

TOPIC HIGHLIGHT

Walter Fries, MD, Series Editor

Enteropathic spondyloarthropathy: A common genetic background with inflammatory bowel disease?

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Abstract

The association between spondyloarthropathy and inflammatory bowel disease (IBD) is largely established, although prevalence is variable because of different population selection and diagnostic methodologies. Most studies indicate that as many as 10%-15% of cases of IBD are complicated by ankylosing spondylitis (AS) or other forms of spondylarthritis (SpA). Of note, ileal inflammation resembling IBD has been reported in up to two thirds of cases of SpA, and it has been suggested that the presence of ileitis is associated with the chronicity of articular complications. Although this observation is of interest to unravel the pathophysiology of the disease, systematic screening of patients with SpA by ileocolonoscopy is not indicated in the absence of gut symptoms, as only a small proportion of patients with subclinical gut inflammation will develop overt IBD over time. The existence of familial clustering of both IBD and AS, the coexistence of both conditions in a patient, the evidence of an increased risk ratio among first- and second-degree relatives of affected AS or IBD patients and finally, the increased cross-risk ratios between AS and IBD, strongly suggest a shared genetic background. So far, however, IL23R is the only identified susceptibility gene shared by both IBD and AS. Although functional studies are still

needed to better understand its pathogenic role, great effort is being spent therapeutically targeting this pathway that may prove effective for both disorders.

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INTRODUCTION

Crohn's disease (CD) and ulcerative colitis (UC) are chronic relapsing inflammatory bowel diseases (IBDs) of unknown etiology that affect up to 1 in 250 of the adult population, with up to 25% of patients being diagnosed during childhood or adolescence^[1]. Key features of UC include diffuse mucosal inflammation that extends proximally from the rectum. In CD, conversely, any site in the gastrointestinal tract may be affected with transmural inflammation, which is typically patchy and segmental^[2]. Joint complications are the most common extra-intestinal manifestations of IBD, and were recognized as far back as the 1920s. Both axial and peripheral joint complications are recognized. This review mainly focuses on the so-called enteropathic spondyloarthropathy, and more specifically, on the possible pathogenic link which may lie in a common genetic background with IBD.

ANKYLOSING SPONDYLITIS (AS)

AS is a seronegative inflammatory arthropathy that affects

the vertebral column, and is characterized by sacroiliitis and progressive ankylosis (fusion) of the vertebral facet joints. It is defined classically by the modified New York Criteria^[3], which include: low back pain for more than 3 mo; relieved by exercise and not improved by rest; limited spinal movement in two planes; and decreased chest expansion. If any of these clinical features is present in association with bilateral grade 2-4 or unilateral grade 3-4 sacroiliitis, then a definitive diagnosis can be made. However, there is some overlap with the more general term of sponyloarthropathy (SpA), as defined by the European Study Group on Spondyloarthropathy^[4]. This involves a combination of inflammatory low back pain and a number of other factors including associated conditions, such as IBD or enteric infection, post-dysenteric reactive arthritis, psoriatic arthritis, and post-urethritis arthritis. The prevalence of AS in the general population is 0.25%-1%^[5,6], but it is increased in IBD patients to 1%-6%, depending on the study population and the method of investigation^[7,8]. In a recent population-based study in Italy^[9], the prevalence of AS was 0.37%, while IBD-associated arthritis accounted for 0.09%. However, the clinical spectrum might be broader than that so far defined. In a population-based inception cohort of IBD patients evaluated in Italy and Netherlands, 18% satisfied the European criteria for SpA, 3.1% satisfied the modified New York criteria for AS, however, 14.4% patients developed one or more SpA-related manifestations, without fulfilling any of the classification criteria^[10].

The traditional method of radiological assessment is by plain radiology of the sacroiliac joints. Magnetic resonance imaging has demonstrated a higher sensitivity^[59], although in the absence of symptoms, its significance is sometimes unclear. Idiopathic AS is more common in male subjects, with an M:F ratio of 3:1, whereas in IBD, the M:F ratio is closer to 1:1. The main lesion of AS is sacroillitis and this is associated with inflammatory low back pain. The symptoms are characterized by an insidious onset over several months, morning stiffness, and exacerbation of pain by rest. The evolution of AS is usually independent of the bowel disease, and more often runs a more benign clinical course than idiopathic AS^[11].

ISOLATED SACROILIITIS

Isolated sacroiliitis may occur in association with IBD, without evidence of progressive spinal disease. Although some patients complain of low back pain, in many cases, they may be asymptomatic, therefore, prevalence is dependent largely upon the investigation. Radiographic surveys suggest a prevalence of 18%^[7], but higher prevalence is estimated by means of scintigraphy, with radioisotope uptake found in up to 52% of patients with CD and 42% with UC^[12]. However, given the large degree of inter- and intra-observer error, and the lack of follow-up information about possible progression to AS, the significance of these findings is unclear. In the majority of patients, it seems a non-progressive condition. In clinical practice, diagnosis is usually made

by plain abdominal radiography, but more often it is detected incidentally.

PERIPHERAL ARTHRITIS

Articular manifestations have been reported in association with IBD for many years, but only in the late 1950s was arthritis proven to be inflammatory, and quite distinct from classical rheumatoid arthritis (RA), to be seronegative. Articular manifestations occur in 5%-20% of IBD patients, and more recently, a new classification proposes two distinct clinical forms with specific genetic associations^[13].

Type I peripheral arthropathy, defined as acute, self-limiting inflammation that affects fewer than five joint, and is associated with IBD relapse and the presence of other extra-intestinal manifestations. More often, large weight-bearing joints are affected, particularly knees, wrists and ankles. The median duration of illness is 5 wk, however, 10%-20% of patients will develop persistent symptoms. One third of patients will report one episode over time.

Type II arthritis is a symmetrical, seronegative, small-joint arthropathy, unrelated to disease activity. The onset may occur at any time during the course of IBD or before, and in CD, it is reported more commonly in colonic disease. It usually runs a more chronic course with a median duration of 3 years. The small joints of the hands are more commonly affected.

ROLE OF INTESTINAL INFLAMMATION

The role of intestinal inflammation and luminal factors in SpA is an area of debate. In a large series of ileocolonoscopy examinations with biopsies in patients with SpA[14,15], inflammatory lesions were found in two thirds of patients, with a similar proportion in those with AS and RA. Moreover, the clinical course of articular disease was independent of the presence of gut inflammation, and a minority of patients (3.7%) developed overt IBD. In another study [16], 123 patients with SpA at initial endoscopy were reassessed clinically, and follow-up endoscopy performed in 49 patients. Articular remission rates were independent of initial gut inflammation and associated with endoscopic and histological remission. In addition, initial chronic gut inflammation implies a high risk of evolution of AS. Nevertheless, a potential confounding factor of these studies is that most patients are treated with non-steroidal anti-inflammatory drugs (NSAIDs) which may promote enteropathy that is hardly distinguishable from primary inflammatory lesions of the gut. Furthermore, in a followup study^[17] of some patients still taking NSAIDs, no inflammatory gut lesions were found in those in clinical remission from articular symptoms, while in contrast, half of the patients with articular inflammation had persistent inflammatory gut lesions, and one quarter developed overt IBD. This suggests that intestinal inflammation is important in idiopathic as well IBD-associated AS, possibly by determining an increased antigenic load across the inflamed gut mucosa.

Post-enteric reactive arthritis is associated with Gramnegative enterobacteria such as Salmonella, Escherichia coli, Yersinia and Campylobacter, in these circumstances, bacterial antigens have been isolated in the affected joints. These conditions are clinically very similar to type I IBD arthritis, and it therefore seems likely that bacterial antigens may be important in the initiation of the inflammatory process. Furthermore, stronger support on the role of bacteria in initiating arthritis in the presence of gut inflammation has been gained from a study of HLA-B*27 transgenic animal models. These knock-out animals spontaneously develop colitis and axial and peripheral arthritis when reared under normal conditions^[18,19]. Interestingly, when they are kept in a germ-free environment, gut and joint inflammation is prevented^[19]. Furthermore, different bacteria induce gut and joint inflammation with different efficiency, with Bacteroides vulgatus being the most efficient and E. coli is ineffective [20]. Thus, it appears likely that similarly to IBD, bacteria are important in the pathogenesis of SpA, with an interaction with the immune system. The link between bacteria, gut/joint inflammation and the immune response, might result from a (common) genetic predisposition.

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GENETIC PREDISPOSITION TO SPONDYLOARTHROPATHY

Idiopathic AS is strongly associated with possession of HLA-B*27, with a 94% prevalence in northern European patients, compared with 10% of healthy controls [21,22]. This association is considerably weaker in IBD-associated AS, ranging between 50% and 80% of patients [23-25]. Conversely, 50% of HLA-B*27-positive IBD patients have AS, compared with 1%-10% of B*27-positive individuals in the general population. Putative mechanisms include B*27 presenting peptide from luminal bacteria, or self proteins causing an inflammatory response, or peptides being presented to the immune system by other antigens such as HLA-DR. Central to these theories is the concept of a triggering bacterial antigen, although evidence is lacking. Patients with isolated sacroiliitis are less likely to be HLA-B*27-positive, and HLA-B*27 seems to be a marker of progressive axial disease rather than sacroiliitis, but longterm studies are needed. Other genes in the HLA region have also been implicated including HLA-DR1, TAP and LMP, but none of these findings have been conclusive. Moreover, subsequent studies have demonstrated other HLA associations in IBD arthritis. The association with HLA-DRB1*0103 is solely with type I arthritis, which is also associated with HLA-B*27, whereas type II is associated with B*44 and MICA^[13,26] (Table 1).

A number of studies have demonstrated a striking overlap within patients and family members with rheumatological, dermatological and gastrointestinal diseases. The susceptibility genes of these disorders appear to overlap with each other^[27]. In a study that explored the prevalence of secondary disorders in 3287 AS individuals^[28], the sub-group of patients with IBD-AS had higher prevalence of iritis (OR = 1.4) or psoriasis (OR = 1.9) than the controls. Moreover, patients with multiple

Table 1 HLA associations in IBD and IBD-associated arthropathy^[11]

	HLA antigens investigated	Percentage in IBD + arthropathy affected patients	Percentage in IBD patients without arthropathy
AS	HLA-B*27	60	7
Type I arthritis	HLA-B*27	26	7
	HLA-B*35	33	15
	HLA-DRB1*0103	35	3
Type II arthritis	HLA-B*44	62	31

disorders predicted the highest prevalence of co-existing disease (i.e. psoriasis, IBD, iritis, or AS) within family members. These data suggest that susceptibility factors are additive or have a synergistic effect on each other, thus pointing to a shared gene hypothesis.

GENETIC PREDISPOSITION TO IBD

IBD is widely believed to originate from a dysregulated immune response to luminal bacteria in a genetically susceptible host^[2]. The inheritance model is non-Mendelian but complex-polygenic, with several genes involved together with environmental factors. Of the other environmental factors thought to have an impact on disease susceptibility, only smoking and appendectomy have a substantive evidence base^[29]. Concordance data in twins (36% for CD and 16% for UC, 4% for both CD and UC for monozygotic and dizygotic twins, respectively) and multiplex IBD families (relative risk to first-degree relative of proband up to 35 for CD and 15 for UC) have provided strong epidemiological evidence for a genetic contribution to IBD susceptibility^[30]. These observations have led to the development of genetic investigations with two broad strategies: one has investigated candidate genes, and the other has used hypothesis-free methods of genome-wide scanning.

Overall, candidate gene strategies have not proved to be particularly fruitful in IBD, but one success has been the identification of an association between the major histocompatibility complex (MHC) region and UC susceptibility, initially in Japanese subjects^[31] and later in Europeans^[32]. The DRB1*0103 allele has been implicated in both severe UC and extra-intestinal (mainly articular) manifestations of IBD. Subsequently, 11 genome-wide scans by non-parametric linkage analysis were performed in the 1990s, and several susceptibility loci were identified in approximately half of the chromosomes^[33].

The *NOD2* gene on chromosome 16q12 was the first susceptibility gene for CD to be identified successfully. It was detected by parallel strategies of positional cloning within a region of linkage and positional candidate gene investigation^[34,35], and the finding was subsequently widely replicated in Caucasian, but not in Asian populations. NOD2 encodes an intracellular receptor that is expressed predominantly in monocytes and Paneth cells^[33]. This has been implicated in the innate immune response to muramyldipeptide (MDP), a component of peptidoglycan

in bacterial cell walls. The CD-associated variants that are clustered in the C-terminal leucine-rich repeat part of the NOD2 protein significantly diminish responsiveness to MDP. On exposure to MDP, oligomerized NOD2 recruits RIP2 (the serine-threonine kinase RICK) and subsequently activates nuclear factor-kB transcription factor via NEMO ubiquitination and IkB degradation. This leads to production of cytokines and cryptidins/defensins, hence facilitating clearance of bacteria. In addition, there is evidence of cross-talk between NOD2 and toll-like receptor pathways. However, the precise mechanism by which NOD2 mutations lead to increased intestinal inflammation is unknown, but it may be that reduced ability to clear bacteria by innate immune mechanisms leads to dysregulation of adaptive immune pathways.

Following fine mapping of the IBD5 linkage region on chromosome 5q31, consistent evidence for association between CD and a haplotype of markers spanning 250 kb has been observed. More recently, the same locus has been associated also with UC[36]. However, because of the strong linkage disequilibrium (LD) across this region, it has been very difficult to identify the causal variant. Peltekova et al^[37] have reported a two-locus risk haplotype in the region of the organic cation transporter (OCTN) genes and suggested that this accounts for the association. The two-locus haplotype comprises L503F (1672 C-T, missense substitution) and G207C (transversion) in the SLC22A4 (OCTN1) and SLC22A5 (OCTN2) genes, respectively. However, there remains significant debate as to whether these transcripts are truly implicated by the genetic evidence, and a number of other immunoactive candidates remain in the frame, including interferon regulatory factor 1 (IRF1) and a number of important cytokine genes (IL-3, IL-4, IL-5 and IL-13) located within the 250-kb risk haplotype.

Progress from the Human Genome Project and Hap-Map Project, combined with markedly decreasing genotyping costs, has made possible the performance of adequately powered genome-wide association studies (GWAs) in complex genetic disorders such as IBD. Several GWAs^[38] and a meta-analysis [39] have already been performed in CD and more recently in UC[40] and pediatric IBD[41]. Genome scans have identified 11 susceptibility genes and loci and highlighted a number of new, previously unsuspected pathways as playing an important role in IBD pathogenesis, including the IL23 pathway in IBD overall and specific aspects of innate immunity (particularly the autophagy genes ATG16L1 and IRGM) in CD. As expected, a number of genes such as IL23r, IL12B, MHC, STAT3, IBD5, MST1, PTPN2, NKX2-3 seem to be shared in the predisposition to both UC and CD (Table 2).

COMMON GENETIC LINK BETWEEN IBD AND SPONDYLOARTHROPATHY

IBD and AS show familial clustering and may coexist in a patient. More intriguingly, healthy first-degree relatives of patients with AS (21%-60%) and CD (10%-54%) have increased permeability of the small intestine [42-44]. These changes might be a consequence of subclinical

Table 2 Candidates genes and loci in CD and UC

	Genes and loci	Associated with CD	Associated with UC
1p31	IL23R	Yes	Yes
1q21	ECM1	-	Yes
2q37	ATG16L1	Yes	No
3p21	Several	Yes	Yes
	included MST1-BSN		
5p13	Intergenic, PTGR4	Yes	No
5q31	Several	Yes	Yes
	included SLC22A5		
5q33	IRGM	Yes	No
5q33	IL12B	Yes	Yes
6q21	HLA-DQ/DR	Yes	Yes
10q21	ZNF365	Yes	Yes
10q24	NKX2-3	Yes	Yes
16q12	NOD2	Yes	No
17q21	Several included STAT3	Yes	Yes
18p11	PTPN2	Yes	Yes

CD: Crohn's disease; UC: Ulcerative colitis.

intestinal inflammation, and conform to the profile of an additive trait in both conditions^[45,46]. Evidence from studies of twins and other first-degree relatives suggests that the genetic basis is somewhat stronger for IBD than for AS^[47-50].

In the pre-GWA era, studies investigating a possible common genetic background in IBD and articular involvement were concentrated mainly on MHC and NOD2. It has been recognized that genes in the HLA region have a greater role for modifying IBD phenotype than in determining overall disease susceptibility. Within UC clinical subgroups, the uncommon DRB1*0103 allele is associated with both extensive and severe disease, with an early need for surgery^[51]. Interestingly, the same allele has also been associated with CD colitis, thus suggesting the molecular basis of a colonic IBD phenotype. Furthermore, type I pauciarticular large-joint arthritis is also associated with this allele and other class I alleles (B*27 and B*35) in LD. However, the low frequency of this allele suggests that this association is unlikely to be clinically useful in predicting disease course. In addition, an increased prevalence of extraintestinal manifestations has been reported previously in colonic IBD, increasing the possibility that the association between DRB1*0103 and articular manifestations may merely mirror the association with colonic disease. Finally, recent evidence from GWA scans has at least refined the signal to the 400-kb haplotype block that contains DRB1*0103, and shows that this locus is common to UC and the colonic (but not small bowel) sub-phenotype of CD^[52].

Crane *et al*^[53] have investigated the hypothesis that the three major variants of the NOD2 gene are involved in AS. A case-controlled study was performed in 229 AS, 197 IBD-associated AS (78 with CD and 119 with UC), and 229 ethnically matched healthy controls. The Gly908Arg variant was associated with UC-associated AS (OR = 4.6, 95% CI = 1.3-16, P = 0.016), with a similar non-significant trend in CD-associated AS (OR = 3.9, 95% CI = 0.8-18, P = 0.08). In contrast, no association was found between

NOD2 variants and primary AS, or other variants with UC- or CD-associated AS. Moreover, carriage of the Pro268Ser variant was associated with greater disease activity. Similarly, in subsequent studies, variants of NOD2 do not appear to confer susceptibility to AS^[54], but rather identify a subgroup of patient with CD-associated AS^[55].

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Recently, the Wellcome Trust Case Control Consortium and the Australo-Anglo-American Spondylitis Consortium have published the first association scan with 14 436 non-synonymous single nucleotide polymorphisms (SNPs) in 922 independent cases of AS, together with autoimmune thyroid disease, multiple sclerosis and breast cancer, against a common control dataset of 1500 healthy individuals $^{\scriptscriptstyle{[56]}}$. The strongest association in AS was observed in the MHC region, centered around the HLA-B genes, but the association of $P < 10^{-20}$ was observed across about 1.5 Mb, probably reflecting the strong effect of HLA-B27, even over distant SNPs with modest LD. To validate less strong signals obtained at the first scan, a further 471 independent AS cases and 625 new controls were genotyped with additional SNPs. In the combined data set, a strong association ($P = 1.2 \times 10^{-8}$ to 3.4×10^{-10}) with SNPs of the ARTS1 gene (OR = 1.4) and IL23R gene (peak P value of 7.5×10^{-9} at the rs11209032 with an OR of 1.3) was found. The association with IL23R remained strong when considering individuals with AS not having IBD (n = 1066). These genes both represent excellent biological candidates, but more importantly, IL23R has been documented recently in CD and psoriasis^[57], which suggests that this gene is a common susceptibility factor for the major seronegative diseases, at least partially explaining their co-occurrence. IL23R is a key factor in the regulation of a newly defined effector T-cell subset, TH17 cells^[33]. They express high levels of the cytokine IL-17 in response to stimulation, in addition to IL-1, IL-6, tumor necrosis factor α, IL-22 and IL-25. In animal models, blocking IL-23 reduces inflammation, which suggests that IL23R variants associated with disease are pro-inflammatory. No functional studies of IL23R variants are available to date, however a promising treatment of CD has been reported with anti-IL-12p40 antibodies, which block IL-12 and IL-23, as these cytokines share the p40 subunit^[58].

A different perspective was employed in a study that explored the possible common genetic background of IBD and AS through a genealogical evaluation in Iceland^[59]. Icelanders are relatively homogeneous with respect to the environment, cultural aspects and genetic factors; moreover, extensive genealogical records and diseases registries are available. By investigating the genealogical database and registry of subjects with AS (n = 205) and IBD (n = 1352), the risk ratios for relatives for each disease and the cross-risk ratios (AS vs IBD and vice versa) were estimated. First-, second- and third-degree relatives of patients with AS, had risk ratios of 94, 25 and 3.5, respectively, of developing AS (each P < 0.0005), while first-, second- and third-degree relatives of patients with IBD had risk ratios of 4.4, 2.2 and 1.4, respectively (each P < 0.0001). More intriguingly, the cross-risk ratio was 3.0 and 2.1 (P < 0.0001), respectively, in first- and second-degree relatives, with a comparable effect for UC and CD. This elevated cross-risk ratio between IBD and AS strongly suggests that there is a genetic component shared by these complex diseases, and should stimulate further molecular and functional studies.

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CONCLUSION

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The clinical association between spondyloarthropathy and IBD is well-established, with studies indicating that as many as 10%-15% of cases of IBD are complicated by AS or other forms of SpA^[60]. Ileal inflammation that resembles IBD has been reported in up to two thirds of cases of SpA, and it has been suggested that the presence of ileitis is associated with the chronicity of articular complications. Moreover, evidence that there is familial clustering of IBD and AS, that both conditions may coexist in patients, that there is an increased risk ratio among first- and second-degree relatives of affected AS or IBD patients and finally, that there is an increased crossrisk ratios between AS and IBD, confirm the existence of a shared genetic predisposition. So far, IL23R is the only identified susceptibility gene shared by IBD and AS. Functional studies are still needed to better understand its functional role, but it is hoped that treatment that targets this pathway may prove effective in both disorders.

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