ulcerative colitis and 74 healthy controls. A variable number of tandem repeats (VNTR) in the IL-1ra gene, and a single base pair polymorphism in the TNF $\alpha$  gene promoter region (-308) and in the first intron of the TNF $\beta$  gene were analysed. Anti-neutrophil cytoplasmic antibodies (ANCA) were detected using an indirect immunofluorescence assay.

**Results** There were no significant differences between ulcerative colitis patients and controls in either polymorphism analysed, nor between ulcerative colitis subgroups as a function of the clinical disease pattern. However, when stratified by their ANCA status, perinuclear ANCA (p-ANCA) ulcerative colitis showed an increased frequency of the genotype 1,2 of the IL-1ra gene compared with ANCA-negative ulcerative colitis (52% versus 28%;

$P = 0.02$ ,  $P_{corr} = 0.1$ ). Furthermore, p-ANCA ulcerative colitis had a statistically significant increase of this genotype compared with cytoplasmic ANCA (c-ANCA)/ANCA-negative ulcerative colitis (52% versus 26.5%;  $P = 0.01$ ,  $P_{corr} = 0.05$ ).

**Conclusions** In the Spanish population studied, the polymorphisms analysed in the IL-1ra, TNF $\alpha$  and TNF $\beta$  genes are unlikely to be important in the overall susceptibility to ulcerative colitis. However, the combination of a subclinical (p-ANCA) and a genetic (IL-1ra gene) marker identified a distinct ulcerative colitis subgroup (p-ANCA; IL-1ra genotype 1,2). These findings provide further evidence of genetic heterogeneity within ulcerative colitis, and support the concept that ANCA may represent a subclinical marker of genetic heterogeneity.  
*Eur J Gastroenterol Hepatol* 11:413-420 © 1999 Lippincott Williams & Wilkins

*European Journal of Gastroenterology & Hepatology* 1999, 11:413-420

**Keywords:** anti-neutrophil cytoplasmic antibodies, cytokine gene polymorphisms, inflammatory bowel disease, ulcerative colitis

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Received 26 May 1998 Revised 31 July 1998

Accepted 13 August 1998

## Introduction

The aetiopathogenesis of the chronic inflammatory bowel diseases (IBDs) ulcerative colitis and Crohn's disease remains unknown. The most comprehensive theory proposed is that the diseases occur in a genetically susceptible subject, as a result of the interaction between environmental triggers and host immunological responses [1]. Although numerous lines of evidence strongly support the contribution of genetic factors in the pathogenesis of ulcerative colitis and Crohn's disease, the pattern of inheritance is still unclear [2].

Currently available evidence indicates that they are not inherited in any simple Mendelian or polygenic models. Moreover, recent studies using the genome-wide screening technique have shown the involvement of multiple genes in different chromosomes [3-5]. In addition, epidemiological and genetic studies support the hypothesis that the IBDs may be genetic heterogeneous disorders of polygenic inheritance [6,7].

For the last few years, the identification of susceptibility genes in IBD has become a major focus of research.

Considering the central role of the immune system in mediating the tissue damage in IBD, most studies have investigated the potential contribution of the HLA class II genes. Several reports from North America [8,9], Europe [10] and Japan [11] have shown that these genes are determinants of disease susceptibility and behaviour in ulcerative colitis. However, data regarding HLA class II associations with ulcerative colitis in different populations have been conflicting.

Other non-HLA genes also involved in the regulation of the immune response have been proposed recently as natural candidates for genetic IBD studies. Although their functional significance is still under evaluation, the description of several polymorphisms within the cytokine genes has allowed the investigation of associations with ulcerative colitis and Crohn's disease [12].

Interleukin-1 receptor antagonist (IL-1ra) is a natural receptor antagonist that modulates the pro-inflammatory effects of interleukin 1. Both experimental and clinical studies have pointed out the importance of IL-1ra in IBD [13]. Of note, an intestinal mucosal imbalance of IL-1 and IL-1ra has been described in patients with ulcerative colitis, which may contribute to the pathogenesis of chronic gut inflammation. The gene encoding the IL-1ra lies on chromosome 2 and contains a variable number of tandem repeats (VNTR) of an 86 base pair sequence in intron 2 [14]. Mansfield *et al.* [15] reported an association between ulcerative colitis and allele 2 of the polymorphic IL-1ra gene. This was the first observed association of ulcerative colitis with a gene outside the major histocompatibility complex (MHC). Although this finding was strengthened by two North American studies [16,17], data from subsequent European reports did not support it [18–23].

Tumour necrosis factor  $\alpha$  (TNF $\alpha$ ) and tumour necrosis factor  $\beta$  (TNF $\beta$ ) are potent pro-inflammatory and immunomodulatory cytokines, implicated in the initiation and regulation of the immune response [12]. The genes for these cytokines are tandemly arranged in the class III region of the MHC, on the short arm of chromosome 6. A number of polymorphisms that might be responsible for differences in the secretion of these cytokines have been described in the TNF locus. Of particular interest, a polymorphism at position –308 in the promoter region of the TNF $\alpha$  gene may be important for the transcriptional control of TNF $\alpha$  [24–26], and has been implicated in genetic susceptibility to some autoimmune diseases [27]. Within the first intron of the TNF $\beta$  gene, an *Nco*I restriction fragment length polymorphism (RFLP) influencing TNF $\beta$  production has been described [28]. In addition, an association between this polymorphism and TNF $\alpha$  production has also been found [29]. Genetic variation within this polymorphism might be

involved in the pathogenesis of certain autoimmune diseases [27].

During recent years, the occurrence of anti-neutrophil cytoplasmic antibodies (ANCA) has been recognized in patients with IBD, particularly ulcerative colitis [30]. The majority of ulcerative colitis-associated ANCA show an immunofluorescence perinuclear pattern (p-ANCA), but cytoplasmic (c-ANCA) and mixed patterns have also been described. The significance of ANCA in IBD, however, remains unclear. Their value as disease markers is supported by the high degree of specificity for IBD in comparison with other colitides, lack of correlation with disease extent and activity, and persistence after colectomy. Furthermore, it has been suggested that p-ANCA may allow stratification of clinically distinct subsets of IBD patients: they have been found to be particularly associated with patients with pouchitis [31], treatment-resistant left-sided ulcerative colitis [32], aggressive disease [33] and Crohn's disease patients with an 'ulcerative colitis-like' clinical phenotype [34]. On the other hand, ANCA may represent a genetic marker in IBD, although this issue is a matter of debate. This concept was raised by the finding of an increased prevalence of these antibodies in healthy relatives of ulcerative colitis patients, suggesting their role as a subclinical marker of genetic disease susceptibility [35,36]. In addition, the reported associations between ANCA and different genetic markers in ulcerative colitis (HLA class II and intercellular adhesion molecule 1 genes) point to their role as a potential marker of genetic heterogeneity [37,38].

In the present study, we report on the distribution of three cytokine gene polymorphisms (IL-1ra, TNF $\alpha$  and TNF $\beta$ ) in a well-defined Spanish population of patients with ulcerative colitis. We have also investigated potential associations between these polymorphisms and subgroups of patients defined by their clinical disease pattern and ANCA status.

## Materials and methods

### Study subjects

Ninety-five non-operated patients with ulcerative colitis attending the Gastroenterology Section and the Department of Gastroenterology of two participating medical centres (Hospital Joan XXIII of Tarragona and Hospital Vall d'Hebron of Barcelona) were included in the study. The patients studied did not have any other conditions known to exhibit ANCA, nor anti-nuclear antibody positive serum samples. All patients were well known to the investigators, their diagnosis having been established based on conventional clinico-pathological criteria. Disease extent was determined by endoscopy and/or radiology, and classified as extensive (proximal to the splenic flexure) or distal. Patients were divided according to the clinical course into relapsing-remitting

and chronic-relapsing requiring immunosuppressive therapy. The main clinical features of the patients are shown in Table 1.

Seventy-four unrelated healthy blood donors without any history of gastrointestinal disease nor family members affected with IBD served as controls. All patients and controls analysed in the present report are non-Jewish Caucasians, and were born and live in the same geographical area (Catalonia).

#### Isolation of DNA

A 10 ml sample of venous blood was collected in an EDTA tube. Within 1 h of drawing, the buffy coat was separated from the blood by centrifugation at 800–900 g for 10 min. Genomic DNA was isolated from the buffy coat using QiaAMP spin columns (Qiagen, Chatsworth, California, USA).

#### Cytokine gene polymorphisms analysis

Genotyping for the cytokine gene polymorphisms was performed using the polymerase chain reaction (PCR).

#### IL-1ra VNTR gene polymorphism

A 100 ng aliquot of the extracted DNA was used as a template for amplifying the second intron of the IL-1ra gene, which contains a variable number of 86 bp sequence that gives rise to this polymorphism [15].

The primers used in the PCR were: 5'-CTCAGC-AACACTCCTAT-3' and 5'-TCCTGGTCTGCAGG-TAA-3'. The reaction was carried out in a final volume of 50  $\mu$ l containing 2 mmol/l MgCl<sub>2</sub>, 0.2 mmol/l of each dNTP (Boehringer Mannheim, Mannheim, Germany), 0.2  $\mu$ mol/l of each primer and 2.5 units of Taq polymerase (Gibco Life Technologies). DNA was amplified for 30 cycles, with an initial denaturation of 30 s at 94°C and a final extension of 10 min at 70°C. Each cycle consisted of 30 s denaturation at 94°C, 1 min annealing at 58°C and 1 min extension at 70°C. PCR products were electrophoresed on a 2% agarose gel. VNTR was detected by ethidium bromide staining.

VNTR IL-1ra analysis revealed a five-allele polymor-

ism which produced five bands of different sizes. A 410 bp band corresponded to the class 1 allele (four repeats), a 240 bp band to the class 2 allele (two repeats), a 500 bp band to the class 3 allele (five repeats), a 325 bp band to the class 4 allele (three repeats), and a 595 bp band to the class 5 allele (six repeats).

#### TNF $\alpha$ gene polymorphism

A transition polymorphism G → A in the -308 position of the gene was detected [15]. A 100 ng aliquot of the extracted DNA was used as a template. The primers used were: 5'-AGGCAATAGGTTTGAGGGCCAT-3' and 5'-TCCTCCCTGCTCCGATTCCG-3'. The reaction was carried out in a final volume of 50  $\mu$ l containing 3 mmol/l of MgCl<sub>2</sub>, 0.5 mmol/l of each dNTP, 0.2  $\mu$ mol/l of each primer and 2.5 units of Taq DNA polymerase. DNA was amplified for 35 cycles, each consisting of 1 min denaturation at 94°C, 1 min annealing at 60°C and 1 min extension at 72°C. Before the first cycle, one cycle of 3 min denaturation at 94°C, 1 min annealing at 60°C and 1 min extension at 72°C was performed. After all the cycles, a final cycle of 1 min denaturation at 94°C, 1 min annealing at 60°C and 5 min extension at 72°C was included. PCR products were digested with a 10-fold excess of *Nco*I restriction enzyme at 37°C for 2–4 h and electrophoresed on a 2.5% agarose gel. *Nco*I RFLPs were detected by ethidium bromide staining.

RFLP-TNF $\alpha$  gene analysis revealed a two-allele polymorphism that produced three bands of different sizes: a 107 bp fragment corresponding to the TNF2 allele (restriction site absent) and a set of 87 bp and 20 bp bands corresponding to the TNF1 allele (restriction site present).

#### TNF $\beta$ gene polymorphism

A 100 ng aliquot of the extracted DNA was used as a template for amplifying the first intron of the TNF $\beta$  gene, which contains a mutation that correlates 100% with a mutation in the second exon of this gene that produces a transversion of A → C [28]. The primers used in the PCR were: 5'-CCGTGCTTCGTGC-TTGGACTA-3' and 5'-AGAGCTGGTGGGGACA-TGTCTG-3'. The reaction was carried out in a final volume of 50  $\mu$ l containing 1.75 mmol/l MgCl<sub>2</sub>, 0.34 mmol/l of each dNTP, 0.38  $\mu$ mol/l of each primer and 2.8 units of Taq polymerase. DNA was amplified for 30 cycles with an initial denaturation of 2 min at 94°C and a final extension of 7 min at 68°C. The cycles were divided into two programmes, one consisting of 10 cycles of 10 s denaturation at 94°C, 30 s annealing at 65°C and 2 min extension at 68°C, and the other consisting of 20 cycles with the same temperatures and times except for the extension time which increased by 20 s per cycle. PCR products were digested with a 10-fold excess of *Nco*I restriction enzyme at 37°C

**Table 1** Characteristics of patients with ulcerative colitis

|                              |          |
|------------------------------|----------|
| Total number                 | 95       |
| Gender (male/female)         | 45/50    |
| Age (years)                  |          |
| Mean                         | 41       |
| Range                        | 16–79    |
| Extent of ulcerative colitis |          |
| Extensive                    | 39 (41%) |
| Distal                       | 56 (59%) |
| Clinical course              |          |
| Relapsing-remitting          | 76 (80%) |
| Chronic-relapsing            | 19 (20%) |

overnight and electrophoresed on a 0.8% agarose gel. *Nco*I RFLPs were detected by ethidium bromide staining.

RFLP-TNF $\beta$  gene analysis revealed a two-allele polymorphism that produced three bands of different sizes: a 740 bp band corresponding to the TNFB1 allele (absence of restriction site) and a set of 555 bp and 185 bp bands corresponding to the TNFB2 allele (restriction site present).

#### ANCA indirect immunofluorescence assay

A standard indirect immunofluorescence (IIF) method was used for detection of ANCA as previously described [39]. In brief, sera were diluted 1:20 in phosphate-buffered saline (PBS), and approximately 35  $\mu$ l of the diluted sera was placed onto test wells on glass slides containing ethanol-fixed neutrophils as antigen substrate (INOVA Diagnostics, San Diego, California, USA). All incubations were performed in humidified boxes at room temperature for 30 min. The slides were then washed with three changes of PBS for 5 min each. After a 30 min incubation period with anti-human immunoglobulin (IgG) conjugated to fluorescein with Evans blue counterstain (INOVA Diagnostics), they were washed again as above, mounted under a cover slip with PBS-glycerin, and finally examined with a fluorescent microscope. Positive and negative controls were included for all assays. The slides were analysed in a blinded fashion by two independent investigators, and a perinuclear or cytoplasmic immunofluorescence staining pattern was regarded as positive. Sera with an equivocal ANCA staining pattern were excluded from the final analysis.

#### Statistical analysis

Statistical comparisons of genotypes, allele frequencies and carriage rates between the study groups were performed using either a  $\chi^2$  test or Fisher's Exact Test when appropriate. For subgroup analysis as a function of clinical disease pattern (extent and clinical course) and ANCA status, correction was made using a Bonferroni correction for multiple analysis. Thus probability values were multiplied by a factor of 5 to obtain corrected probability values. A probability value of 0.05, after correction if necessary, was considered to be the threshold for statistical significance.

## Results

### Comparisons between ulcerative colitis patients and controls

The distribution of the IL-1ra, TNF $\alpha$  and TNF $\beta$  genotypes and allelic frequencies in patients with ulcerative colitis and healthy controls is shown in Tables 2 and 3. There were no significant differences in the IL-1ra VNTR genotypes and allelic frequencies between the two groups (Table 2). In patients with ulcerative colitis, the frequency of allele 2 (30.5%) was similar to that in the controls (31%). Moreover, no significant difference was observed between ulcerative colitis patients and controls in the allele 2 carriage rate (50.5% versus 53%). The polymorphisms studied in the TNF $\alpha$  and TNF $\beta$  genes did not either reveal any associations with ulcerative colitis when compared with the control group (Table 3).

### Comparisons within subgroups of ulcerative colitis patients as a function of the clinical disease pattern and ANCA status

On subgroup analysis based on the clinical disease pattern, no associations between the IL-1ra VNTR genotypes and allelic frequencies, and groups defined by extent and clinical course were found. In patients with extensive colitis, the frequency of allele 2 (29%) was similar to that in the patients with distal colitis (31%). Nineteen of 39 patients (49%) with extensive colitis and 29 of 56 patients (52%) with distal disease were carriers of at least one copy of allele 2.

When we divided patients according to their ANCA status, we observed that p-ANCA ulcerative colitis patients had an increased frequency of the genotype 1,2 compared with ANCA-negative patients (52% versus 28%;  $P = 0.02$ ,  $P_{\text{cor}} = 0.1$ ) (Table 4). Similarly, p-ANCA ulcerative colitis patients had a higher frequency of the genotype 1,2 than c-ANCA ulcerative colitis patients (52% versus 22%), although the difference was not statistically significant probably due to the small numbers analysed. For further analysis, we combined c-ANCA and ANCA-negative patients, since both groups showed a similar genotype distribution, and compared them with p-ANCA ulcerative colitis patients. The result indicated that p-ANCA ulcerative colitis patients had a statistically significant increase of the genotype 1,2 compared with c-ANCA/ANCA-nega-

Table 2 IL-1ra genotypes and allele frequencies in patients and controls

|                                 | 1,1 | 1,2 | 1,3 | 1,5 | 2,2 | 3,3 | Genotype |      |   |   |   | Allelic frequencies (%) |   |   |  |  |
|---------------------------------|-----|-----|-----|-----|-----|-----|----------|------|---|---|---|-------------------------|---|---|--|--|
|                                 |     |     |     |     |     |     | 1        | 2    | 3 | 5 | 1 | 2                       | 3 | 5 |  |  |
| Healthy controls ( $n = 73$ )   | 31  | 33  | 2   | 1   | 6   | 0   | 67       | 31   | 1 | 1 |   |                         |   |   |  |  |
| Ulcerative colitis ( $n = 95$ ) | 44  | 38  | 2   | 0   | 10  | 1   | 67.5     | 30.5 | 2 | 0 |   |                         |   |   |  |  |

**Table 3** TNF $\alpha$  and TNF $\beta$  genotypes and allele frequencies in patients and controls

|                                     | Genotype |     |     | Allelic frequencies (%) |      |
|-------------------------------------|----------|-----|-----|-------------------------|------|
|                                     | 1,1      | 2,2 | 1,2 | 1                       | 2    |
| <b>TNF<math>\alpha</math></b>       |          |     |     |                         |      |
| Healthy controls ( <i>n</i> = 74)   | 52       | 4   | 18  | 82.5                    | 17.5 |
| Ulcerative colitis ( <i>n</i> = 93) | 71       | 3   | 19  | 86.5                    | 13.5 |
| <b>TNF<math>\beta</math></b>        |          |     |     |                         |      |
| Healthy controls ( <i>n</i> = 71)   | 7        | 41  | 23  | 26                      | 74   |
| Ulcerative colitis ( <i>n</i> = 92) | 7        | 46  | 39  | 29                      | 71   |

tive ulcerative colitis (52% versus 26.5%;  $P = 0.01$ ,  $P_{\text{corr}} = 0.05$ ) (Fig. 1). Finally, p-ANCA/IL-1ra genotype 1,2 ulcerative colitis was not associated with any clinical disease pattern when compared with the remaining ulcerative colitis patients (data not shown).

The genotype and allelic frequencies of the TNF $\alpha$  and TNF $\beta$  genes did not reveal any significant differences between subgroups defined by their clinical disease pattern, nor their ANCA status (data not shown).

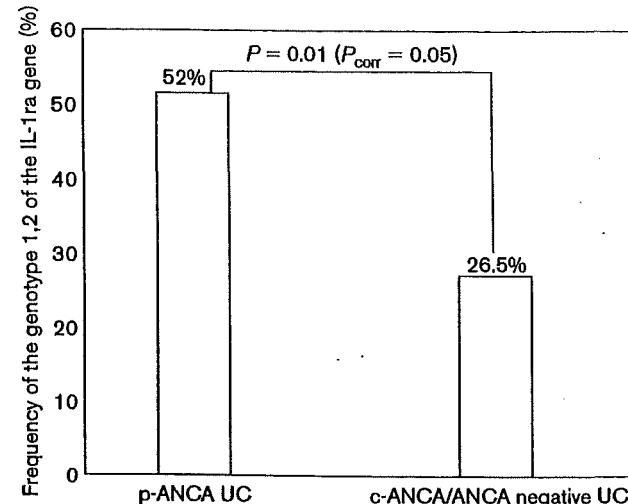
#### ANCA

Four patients had an equivocal ANCA staining pattern and were excluded from further analysis. Fifty-five of 91 (60.5%) ulcerative colitis patients showed the presence of circulating ANCA. Perinuclear staining around neutrophil nuclei was the predominant IIF pattern observed (50.5%), whereas a cytoplasmic staining was seen for nine samples (10%). There was no correlation between ANCA positivity and course, extent, and activity of the disease (data not shown).

#### Discussion

Considering the key role of cytokines in the control of the mucosal inflammatory response in IBD, genes involved in the regulation of their activity have recently been proposed as tentative candidate loci for genetic IBD studies. Mansfield *et al.* [15] first reported an association between the polymorphic gene for IL-1ra and ulcerative colitis in a British population. The rare allele 2 was over-represented in patients with ulcerative colitis (35%) compared with controls (24%). Furthermore, since this association was greatest in patients

**Fig. 1**



Frequency of the genotype 1,2 of the IL-1ra gene in p-ANCA ulcerative colitis and c-ANCA/ANCA-negative ulcerative colitis. p-ANCA ulcerative colitis patients showed an increased frequency of the genotype 1,2 ( $P = 0.01$ ,  $P_{\text{corr}} = 0.05$ ) compared with c-ANCA/ANCA-negative ulcerative colitis patients.

with total colitis, the authors suggested that allele 2 of the IL-1ra gene might represent a genetically specified severity factor in ulcerative colitis. This overall association was supported by two North American studies [16,17] which showed a significant increase in the allele 2 carriage rate in ulcerative colitis patients compared with controls. In contrast, however, other European studies from Germany [18,22], England [20,21], The Netherlands [19] and France [23] failed to detect a significant association of this allele with ulcerative colitis. The results of the present study are in agreement with the latter reports. Allele 2 frequencies and carriage rates were similar in patients with ulcerative colitis and healthy controls (30.5% versus 31% and 50.5% versus 53%, respectively). In addition, no differences were detected between patients with extensive and distal colitis (49% versus 52%). Our present results are also consistent with those of another study in a Spanish population, which showed no association between allele 2 and ulcerative colitis [40].

**Table 4** IL-1ra genotypes in p-ANCA ulcerative colitis, c-ANCA ulcerative colitis and ANCA-negative ulcerative colitis patients

|   | Genotype 1,2 | Genotypes 1,1,3 2,2 and 3,3 |
|---|--------------|-----------------------------|
| ANCA-negative ulcerative colitis ( <i>n</i> = 36) | 10 (28%)     | 26 (72%)                    |
| p-ANCA ulcerative colitis ( <i>n</i> = 46)        | 24 (52%)*    | 22 (48%)                    |
| c-ANCA ulcerative colitis ( <i>n</i> = 9)         | 2 (22%)      | 7 (78%)                     |

\*p-ANCA ulcerative colitis versus ANCA-negative ulcerative colitis:  $P = 0.02$ ,  $P_{\text{corr}} = 0.1$ .

The reasons for the discrepancies between these studies are unclear. Methodological reasons are unlikely to be responsible, since all of them used the same molecular genotyping procedures. There are several possible explanations for the divergent results. First, ethnic differences, which account for many of the inconsistencies reported in HLA association studies in ulcerative colitis, may in part explain them. Thus, the North American studies involved a mixed Jewish/non-Jewish population from Pittsburgh and a Hispanic one from Los Angeles, whereas the European studies included predominantly non-Jewish white European subjects. Moreover, Tountas *et al.* [41] have recently reported that the association with allele 2 of the IL-1ra gene was only relevant in a Jewish subgroup from a Caucasian population in Los Angeles, but not in the whole study cohort. Second, the different results could be due to disease heterogeneity. From a clinical point of view, ulcerative colitis is a heterogeneous disease, which may be a reflection of underlying genetic heterogeneous background. For instance, there is evidence that genes in the HLA region may influence disease behaviour in ulcerative colitis: the HLA-DRB1\*1502 allele has been found to be associated with disease intractability [11] and corticosteroid treatment [42], whereas the DR3-DQ2 haplotype has been found to predict extensive disease [10]. Similarly, the allele 2 of IL-1ra might only be associated with a particular subgroup of ulcerative colitis patients. In fact, three of the above studies showed a significant association of allele 2 exclusively with extensive disease [19,21] or disease intractability [23], but not with the whole group of ulcerative colitis patients. Finally, it is possible that the reported weak association in some studies reflects the fact that the IL-1ra gene does not contribute in itself to genetic susceptibility to ulcerative colitis, but rather is a marker of other closely linked genes on chromosome 2 of primary importance, or alternatively, the synergistic association of specific alleles of the IL-1ra gene with other nearby genetic markers predisposes to ulcerative colitis. Supporting this last hypothesis, different associations of allelic variants of the IL-1 $\beta$  and IL-1ra genes in both ulcerative colitis and Crohn's disease patients compared to healthy controls have recently been reported [23,43].

Genetic variation within the TNF locus may be involved in the pathogenesis, or clinical manifestations, of some autoimmune and infectious diseases [27]. In IBD, there are relatively few studies of TNF $\alpha$  and TNF $\beta$  gene polymorphism associations with either ulcerative colitis or Crohn's disease. Plevy *et al.* [44] have recently reported an association of the TNF microsatellite haplotype a2b1c2d4e1 with Crohn's disease, which is the strongest genetic risk factor described so far in Crohn's disease. Bi-allelic single-base polymorphisms of either TNF $\alpha$  [15,20,21,45,46] or

TNF $\beta$  genes [45–47] have shown weak [45] or no association [15,20,21,46,47] with ulcerative colitis. In agreement with these previous studies, we found no differences between ulcerative colitis patients and controls in the TNF $\alpha$  and TNF $\beta$  polymorphisms analysed. Taken as a whole, these data indicate that bi-allelic single-base polymorphisms of the TNF genes are not important determinants of overall disease susceptibility to ulcerative colitis.

A number of observations support the concept of genetic heterogeneity within IBD [2]. According to these, IBD is regarded not as a single disease, but rather as several aetiologically and genetically distinct diseases presenting a similar clinical picture. Furthermore, there is an increasing body of evidence suggesting genetic heterogeneity within each disease. The most relevant clues have come from genetic marker studies, which have demonstrated different HLA associations for ulcerative colitis and Crohn's disease, and distinct associations between subsets of ulcerative colitis as discussed earlier. Likewise, there are hints that subclinical markers, such as ANCA, may contribute to establish genetic heterogeneity within ulcerative colitis. This was first suggested by Shanahan *et al.* [35], who described a familial distribution of these antibodies: the relatives of ANCA-positive ulcerative colitis patients had an increased prevalence of the presence of ANCA compared with those of ANCA-negative patients. Additional evidence was provided by the same investigators from Los Angeles, who reported distinct associations between ANCA and various genetic markers. Thus, both ANCA-positive and ANCA-negative ulcerative colitis were associated with the HLA-DR2 and the HLA-DR4 alleles respectively in a mixed Jewish/non-Jewish population from Los Angeles [37]. In another study, ANCA-negative ulcerative colitis exhibited an increased frequency of allele R241 in codon 241 of the intercellular adhesion molecule 1 gene [38]. However, the role of ANCA as a subclinical marker of genetic heterogeneity in ulcerative colitis has been questioned, because further studies did not establish any relationship between ANCA and HLA status, particularly with the HLA-DR2 allele [9,19]. The discrepancies between the studies may reflect methodological differences and disease heterogeneity. Ethnic differences may also be relevant, as shown by Satsangi *et al.* [48] who recently reported that in North European patients with ulcerative colitis there is an association between ANCA and the HLA-DR3 DQ2 TNF2 haplotype, but not with HLA-DR2.

The results of the present study provide further support for the notion of ANCA as a subclinical marker of genetic heterogeneity within ulcerative colitis. We have shown an association between an inherited polymorphism of the IL-1ra gene and an immunologically

defined subgroup of ulcerative colitis patients: p-ANCA ulcerative colitis was positively associated with the genotype 1,2 (52%) compared with c-ANCA/ANCA-negative ulcerative colitis (26.5%). In contrast to our results, no association between p-ANCA and the IL-1ra gene polymorphism was found in reports from North America [16], Germany [18] and The Netherlands [19]. In a British study [21], the proportion of carriers of allele 2 was increased in the ANCA-positive group (38.2%) compared with the ANCA-negative group (11.8%). Here again, as for the HLA association studies, the conflicting results may reflect methodological differences, disease heterogeneity and/or variability between different study populations and ethnic groups.

The association of ANCA with ulcerative colitis is now well established. The majority of ulcerative colitis-associated ANCA exhibit a perinuclear immunofluorescence pattern, but cytoplasmic and mixed patterns have also been described [49–53]. There is no consensus, however, on which patterns should be considered associated with ulcerative colitis. While most authors only consider the perinuclear type, others also include the less frequent cytoplasmic or mixed patterns. The findings of our study provide evidence supporting this last view. When we first compared ANCA-positive ulcerative colitis with ANCA-negative ulcerative colitis patients, we did not find any association between ANCA and the cytokine gene polymorphisms analysed. It was only after the stratification of ulcerative colitis by their different ANCA immunofluorescence patterns, p-ANCA and c-ANCA, that we detected an association between p-ANCA and a specific IL-1ra genotype. c-ANCA and ANCA-negative ulcerative colitis patients showed a similar 1,2 genotype distribution, which was opposite to that of p-ANCA ulcerative colitis patients. However, these data should be interpreted with caution, first due to the small number analysed, and second because attempts to differentiate clinical disease patterns between p-ANCA ulcerative colitis patients and c-ANCA ulcerative colitis patients have so far been unsuccessful. Nevertheless, considering that the nature of the antigen(s) to which ANCA react in ulcerative colitis remains unknown, although it is likely that p-ANCA and c-ANCA are directed against different antigens, it does not seem reasonable to exclude any type of ANCA pattern when an unequivocal immunofluorescence staining is found.

In summary, this study shows that cytokine gene polymorphisms of the TNF $\alpha$ , TNF $\beta$  and IL-1ra are not important factors in determining genetic susceptibility to ulcerative colitis in the Spanish population studied. On the other hand, our findings are in accordance with the concept of genetic heterogeneity within ulcerative colitis, and provide further evidence that

ANCA may represent a serological marker of genetic heterogeneity in this disease.

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UNIVERSITAT ROVIRA I VIRGILI  
MARCADORES INMUNOGENETICOS EN LA ENFERMEDAD INFLAMATORIA INTESTINAL: ESTUDIO SOBRE LOS ANTICUERPOS  
ANTICITOPLASMA DE NEUTROFILO Y POLIMORFISMOS GENETICOS DE CITOCINAS (IL-1RA, TNF $\alpha$  Y TNF $\beta$ ) EN UNA POBLACIÓN  
DE PACIENTES ESPAÑOLES CON COLITIS ULCEROSA Y ENFERMEDAD DE CROHN  
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ISBN:978-84-691-2705-6/DL: T.398-2008

## **5. DISCUSION**

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## **ESTUDIO 1.**

Los resultados de este primer trabajo han demostrado la presencia de ANCA en 49 de 75 pacientes (65%) con CU, en 5 de 41 pacientes con EC (12%) y únicamente en un sujeto del grupo control (2,5%). Estos hallazgos coinciden con los de la mayoría de las series de la literatura, en las que estos anticuerpos tienen una alta prevalencia en la CU (50-80%)<sup>49,50,200-204,285-288,290,291,293-295,297,299-303,306-310,312,313,316</sup>, se detectan con mucho menor frecuencia en la EC (5-25%)<sup>49,50,202-204,207,285-291,293,298,299,301-306,308,310,311,316,318</sup>, y no se asocian a otras patologías del tracto gastrointestinal. Por el contrario, contrastan con los de otros trabajos que han comunicado una prevalencia sensiblemente inferior en la CU (30-40%)<sup>202,207,208,289,304,305</sup>, y una mayor frecuencia a la reportada habitualmente en la EC (40-55.5%)<sup>292,295,297,300,307,312-314</sup>.

Las causas de tan notables diferencias sobre la prevalencia de los ANCA en la EII no han sido del todo esclarecidas. Se han propuesto varias explicaciones posibles y no excluyentes. En primer lugar, la utilización de distintas técnicas para su detección puede ser parcialmente responsable. Como ya se ha señalado en la introducción, existen discrepancias en cuanto a la sensibilidad y especificidad de la IFI y el ELISA<sup>290,358</sup>. Sin embargo, el hecho de que también se perciban marcadas diferencias entre laboratorios que emplean únicamente la IFI, técnica con la que se consiguen resultados altamente reproducibles<sup>290,296</sup>, sugiere que éstas no se deben únicamente a diferencias metodológicas. En segundo lugar, la divergencia de resultados puede atribuirse a diferencias reales de prevalencia en las distintas poblaciones estudiadas, entre las que cabe considerar diferencias

raciales y/o étnicas. Así, la frecuencia de ANCA reportada en la CU varía en distintas áreas geográficas, siendo del 72-85 % en Norteamérica<sup>49,204,285</sup>, 58-83 % en Alemania<sup>203,291,293</sup>, 45-79 % en Holanda<sup>290,292,296</sup> y 41-76 % en Inglaterra<sup>286,297,305,366</sup>. La prevalencia reportada en nuestro país oscila entre un 41 % y 73 %<sup>296,302,303,318,352</sup>. Estas cifras, exceptuando el estudio de García Herola y cols.<sup>318</sup>, son superiores a las descritas en los otros países europeos del área mediterránea: 39,8-48 % en Italia<sup>298,304,365</sup>, 46-52 % en Francia<sup>288,296,364</sup>, y 30 % en Grecia<sup>289</sup>. Estudios en los que se han analizado simultáneamente sueros de distintas poblaciones en laboratorios independientes han confirmado diferencias regionales significativas<sup>296,363</sup>. Finalmente, no se puede excluir que las diferencias de prevalencia puedan deberse a sesgos de tamaño y de selección de los pacientes estudiados. No obstante, esta última posibilidad es menos probable, teniendo en cuenta que no existe una relación demostrada entre el status ANCA y las principales variables demográficas y clínicas de la enfermedad.

Lógicamente, el valor de los ANCA como marcadores serológicos útiles para el diagnóstico de la CU, está en función de la prevalencia encontrada en los pacientes con CU y con EC, que como se ha discutido, varía notablemente entre las distintas series, muy posiblemente como consecuencia de diferencias metodológicas y/o poblacionales. En nuestro estudio, la sensibilidad y especificidad de los ANCA para la CU fue de un 65 % y de un 88 % respectivamente. El valor predictivo positivo fue del 91 %, y el valor predictivo negativo del 58 %. De esta forma, nuestros resultados coinciden con los de la mayoría de trabajos publicados que han reportado una sensibilidad y especificidad de los ANCA para el diagnóstico de la CU de entre un 50-80 % y un 80-95 %

respectivamente<sup>49,204,285,287,288,290,296,298,302,303,309,311,318</sup>. Por contra, los autores que detectan una baja prevalencia de los anticuerpos en la CU y/o una mayor frecuencia a la reportada habitualmente en la EC, señalan obviamente, que si bien los ANCA pueden ser de utilidad para diferenciar la CU de ciertas colítides, su valor discriminatorio frente a la EC es limitado<sup>207,295,304,306,312,313</sup>.

A pesar de que nuestro estudio, al igual que otros, sugiere que la determinación de los ANCA puede contribuir al diagnóstico CU, ciertamente su utilidad en la práctica clínica tiene una serie de limitaciones que merecen ser comentadas. En primer lugar, es importante señalar que las técnicas utilizadas en la actualidad para la detección de los ANCA en la EII tienen el inconveniente de no ser antígeno-específicas. En este sentido, los estudios más recientes que ubican el antígeno de los ANCA asociados a la EII en el núcleo celular<sup>326-330</sup>, han creado nuevas expectativas para conseguir finalmente su identificación, lo que debería permitir en último término el desarrollo de técnicas más específicas para soslayar los problemas metodológicos. En segundo lugar, la hipotética utilidad de los marcadores serológicos para el diagnóstico de la CU y la EC es discutible. En efecto, a diferencia de otras patologías (conectivopatías u otras enfermedades autoinmunes organoespecíficas por citar algunos ejemplos) en las que diversos autoanticuerpos tienen una considerable utilidad clínica, el valor potencial de los marcadores serológicos en la EII parece más limitado, teniendo en cuenta que el diagnóstico tanto de la CU como de la EC no plantea por lo general grandes dificultades cuando se combinan criterios convencionales clínicos, radiológicos, endoscópicos y anatomiopatológicos. Por ello, la mayor utilidad de los marcadores serológicos en la EII, y en concreto la de los ANCA, consistiría en posibilitar el

diagnóstico diferencial en aquellas situaciones en las que realmente existen dificultades diagnósticas. Primero, deberían facilitar el diagnóstico diferencial de la EII con otras colítides, principalmente las infecciosas enteroinvasivas y algunas colitis isquémicas de curso evolutivo crónico. Como ya se ha señalado en otros apartados de este texto, los ANCA parecen cumplir este objetivo, ya que no se detectan en otras colopatías agudas y/o crónicas. Unicamente se ha sugerido su asociación con las colitis microscópicas<sup>285</sup>, si bien este hallazgo no ha sido posteriormente ratificado<sup>512</sup>. Segundo, deberían posibilitar el diagnóstico diferencial entre la CU y la EC con afectación colónica, cuando las técnicas diagnósticas habituales no son del todo concluyentes. En este sentido, la alta prevalencia de los anticuerpos en los pacientes con EC que tienen un fenotipo *UC-like* reportada por algunos autores<sup>314,359</sup>, obviamente limitaría su utilidad. Esta observación, sin embargo, no ha sido confirmada por otros investigadores<sup>360,361</sup>. Finalmente, la mayor utilidad de los ANCA consistiría en poder establecer el diagnóstico definitivo de CU o EC en los pacientes que tienen una de colitis indeterminada. No obstante, esta cuestión es difícil de evaluar, y hasta la fecha no se ha publicado ningún estudio al respecto.

En resumen, si bien los ANCA pueden contribuir al diagnóstico de la CU, posibilitando el diagnóstico diferencial con otras colítides, su valor clínico para diferenciar las formas de CU difícilmente distinguibles de la EC no se ha establecido. Es posible que la combinación de la detección de los ANCA con otros marcadores serológicos, como por ejemplo los anticuerpos anti-*Saccharomyces cerevisiae* (ASCA) que tienen una alta especificidad para la EC, pueda aumentar el rendimiento diagnóstico de los marcadores serológicos en la EII, tal como se ha sugerido recientemente en diversos trabajos<sup>341,513,514</sup>.

En nuestro estudio, al igual que en la mayoría de los trabajos publicados, no encontramos relación entre la seropositividad de los ANCA en la CU, y el tiempo de evolución, el curso clínico, la extensión, la actividad de la enfermedad, las manifestaciones extraintestinales, o el tratamiento farmacológico recibido. Tampoco existió relación entre el título o patrón de inmunofluorescencia y los parámetros clínicos valorados. Sin embargo, algunos autores sí han detectado relación con alguna de las variables analizadas. Tural<sup>303</sup> y Rump y cols.<sup>293</sup> encuentran una correlación entre la positividad de los ANCA y la actividad de la enfermedad. Rump y cols.<sup>293</sup> describen además su negativización en pacientes que entran en remisión tras tratamiento esteroidal. De forma similar, otros autores hallan relación entre el título de los ANCA y la actividad clínica de la CU<sup>203,287,293,295</sup>. Por otra parte, se ha sugerido que el status ANCA se relacionaría con la evolución de la enfermedad, de tal forma que su presencia se asociaría con un curso clínico más agresivo: se ha reportado una mayor prevalencia entre los pacientes que tienen más exacerbaciones anuales<sup>298,515</sup>, y una muy baja prevalencia en enfermos que presentan una remisión clínica prolongada<sup>516</sup>. Finalmente, Sandborn y cols.<sup>517</sup> han encontrado una frecuencia incrementada en pacientes con colitis izquierda resistente al tratamiento médico, sugiriendo una posible asociación entre los ANCA y una resistencia relativa al tratamiento farmacológico. No obstante, como previamente se ha hecho referencia, la tendencia más constante observada en la bibliografía es la ausencia de relación entre el status ANCA y las características clínicas de la enfermedad. Lógicamente, la ausencia de relación entre la positividad y/o el título de los ANCA con la actividad de la CU, inhabilitan una hipotética utilidad de estos anticuerpos.

como marcadores serológicos para la monitorización de la respuesta terapéutica y evolución clínica.

## **ESTUDIO 2.**

En este segundo trabajo se evaluó el posible papel de los ANCA como marcadores subclínicos de susceptibilidad genética a la EII en nuestro medio. Para ello se establecieron tres grupos de estudio. En el primero, formado por pacientes con EII, se detectó la presencia de ANCA en 34 de 53 pacientes (64%) con CU, y en 3 de 24 de pacientes (12,5%) con EC. El segundo grupo incluyó 215 familiares de primer grado de los pacientes con EII. Se encontró la presencia de los anticuerpos en 6 de 155 familiares (3,9%) de pacientes con CU, y en 4 de 60 familiares (6,7%) de pacientes afectados de EC. De esta forma, globalmente se detectó la presencia de ANCA en 10 de los 215 familiares estudiados de los pacientes con EII, lo que representa un 4,6%. Finalmente, en el grupo control, los ANCA se detectaron únicamente en uno de 40 sujetos sanos donantes de sangre (2,5%), en ninguno (0%) de 22 cónyuges de pacientes con EII (grupo control ambiental), y en ninguno (0%) de los 11 pacientes con enfermedad celíaca que también fueron evaluados. De esta forma, la presencia de ANCA fue estadísticamente más frecuente en los pacientes con CU respecto a todos los demás grupos de estudio. La prevalencia de los anticuerpos no se encontró incrementada en los familiares sanos de los pacientes con respecto al grupo control.

A pesar de los considerables esfuerzos realizados durante la última década con el objetivo de identificar los locus genéticos que expliquen el carácter hereditario de la CU y la EC, la naturaleza de los genes implicados sigue siendo desconocida.

Consecuentemente, a diferencia de lo que sucede actualmente con numerosas enfermedades hereditarias monogénicas en las que el riesgo de recurrencia para los miembros de una familia específica puede determinarse con relativa facilidad, en la EII no se disponen de marcadores genéticos que permitan identificar a los sujetos susceptibles de desarrollar la enfermedad. Por ello, el estudio de diversos marcadores subclínicos en los familiares sanos de los pacientes, parámetros que permiten detectar a los sujetos con un genotipo anormal en ausencia de expresión fenotípica de una enfermedad, y que se han mostrado útiles en otros trastornos genéticos multifactoriales, ha sido objeto de una considerable atención<sup>375</sup>. Se han propuesto diversos candidatos que incluyen el sistema del complemento<sup>518</sup>, las glicoproteínas colónicas<sup>519</sup>, la flora anaerobia intestinal<sup>520</sup>, las subclases de inmunoglobulinas IgG<sup>521,522</sup>, el estudio de la permeabilidad intestinal<sup>523-529</sup>, y varios anticuerpos como los anti-linfocitotóxicos<sup>530</sup>, anticuerpos dirigidos contra antígenos epiteliales intestinales (ECAC)<sup>531</sup>, contra el páncreas<sup>532,533</sup>, anti-tropomiosina<sup>534</sup>, anti-*goblet cells*<sup>535</sup>, anti-*Saccharomyces cerevisiae*<sup>536</sup>, e incluso los ANA<sup>537</sup>. Sin embargo, para ninguno de estos potenciales marcadores subclínicos se han obtenido resultados consistentes.

El valor de los ANCA como marcadores subclínicos de susceptibilidad genética a la CU fue inicialmente sugerido por el grupo de Shanahan y cols.<sup>362</sup> que encontraron una frecuencia significativamente más alta de los anticuerpos en los familiares sanos de los pacientes que en sujetos controles. Estos autores reportaron la presencia de los anticuerpos en 14 de 93 (15,7%) de los familiares sanos de pacientes con CU en una población de Los Angeles, y en 9 de 43 (20,9%) de los de una población canadiense de

Calgary. Estos hallazgos fueron confirmados dos años más tarde por Seibold y cols.<sup>363</sup> en Alemania: detectaron la presencia de ANCA en el 30% de los familiares sanos de pacientes con CU, y en el 25% de los de pacientes con CEP. No obstante, contrariamente a estos dos trabajos, cuatro estudios realizados en Francia<sup>364</sup>, Italia<sup>365</sup> e Inglaterra<sup>366,367</sup>, no evidenciaron una prevalencia incrementada de ANCA en los familiares sanos de pacientes con CU (0-6,6%). Nuestro estudio, al igual que estos últimos trabajos, tampoco ha mostrado una mayor frecuencia de los anticuerpos en los familiares de los enfermos con CU, ni en los de los de pacientes con EC, con respecto al grupo control. Más recientemente, otros autores han comunicado, ya sea en forma de artículos originales o de comunicaciones, resultados igualmente negativos<sup>532,538-540</sup>. Por otra parte, Yang y cols.<sup>541</sup> han reportado que la frecuencia de ANCA no está incrementada en hermanos gemelos monocigotos sanos de hermanos con CU, resultados que están en contra del hipotético papel de estos anticuerpos como marcadores genéticos en la EII.

En resumen, los resultados de los estudios del grupo de Shanahan y del de Seibold sugiriendo el papel de los ANCA como marcadores de susceptibilidad genética a la CU, y por extensión a la CEP, no se han reproducido en otros estudios europeos. Las diferencias entre estos trabajos, al igual que las encontradas con respecto a la prevalencia de los ANCA en los propios pacientes, también se han atribuido a diferencias metodológicas y/o poblacionales. Considerando esta última explicación, es posible que los ANCA representen marcadores genéticos en la CU únicamente en determinadas poblaciones. En cualquier caso, en la mayoría de las poblaciones estudiadas, incluida la nuestra, los ANCA no representan marcadores de susceptibilidad genética a la EII.

## **ESTUDIO 3.**

Durante los últimos años, los genes que codifican para diversas citocinas con importante actividad inflamatoria y/o inmunoreguladora, moléculas que participan de forma activa en la patogenia de la EII, se han considerado como importantes candidatos potenciales a la susceptibilidad genética de la CU y la EC. Los importantes avances realizados en el campo de la biología molecular, han llevado por una parte, a la clonación y secuenciación de estos locus genéticos, y por otra, la descripción de polimorfismos de los mismos, permitiendo de esta forma el estudio de posibles asociaciones con las enfermedades inflamatorias idiopáticas crónicas del intestino. Los trabajos publicados hasta la fecha han evaluado polimorfismos de los genes que codifican para el TNF $\alpha$ , el TNF $\beta$ , la IL-1 $\beta$ , el IL-1ra, la IL-2, y la IL-10<sup>284,421,422</sup>.

Con respecto al gen del IL-1ra, desde que en el año 1994 Mansfield y cols.<sup>460</sup> reportaran una asociación entre el alelo 2 del polimorfismo VNTR en el intrón 2 del IL-1RN y la CU en una población de Sheffield, otros investigadores han comunicado resultados discordantes. Entre los estudios positivos, dos grupos norteamericanos<sup>461,462</sup> evidenciaron una mayor frecuencia de portadores del alelo 2 en la CU, confirmando los hallazgos de los investigadores ingleses. Recientemente, el grupo de Mansfield ha estudiado una serie considerablemente más amplia de pacientes con CU, ratificando los datos de su primer estudio<sup>542</sup>. Sin embargo, los resultados obtenidos al evaluar este polimorfismo en otras poblaciones europeas, de Alemania<sup>463,464</sup>, Inglaterra<sup>465,466</sup>, Holanda<sup>373</sup>, Francia<sup>467</sup> y España<sup>468</sup>, no han encontrado esta asociación. En nuestro estudio,

al igual que en estos últimos trabajos, tampoco encontramos una asociación entre el alelo 2 del IL-1RN y la CU. En concreto, la frecuencia del alelo 2 en la CU (30,5%) fue similar a la detectada en el grupo control (31%), y la frecuencia de los portadores de este alelo en la CU (50,5%) fue también equiparable a la observada en los controles (53%).

Las discrepancias entre estos trabajos difícilmente se pueden atribuir a diferencias metodológicas, ya que las técnicas de biología molecular utilizadas en todos ellos son muy similares. Diferencias poblacionales, en concreto étnicas, así como la heterogeneidad clínica y genética propias de la EII, parecen ser más relevantes<sup>469</sup>. Con respecto a las posibles diferencias étnicas, en los dos trabajos realizados en Estados Unidos se evaluaron una población mixta de judíos/no judíos de Pittsburgh y una población hispánica de los Angeles, mientras que en los estudios europeos se incluyeron mayoritariamente sujetos blancos no judíos del norte de Europa. Más aún, Tountas y cols.<sup>543</sup> han reportado que la asociación entre el alelo 2 y la CU era relevante únicamente en el subgrupo de pacientes judíos de la población caucásica que estudiaron. En cuanto a la explicación que considera la heterogeneidad clínica y genética de la CU, ya en el estudio inicial del grupo de Mansfield<sup>460</sup>, la asociación entre el alelo 2 y la CU era mucho más manifiesta en los pacientes con una afectación extensa del colon (pancolitis) que en los que tenían una colitis distal. De igual forma, en dos de los estudios europeos en los que no se objetivó una asociación del alelo 2 con la CU, sí se observó una asociación con la forma de afectación extensa de la enfermedad<sup>373,466</sup>, y en otro trabajo, con la intratabilidad de la misma<sup>467</sup>. Así, los autores de estos trabajos han sugerido que el alelo 2 podría representar un marcador de "gravedad" en la CU. Su asociación con las formas más "graves" de CU,

sin embargo, no se ha objetivado en los demás estudios, incluido el nuestro. Finalmente, otra posible explicación a las discrepancias entre los estudios, propone que las asociaciones positivas comunicadas por algunos autores entre el alelo 2 y la CU, se deben a que el IL1RN, no siendo directamente responsable de la susceptibilidad a la enfermedad, está en desequilibrio de ligamiento con algún otro gen de importancia primaria en el cromosoma 2, o alternativamente, la acción sinérgica del ILRN con otros genes cercanos es la que determina la susceptibilidad genética a la CU. Sosteniendo esta última hipótesis, Bioque y cols.<sup>544</sup>, y Heresbach y cols.<sup>467</sup>, han descrito una asociación de distintas variantes alélicas de polimorfismos genéticos del IL1B y IL1RN en la CU, sugiriendo que puede ser la combinación de genotipos IL1B/IL1RN la que define las bases biológicas de la predisposición a la enfermedad.

Considerando que el TNF juega un importante papel en la patogenia de la EII, y que la variación genética de ciertos polimorfismos del TNFA y del TNFB se ha asociado a diversas enfermedades autoinmunes e infecciosas, estos dos locus se han considerado candidatos potenciales en la EII<sup>495</sup>. Sin embargo, los resultados de los diversos estudios de la literatura sobre polimorfismos RFLP del TNFA y del TNFB en la EII, realizados básicamente en poblaciones del norte de Europa, han mostrado una muy discreta o nula asociación con la CU y la EC<sup>460,465,466,506-508,510,511</sup>. En concordancia con estos estudios, en el nuestro no hemos detectado ningún tipo de asociación alélica ni genotípica de los dos polimorfismos analizados con la CU. A partir del análisis combinado de todos estos estudios, se infiere que los polimorfismos bialélicos del locus del TNF no son determinantes mayores de susceptibilidad global a la CU, ni a la EC. Es importante

señalar, no obstante, que esta asunción no descarta que los genes que codifican para estas citocinas puedan jugar un papel en la genética de la EII. En efecto, Plevy y cols.<sup>546</sup> han reportado una asociación del haplotipo a2b1c2d4e1 de microsatélites del TNF con la EC, que representa el mayor riesgo genético descrito hasta la fecha en esta enfermedad. Recientemente, Heresbach y cols.<sup>507</sup> no han podido reproducir los mismos resultados en un estudio realizado en Francia.

Uno de los avances más importantes realizados durante los últimos años en el estudio de la genética de la EII ha sido el reconocimiento de que la CU y la EC son enfermedades genéticamente heterogéneas. Como ya se ha señalado en otros apartados de este texto, la heterogeneidad genética de las dos enfermedades se sustenta en diversas evidencias aportadas por estudios experimentales, clínico-epidemiológicos, y genéticos. Así mismo, también se ha destacado que los marcadores subclínicos, y en concreto los ANCA, pueden contribuir a definir la heterogeneidad genética de la CU y la EC. Shanahan y cols.<sup>362</sup> fueron los primeros autores que lo sugirieron, al encontrar una mayor frecuencia de los anticuerpos en los familiares de pacientes con CU que eran ANCA+ que en los familiares de los pacientes ANCA- (21.4% vs 7%). Posteriormente, varios estudios han mostrado que se pueden definir subgrupos homogéneos de pacientes con CU, a partir de la asociación de marcadores genéticos (genes HLA, ICAM-1, y motilina)<sup>368,369,370,374,547,548</sup> y el status ANCA, y sugerir en consecuencia que la CU-ANCA+ y la CU-ANCA- son grupos genéticamente distintos. Sin embargo, otros trabajos no han conseguido establecer asociaciones de estas características, cuestionando

así el papel de los ANCA como marcadores de heterogeneidad genética<sup>371-373</sup>. Nuevamente aquí, las discrepancias entre estos trabajos se han atribuido a diferencias metodológicas y/o poblacionales.

Los resultados de nuestro estudio apoyan el papel de los ANCA como marcadores subclínicos de heterogeneidad genética en la CU, y consecuentemente proporcionan evidencia adicional al concepto de heterogeneidad genética de la enfermedad. En efecto, se encontró una asociación estadísticamente significativa entre el polimorfismo VNTR del IL-1RN y un subgrupo de pacientes con CU definidos por el status ANCA: los pacientes pANCA+ se asociaron con el genotipo 1,2 cuando se compararon con los pacientes ANCA-/c-ANCA (52% vs 26,5%; p=0,01; p<sub>c</sub>=0,05). Estos hallazgos contrastan con los de otros autores que no han objetivado asociaciones entre la CU-pANCA y variantes genotípicas del polimorfismo del IL-1RN<sup>373,461,463</sup>. Unicamente Roussomoustakaki y cols.<sup>466</sup> han encontrado que la proporción de portadores del alelo 2 está aumentada en la CU-ANCA+ comparada con la CU-ANCA -.

La ventaja principal de contemplar a la CU y la EC como enfermedades genéticamente heterogéneas, consiste en la posibilidad de estratificar a los pacientes por la naturaleza de su alteración genética subyacente, por ejemplo como se ha descrito previamente, mediante el estudio de asociaciones con marcadores genéticos y subclínicos, para conseguir mejorar los conocimientos sobre los mecanismos fisiopatológicos implicados en cada forma etiológica. Además, la identificación de grupos genéticamente homogéneos debería permitir el empleo de tratamientos más racionales y ensayar nuevas estrategias terapéuticas acorde con las alteraciones fisiopatológicas inherentes a cada uno

de ellos. En este sentido, los estudios comentados más arriba, a pesar de que consiguen definir subgrupos homogéneos de CU a partir de marcadores genéticos y los ANCA, no encuentran que los subgrupos "genéticos" tengan características fenotípicas específicas, lo que sin duda debería ser el principal objetivo de este tipo de trabajos. Por citar un ejemplo, recientemente Plevy y cols.<sup>549</sup> han reportado que el estudio combinado de microsatélites del gen del TNF $\alpha$  y del status ANCA, identifica a un subgrupo de pacientes con EC caracterizados por una pobre respuesta al tratamiento con anticuerpos monoclonales anti-TNF $\alpha$ . Lógicamente, los resultados de este trabajo deberían ser ratificados para cobrar relevancia, y únicamente se cita aquí el mismo, para ilustrar lo que puede llegar a aportar este campo de la investigación en el estudio, y sobre todo, en el manejo de la EII. Por todo lo expuesto, se comprende el interés que existe en lograr identificar marcadores genéticos y subclínicos, como los ANCA, que nos permitan alcanzar en el futuro estos objetivos.

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## **6. CONCLUSIONES**

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**ESTUDIO 1.**

- 1.- La presencia de ANCA se asocia a la CU y en mucha menor proporción a la EC en la población catalana estudiada. Su determinación mediante IFI puede ser de utilidad para el diagnóstico diferencial entre las dos enfermedades en nuestro medio.
- 2.- La seropositividad de los ANCA no se asocia con las diferentes características demográficas ni clínicas de la CU.

**ESTUDIO 2.**

- 1.- La prevalencia de los ANCA no se encuentra incrementada en los familiares sanos de primer grado de los pacientes con EII en la población catalana estudiada. Estos anticuerpos no representan marcadores subclínicos de susceptibilidad genética a la EII en esta población.

**ESTUDIO 3.**

- 1.- Los polimorfismos de los genes del TNF $\alpha$ , TNF $\beta$ , e IL-1ra analizados no tienen un papel determinante en la susceptibilidad genética global a la CU en la población catalana estudiada.

2.- La combinación de un marcador genético (IL-1RN) y subclínico (ANCA) identifica a un subgrupo de pacientes con CU (genotipo 1,2 del gen IL-1ra; ANCAp). Este resultado:

2.1. Proporciona evidencia adicional al concepto de heterogeneidad genética en la CU.

2.2. Apoya el papel de los ANCA como marcadores subclínicos de heterogeneidad genética en la CU.

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