Transmission disequilibrium test of stromelysin-1 gene variation in relation to Crohn’s disease

S LF Pender, P JP Croucher, S Mascheretti, J D Prothero, S A Fisher, T T MacDonald, S Schreiber, Shu Ye

C rohn’s disease (MIM 266600) and ulcerative colitis (MIM 191390) are the major forms of inflammatory bowel disease (MIM 601458), the prevalence of Crohn’s disease being more than 1/1000 in the Western countries. Inflammatory bowel disease is characterised by chronic relapsing intestinal inflammation, and its pathogenesis probably involves microbial, immunological, environmental, and genetic factors. Recent genetic association studies have shown that sequence variations in the Caspase Activating Recruitment Domain (CARD15) gene (MIM605956, formerly named NOD2) on chromosome 16q are a strong genetic factor for Crohn’s disease but not for ulcerative colitis. CARD15 represents the first major Crohn’s disease susceptibility gene identified, and its identification might facilitate the uncovering of other genetic factors for the disease.

The matrix metalloproteinases (MMP) are a group of matrix degrading enzymes that play an important role in the pathogenesis of various inflammatory diseases including osteoarthritis, rheumatoid arthritis, atherosclerosis, cancers, and inflammatory bowel disease. We have shown that, of four MMPs studied (interstitial collagenase, gelatinase A and B, and stromelysin-1), stromelysin-1 in particular is directly involved in mucosal destruction following T cell activation in the human fetal gut. Furthermore, patients with Crohn’s disease have increased expression of stromelysin-1 in the mucosa at both the mRNA and protein levels. Microarray techniques have demonstrated that stromelysin-1 expression is increased 8.7-fold in the mucosa of patients with Crohn’s disease compared with healthy controls (Pender SLF, unpublished data), and have also shown that stromelysin-1 expression is 8.2-fold higher relative to controls in PWM-stimulated human fetal gut explant culture. Thus, although the stromelysin-1 gene on chromosome 11q23 is not located within the particular chromosomal regions (19p13, 16q12, 16p, 14q11–q12, 12p13.2–q24.1, 6p, 5q31, and 1p36) that have been shown to be in linkage with inflammatory bowel disease (MIN 266600), it is a strong functional candidate gene that might have an influence on this multifactorial disorder.

We have previously identified a functional polymorphism in the promoter of the stromelysin-1 gene. The polymorphism arises from insertion or deletion of an adenosine within a cluster of adenosines located at position −1612 and upwards, relative to the transcriptional start site of the gene, with one allele having a cluster of five adenosines (5A) and the other allele having six adenosines (6A). In vitro assays have shown that the 5A allele has a higher promoter activity than the 6A allele, with differential binding of a nuclear protein to the two allelic promoters.

Given that increased stromelysin-1 expression plays an important role in the development of Crohn’s disease and that the 5A/6A polymorphism has an allele specific effect on stromelysin-1 expression, individuals carrying the 5A allele might have increased susceptibility to Crohn’s disease. We tested this hypothesis in the present study.
UK), and several additional German centres. The characteristics of the subjects have been described previously.\(^5\)\(^\text{13–16}\)

Informed, written consent was obtained from all study participants. Recruitment protocols were approved by ethics committees at the participating centres before the study began. The diagnosis of inflammatory bowel disease and the classification into Crohn’s disease and ulcerative colitis were determined by standard diagnostic criteria.\(^12\)\(^\text{14}\) Clinical, radiological, and endoscopic examinations (type of lesions, distribution) were required for unequivocal confirmation of the diagnosis of either ulcerative colitis or Crohn’s disease. Histological findings also had to be confirmatory or compatible with this diagnosis. In cases of uncertainty, the diagnosis of indeterminate colitis was assigned and the patient excluded from the study.

**Genotyping**

Genomic DNA was prepared from 10 ml of fresh or frozen peripheral venous blood using the Puregene system (Gentra Systems, Minneapolis, Minnesota, USA). Individual DNA samples were arrayed in 96-well microtitre plates. The stromelysin-1 gene 5A/6A polymorphism was genotyped by TaqMan 5’-nuclease assay using the following primers and probes (designed on the reverse strand): forward primer 5’ GCCACCACTCGTTCTCTGTC 3’, reverse primer 5’ CACGCACCTGGCTAAAGA 3’, first probe (6A) 5’-TGGTTTTTCGCCCTAC 3’, second probe (5A) 5’-CAAGACATGG 3’, first probe (6A) 5’-CAAGACATGG 3’, second probe (5A) 5’-CAAGACATGG 3’, and in the German and British families were undertaken using the TRANSMIT program\(^2\)\(^\text{21}\) with the robust variance estimator option. TDT of the 5A/6A polymorphism in relation to various phenotypes of Crohn’s disease in the German trios was also carried out using the TRANSMIT program. Significances were verified using 10,000 bootstrap replicates.

Possible interaction between the stromelysin gene and the CARD15 gene was examined by stratifying the patients according to their CARD15 genotype. Individuals carrying one or more copies of the R702W, G908R, or 1007insC mutations\(^4\)\(^\text{6}\) were classified as CARD15+, and individuals not carrying these mutations as CARD15−.

**RESULTS**

**Analyses in German sporadic inflammatory bowel disease trios**

Transmission disequilibrium tests in the German sporadic inflammatory bowel disease trios showed a highly significant association between Crohn’s disease and overtransmission of the 5A allele (p = 0.0012, table 2). No significant association between ulcerative colitis and the stromelysin-1 gene was detected.

There was an interaction between stromelysin-1 and CARD15 genes, such that the association of the stromelysin-1 gene 5A allele with Crohn’s disease was apparent only in individuals carrying one or more mutations in the CARD15 gene (p = 0.0054, table 3). In CARD15 mutation carriers, overtransmission of the 5A allele was associated with various Crohn’s disease traits, including stenosis (p = 0.0027), fistulising disease (p = 0.0007), previous surgical resection (p = 0.0023), and disease of the ileum (p = 0.0001) and right colon (p = 0.0115; NS after correcting for multiple testing) (table 3).

There was no evidence of interaction between the stromelysin gene and smoking in relation to the development of Crohn’s disease. In individuals carrying one or more mutations in the CARD15 gene, there was significant overtransmission of the 5A allele in the trios, regardless whether the offspring had smoked (observed/expected 5A allele transmission, 69/59.65; p = 0.0147) or had never smoked (observed/expected 5A allele transmission ratio, 76/65.87; p = 0.0239).

In non-carriers of the CARD15 gene mutations, there was no significant overtransmission of the 5A allele in the trios, regardless of whether the offspring had smoked or not (p = 0.6231, p = 0.6379, respectively).

**Analyses in the multiplex inflammatory bowel disease families**

No significant association between the stromelysin-1 5A/6A polymorphism and Crohn’s disease or ulcerative colitis was detected in the German and British families with familial inflammatory bowel disease (table 2), and this was not affected by stratification for CARD15 genotype.

**DISCUSSION**

In this study we showed an association of Crohn’s disease susceptibility with the stromelysin-1 gene 5A/6A polymorphism in a cohort of German sporadic Crohn’s disease trios. As increased stromelysin-1 gene expression plays an important role in the pathogenesis of inflammatory bowel disease, these findings support the hypothesis that stromelysin-1 gene mutations contribute to inflammation in inflammatory bowel disease.

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**Table 1** Subjects genotyped for the stromelysin-1 gene 5A/6A polymorphism

<table>
<thead>
<tr>
<th>Disease</th>
<th>Number of trios or families</th>
<th>Number of affected offspring per family</th>
<th>Number of trios or families where both parents were genotyped</th>
</tr>
</thead>
<tbody>
<tr>
<td>German sporadic</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>CD</td>
<td>320</td>
<td>1</td>
<td>318 (1e, in 99.4% of the collection)</td>
</tr>
<tr>
<td>UC</td>
<td>148</td>
<td>1</td>
<td>147 (1e, in 99.3% of the collection)</td>
</tr>
<tr>
<td>German multiplex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IBD trios</td>
<td>135</td>
<td>1</td>
<td>115 (e, in 85.2% of the collection)</td>
</tr>
<tr>
<td>UC</td>
<td>83</td>
<td>1</td>
<td>70 (1e, in 84.3% of the collection)</td>
</tr>
<tr>
<td>British multiplex</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>IBD families</td>
<td>91</td>
<td>1</td>
<td>78 (1e, in 85.7% of the collection)</td>
</tr>
<tr>
<td>UC</td>
<td>49</td>
<td>1</td>
<td>42 (1e, in 85.7% of the collection)</td>
</tr>
</tbody>
</table>

CD, Crohn’s disease; IBD, inflammatory bowel disease; UC, ulcerative colitis.
role in the development of Crohn’s disease, the association of the stromelysin-1 gene 5A allele with increased Crohn’s disease susceptibility is likely to reflect increased expression of stromelysin-1 in 5A allele carriers, which would be consistent with results of functional studies showing that the 5A allele had a higher transcriptional activity than the 6A allele. We also found that there is an interaction between the stromelysin-1 gene and the CARD15 gene in determining Crohn’s disease susceptibility. The underlying mechanism for this observation is unclear. One possibility would be that non-genetic factors play a greater role in the non-carriers of the CARD15 gene mutations than in the carriers, making the modest effect of the stromelysin-1 gene less detectable in the non-carriers of the CARD15 gene mutations. The possibility that stromelysin-1 and CARD15 interact at the cellular or molecular level could not be ruled out.

As smoking is an established environmental risk factor for Crohn’s disease, and previous studies have shown an interaction between the 5A/6A polymorphism and smoking in relation to the risk of coronary heart disease, we explored whether there was an interaction between the 5A/6A polymorphism and smoking in Crohn’s disease, but did not find evidence of such an interaction.

The association between the stromelysin-1 gene 5A/6A polymorphism and Crohn’s disease was not detected in the multiplex families in this study. There are several possible explanations for the presence of an association of Crohn’s disease with the stromelysin-1 gene 5A/6A polymorphism in the sporadic Crohn’s disease trios, and the absence of such an association in the multiplex families. First, it is possible that the stromelysin-1 gene 5A/6A polymorphism is associated with a subset of Crohn’s disease phenotypes that are enriched in the sporadic Crohn’s disease trios but underrepresented in the multiplex Crohn’s disease families. However, we did not find a significant difference between the trios and the multiplex families in the frequencies of the phenotypes listed in table 3. Second, as the trios represent sporadic inflammatory bowel disease whereas the multiplex families represent familial disease, it is possible that other not yet identified genes have greater effects on the development of Crohn’s disease in the multiplex families than in the sporadic Crohn’s disease trios, and thus the modest effect of the stromelysin-1 gene would be more easily detectable in the latter than in the former. Another possible explanation might be the lack of statistical power in the family samples, as the sample sizes of the German and British multiplex families and the case-control set were substantially smaller than those of the trio collection. In addition, in about 15% of the German and British families only one parent was genotyped, which would further reduce the statistical power in these samples. In comparison, in nearly 100% of the trios, both parents were genotyped.

In this study, no association between ulcerative colitis and the stromelysin-1 gene 5A/6A polymorphism was detected. Although Crohn’s disease and ulcerative colitis are both major forms of inflammatory bowel disease, previous studies have shown that CARD15 gene mutations are associated with Crohn’s disease but not with ulcerative colitis, suggesting that they have different pathological mechanisms.

Functional studies have revealed that the 5A allele has a higher transcriptional activity than the 6A allele, with preferential binding of a transcription repressor to the latter. Stromelysin-1 plays an important role in the development of several diseases where the pathogenesis involves inflammation and matrix degradation and remodeling. An association between the 5A/6A polymorphism and phenotypes of coronary heart disease has been shown in various studies, such that carriers of the 5A allele have increased risk of myocardial infarction—a clinical event associated with matrix degradation in coronary atherosclerotic plaques—whereas 6A homozygotes have greater atherosclerotic plaque growth, which is associated with matrix accumulation. Taken together, the functional data and genetic epidemiological observations indicate that genetic variation in the promoter of the stromelysin-1 gene can alter the levels of stromelysin-1 expression, leading to an imbalance between synthesis and degradation of vascular matrix—that is, an imbalance favouring matrix degradation in individuals carrying the 5A allele, contrasted by an imbalance favouring matrix accumulation in 6A homozygotes.

In addition to atherosclerosis, several other pathological conditions have been associated with the stromelysin-1 gene 5A/6A polymorphism. For example, a recent study showed that this polymorphism is associated with susceptibility and progression of primary sclerosing cholangitis. An association between this genetic variation and rheumatoid arthritis has also been reported. The results of our present study suggest that the stromelysin-1 5A/6A polymorphism might also be related to Crohn’s disease. However, the findings of this study need confirmation in an independent study before the stromelysin-1 gene may be considered an established

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**Table 2** Results of transmission disequilibrium test

<table>
<thead>
<tr>
<th>Group (IBD)</th>
<th>O/E</th>
<th>p Value*</th>
<th>Group (UC)</th>
<th>O/E</th>
<th>p Value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>German sporadic IBD trios</td>
<td>279/250.63</td>
<td>0.0012</td>
<td>129/128.98</td>
<td>0.9955</td>
<td></td>
</tr>
<tr>
<td>German multiplex IBD families</td>
<td>252/247.51</td>
<td>0.5133</td>
<td>124/119.91</td>
<td>0.4331</td>
<td></td>
</tr>
<tr>
<td>British multiplex IBD families</td>
<td>151/152.69</td>
<td>0.7600</td>
<td>62/64.46</td>
<td>0.4642</td>
<td></td>
</tr>
</tbody>
</table>

*After 10 000 bootstrap replicates.

**Table 3** Results of transmission disequilibrium test in German sporadic inflammatory bowel disease trios stratified for CARD15 genotype

<table>
<thead>
<tr>
<th>CARD15</th>
<th>O/E</th>
<th>p Value*</th>
</tr>
</thead>
<tbody>
<tr>
<td>+</td>
<td>166/147.49</td>
<td>0.0054</td>
</tr>
<tr>
<td>+</td>
<td>170/167.04</td>
<td>0.6718</td>
</tr>
<tr>
<td>+</td>
<td>116/98.56</td>
<td>0.0027</td>
</tr>
<tr>
<td></td>
<td>100/100.89</td>
<td>0.871</td>
</tr>
<tr>
<td>+</td>
<td>103/84.60</td>
<td>0.0007</td>
</tr>
<tr>
<td>+</td>
<td>90/90.39</td>
<td>0.942</td>
</tr>
<tr>
<td>+</td>
<td>106/89.39</td>
<td>0.0023</td>
</tr>
<tr>
<td></td>
<td>89/87.87</td>
<td>0.8284</td>
</tr>
<tr>
<td>+</td>
<td>147/124.78</td>
<td>0.0001</td>
</tr>
<tr>
<td>+</td>
<td>124/124.84</td>
<td>0.891</td>
</tr>
<tr>
<td>+</td>
<td>124/109.3</td>
<td>0.0115</td>
</tr>
<tr>
<td>+</td>
<td>114/114.84</td>
<td>0.8805</td>
</tr>
<tr>
<td>+</td>
<td>57/52.19</td>
<td>0.2165</td>
</tr>
<tr>
<td>+</td>
<td>113/113.56</td>
<td>0.9206</td>
</tr>
</tbody>
</table>

*After 10 000 bootstrap replicates.

CARD15 mutation, + indicates carriers of the R702W, G908R, or 1007insC mutation; − indicates non-carriers.

O/E, observed/expected 5A allele transmission ratio.
Acknowledgements

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Conflicts of interest: none declared

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