**INFLAMMATORY BOWEL DISEASE**

**DLG5 variants do not influence susceptibility to inflammatory bowel disease in the Scottish population**

C L Noble, E R Nimmo, H Drummond, L Smith, I D R Arnott, J Satsangi

**Introduction:** Recent data have suggested that specific haplotypic variants of the DLG5 gene on chromosome 10q23 may be associated with susceptibility to inflammatory bowel disease (IBD) in Germany. Haplotype D, notably characterised by the presence of a G→A substitution at nucleotide 113, was associated with susceptibility to Crohn’s disease (CD) whereas an extended haplotype A conferred protection.

**Aims:** Association of DLG5 haplotypic variants with disease susceptibility, genotype-phenotype relationships, and epistasis with CARD15 was investigated in the Scottish population.

**Patients and methods:** A total of 374 CD, 305 ulcerative colitis (UC), and 294 healthy controls (HC) were studied. Genotyping for the variants rs1248696 (113A, representing haplotype D) and the single nucleotide polymorphism tag rs2289311 (representing haplotype A) were typed using the Taqman system.

**Results:** On analysis of the DLG5 variant 113A, there were no associations with IBD when allelic frequency (11.4% IBD vs 13.2% HC; p = 0.30) and carrier frequency (19.2% IBD vs 24.6% HC; p = 0.069) were analysed. No associations were observed between 113A variant allelic frequency (p = 0.37), carrier frequency (p = 0.057), and CD. In fact, 113A heterozygosity rates were lower in CD (16%) and IBD (16.9%) than in HC (23%) (p = 0.029 and p = 0.033, respectively). No associations between DLG5 and UC were observed. Haplotype A was not protective and there was no evidence of epistasis between DLG5 and CARD15.

**Conclusions:** The present data contrast strongly with previous data from Germany. DLG5 113A is not associated with disease susceptibility and haplotype A does not confer resistance. Further work is required to evaluate the significance of DLG5 in other populations from geographically diverse regions.
contains 32 exons, and is expressed most strongly in placental tissue and less so in heart, skeletal muscle, liver, small bowel, and colon.26

Stoll and colleagues22 identified two extended DLG5 haplotypes that influenced disease susceptibility in the German population. The first haplotype (named haplotype D) was notably rare for the presence of a G→A substitution at nucleotide 113 that resulted in an amino change at position 30 from arginine to glutamine (R30Q). On analysis of carrier frequency, Stoll et al found the 113A variant to be associated with CD (25% CD v 17% healthy controls; χ² = 0.001) in a case control study and trends between 113A transmission and IBD (p = 0.09) and CD (p = 0.065) were observed on transmission disequilibrium testing.22 In silico analysis suggests that the 113A (R30Q) variant may impair DLG5 scaffolding function, but as yet no expression or functional studies in IBDs have been conducted. Evidence of epistasis between the 113A variant of DLG5 and CARD15 variants was also observed in the CD cohort.22

The second haplotype (haplotype A) was tagged by eight marker SNPs and was observed to be significantly under transmitted in the IBD group (p = 0.006), suggesting the haplotype may be protective.22 No phenotypic associations were investigated and as yet no replication data have been published. In the present study, we have assessed the contribution of the DLG5 polymorphisms rs1248696 (113A) and rs2289311 (one of the marker SNPs for the protective haplotype A) in determining genetic susceptibility to CD and UC in the Scottish population which has a high incidence of IBD. We have also investigated genotype-phenotype associations in our rigorously defined IBD population and assessed epistasis with established CARD15 mutations.

PATIENTS AND METHODS

A total of 679 patients with well characterised IBD (IBD) and 294 controls were recruited. All IBD patients attended the clinic at the Western General Hospital, Edinburgh, a tertiary referral centre for IBD in the South East of Scotland. The group comprised of 374 patients with CD and 305 with UC. The diagnosis of IBD adhered to the criteria of Lennard-Jones.21 CD patients were classified according to the Vienna classification which involves age at diagnosis (A1, <40 years; A2, >40 years), location (L1, terminal ileum; L2 colon; L3, ileocecal; L4, upper gastrointestinal), and behaviour (B1, non-stricturing, non-penetrating; B2, stricturing; B3, penetrating).22 UC disease severity was judged by the criteria proposed by Truelove and Witts.23 Phenotypic data were collected by patient questionnaire, interview, and case note review, and comprised of demographics, date of onset of symptoms and diagnosis, disease location, disease behaviour, progression, extraintestinal manifestations, surgical operations, smoking history, joint symptoms, family history, and ethnicity. The study protocol was approved by Lothian Research Ethics Committee (LREC 2000/4/192).

Demographics: CD and UC

The demographics of the CD and UC patients are shown in table 1. Duration of follow up was defined as the time from diagnosis to the time of the most recent clinic review (median duration 11.8 years in the CD group and 7.5 years in the UC group). The CD group consisted of 181 males and 193 females and the UC group 171 males and 134 females, with a median age at diagnosis of 34 years. Vienna disease classification was available for 347 (93%) CD patients at diagnosis and 374 (100%) CD patients at follow up. Full phenotypic data were available for the UC cohort.

Control subjects

A total of 294 controls (163 blood donors from the south east of Scotland and 131 healthy controls subjects) were enrolled. Allelic frequencies of DLG5 variant SNPs 113A, rs2289311, OCTN1 variant rs1050152, OCTN2 variant rs26313667, and IBD5 marker SNP IGR2198 are shown in table 2.

Genotyping

Genomic DNA was extracted from peripheral venous blood by a modified salting out technique and resuspended in 1×TE (10 mM Tris (pH 8.0), 1 M EDTA (pH 8.0)) at a final concentration of 100 ng/μl. SNPs rs1248696 (113G→A representing haplotype A) and rs2289311 (chosen because of its reliability in genotyping to represent the protective haplotype A; M Stoll, personal communication) were typed using the Taqman system. IBD patients and controls were
typed for polymorphisms of the CARD15 gene (R702W, G908R, and 1007fsinsC) using previously described methods. All genotyping except R702W was carried out using the Taqman system. R702W genotyping was performed by restriction fragment length polymorphism polymerase chain reaction. Restriction digestion was performed using 1 μM MspI at 37°C overnight and polymerase chain reaction fragments run on 4% NewSieve 3:1 agarose gels. These were stained with ethidium bromide and viewed under ultraviolet light. An image was recorded digitally.

**Data analysis**

The two SNPs rs1248696 and rs2289311 were analysed for associations with IBD overall, CD, UC, and disease phenotype. Allelic frequency, carrier frequency, heterozygosity, and homozygosity rates were studied. Each allele was shown to be in Hardy-Weinberg equilibrium. Genotype-phenotype associations were analysed by x² analysis using the Minitab statistical software package version 13/02 (Minitab Ltd, Coventry, UK). To identify significant independent variables associated with genotype, univariate and multivariate analysis was carried out. Evidence for DLG5 epistasis with CARD15 was investigated by stratifying DLG5 variants by carriage of one or more of the common CARD15 variants—R702W, G908R, and 1007fsinsC. Allelic frequencies of the DLG5 variants were compared between the subgroups of patients with and without CARD15 variants by x² analysis. The null hypothesis was that the frequency of DLG5 variants did not differ between these subgroups. Phenotypic associations of DLG5 variants were also stratified for the presence and absence of CARD15 variants.

### Table 2: Demographics and allelic frequencies in the blood transfusion samples and healthy volunteer control samples

<table>
<thead>
<tr>
<th>Age (y) (median IQR)</th>
<th>Sex (M/F)</th>
<th>Allelic frequency</th>
<th>Carrier frequency</th>
<th>Heterozygosity frequency</th>
<th>Homozygosity frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Blood transfusion</td>
<td>Healthy control samples</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>35 (26-47)</td>
<td>83/79</td>
<td>14.4%</td>
<td>30.4%</td>
<td>43.5%</td>
<td>49%</td>
</tr>
<tr>
<td>36 (29-51)</td>
<td>52/55</td>
<td>12%</td>
<td>33%</td>
<td>42.4%</td>
<td>46%</td>
</tr>
</tbody>
</table>

IQR, interquartile range.

Allelic frequencies of DLG5 variant single nucleotide polymorphisms (SNPs) 113A, rs2289311, OCTN1 variant rs1050152, OCTN2 variant rs26313667, and IBDS marker SNP IGR2198 are shown to illustrate the consistency between the blood transfusion controls and the healthy volunteer controls.

**RESULTS**

**Disease susceptibility: haplotype D (113A)**

On analysis of the DLG5 variant 113A there were no associations with IBD when allelic frequency (11.4% IBD v 13.2% healthy controls (HC); p = 0.30), carrier frequency (19.2% IBD v 24.6% HC; p = 0.069), and homozygosity rates (2.3% IBD v 1.5% HC; p = 0.48) were analysed (table 3). A negative association was observed between heterozygous rates of 113A and IBD (16.9% IBD v 23% HC; p = 0.033). Furthermore, a negative correlation was observed between heterozygous 113A variants and CD (16% CD v 23% HC; p = 0.029). No associations were observed between 113A variant allelic frequency (11.4% CD v 13.2% HC; p = 0.37), carrier frequency (18.3% CD v 24.6% HC; p = 0.057), homozygous rates (p = 0.36), and CD. No associations between 113A and UC were observed—allelic frequency (12.8% UC v 13.2% HC; p = 0.34), carrier frequency (20.3% UC v 24.6% HC; p = 0.23), heterozygous rates (18% UC v 23% HC; p = 0.45), and homozygous rates (23% UC v 15% CD; p = 0.5).

**DLG5 haplotype A**

Haplotype A allelic frequencies, represented by rs2289311 variants, did not differ between HC (31.5%) and IBD (35%); p = 0.17, CD (36.9%; p = 0.078), or UC (33.4%; p = 0.51) patients. No significant differences were observed between carriage rates of rs2289311 variants—HC (52%), IBD (57.2%; p = 0.18), CD (60.9%; p = 0.052), and UC (54%; p = 0.65). The frequency of patients who were heterozygotes or homozygotes for rs2289311 polymorphisms did not differ between IBD and HC groups (heterozygous HC 41.1% IBD 44.8% (p = 0.43), CD 48% (p = 0.13), and UC 42.1% (p = 0.83); homozygous HC 10.9% IBD 12.6% (p = 0.49), CD 12.6% (p = 0.61), and UC 12.9% (p = 0.50).

**Phenotypic analysis**

On univariate analysis of CD patients, no association was observed between DLG5 113A variants and the Vienna classification for age of diagnosis, location of disease, or disease behaviour. Location of disease and disease behaviour in CD patients was analysed at the time of diagnosis and at the most recent follow up and there was no association between DLG5 113A variants and disease progression. No association was observed between DLG5 113A variants and age at diagnosis in the IBD and UC groups and there was no association between DLG5 113A variants, disease extent, and severity in UC patients.

DLG5 113A variants displayed a trend towards being less common in IBD patients with joint problems (large joint arthralgias related to disease activity, small joint arthralgias unrelated to disease activity, ankylosing spondylitis, and sacroiliitis) (n = 127) compared with those who had no joint problems when allelic frequency was analysed (7.5% v 11.8%; p = 0.36). On univariate analysis of CD patients, no association was observed between DLG5 113A variants and the Vienna classification for age of diagnosis, location of disease, or disease behaviour. Location of disease and disease behaviour in CD patients was analysed at the time of diagnosis and at the most recent follow up and there was no association between DLG5 113A variants and disease progression. No association was observed between DLG5 113A variants and age at diagnosis in the IBD and UC groups and there was no association between DLG5 113A variants, disease extent, and severity in UC patients.

**Table 3: DLG5 113A variant allele frequency, carrier frequency, heterozygote frequency, and homozygote frequency in the inflammatory bowel disease, Crohn’s disease, ulcerative colitis, and control populations**

<table>
<thead>
<tr>
<th>Allelic frequency</th>
<th>Carrier frequency</th>
<th>Heterozygosity frequency</th>
<th>Homozygosity frequency</th>
</tr>
</thead>
<tbody>
<tr>
<td>Controls</td>
<td>IBD (p value)</td>
<td>Crohn’s disease (p value)</td>
<td>Ulcerative colitis (p value)</td>
</tr>
<tr>
<td>Allergic frequency</td>
<td>13.2%</td>
<td>11.4%</td>
<td>11.4%</td>
</tr>
<tr>
<td>Carrier frequency</td>
<td>63/256 (24.6%)</td>
<td>125/652 (19.2%)</td>
<td>65/356 (18.3%)</td>
</tr>
<tr>
<td>Heterozygosity rates</td>
<td>59/256 (23%)</td>
<td>110/650 (16.7%)</td>
<td>57/356 (16%)</td>
</tr>
<tr>
<td>Homozygosity rates</td>
<td>4/256 (1.5%)</td>
<td>15/650 (2.3%)</td>
<td>8/356 (2.2%)</td>
</tr>
</tbody>
</table>

The p values shown are calculated between the control group and each respective disease group.
p = 0.053). When allelic frequency of 113A variants was analysed in UC patients with primary sclerosing cholangitis, a trend towards these patients having fewer 113A variants was observed (0% (n = 7) v 11.4%; p = 0.17). On analysis of the haplotype A, no genotype-phenotype associations were observed in the CD and UC patient groups. Multiple logistic regression analysis did not identify any variables that were independently associated with haplotype D (113A) or haplotype A.

There was no evidence of epistasis between DLG5 113A variants and carriage of the three common CARD15 variants Gly908Arg, Arg702Trp, and Leu1007fsinsC—CARD15 carriage positive DLG5 113A allelic frequency 9.7% (n = 108) versus CARD15 carriage negative DLG5 113A allelic frequency 11.6% (n = 584) (p = 0.43). When CD patients were stratified for CARD15 variant carriage, no significant genotype-phenotype relationships were found with DLG5 113A.

**DISCUSSION**

The present study has demonstrated that in the Scottish population, traditionally characterised by low rates of admixture, the DLG5 variant 113A, representing haplotype D, is not a critical determinant of susceptibility in either CD or UC. In fact, heterozygous rates of 113A were significantly higher in the healthy control population when compared with the IBD cohort and the CD cohort. Haplotype A represented by the SNP rs2289311 was not protective in our CD or UC population.

These data differ markedly from those of Stoll et al who showed that in a German population, DLG5 113A variants were overtransmitted to individuals with IBD, and in a case control study there were significantly higher rates of 113A carriage in the IBD group compared with the control group (25% v 17%; p = 0.001). Considerations, including sample size and phenotypic differences, between the present study and that of Stoll et al, may be responsible for the observed discrepancy in results but a more plausible explanation would be genetic heterogeneity between the populations of Germany and Scotland. This has been clearly illustrated by data now available with respect to the three common polymorphisms of the NOD2/CARD15 gene Gly908Arg, Arg702Trp, and Leu1007fsinsC—CARD15 carriage positive DLG5 113A allelic frequency 9.7% (n = 108) versus CARD15 carriage negative DLG5 113A allelic frequency 11.6% (n = 584) (p = 0.43). When CD patients were stratified for CARD15 variant carriage, no significant genotype-phenotype relationships were found with DLG5 113A.

In conclusion, in our North European study population, we were unable to replicate Stoll’s data that the DLG5 variant 113A confers susceptibility to IBD. Haplotype A represented by the SNP rs2289311 did not confer protection in our population. Furthermore, the identity of other genetic determinants in the Northern European IBD population remains under detailed investigation.

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Conflict of interest: None declared.

**REFERENCES**


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