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Citation for published version:

Digital Object Identifier (DOI):
10.1136/gut.2007.122069

Link:
Link to publication record in Edinburgh Research Explorer

Document Version:
Publisher's PDF, also known as Version of record

Published In:
Gut

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IL23R Arg381Gln is associated with childhood onset inflammatory bowel disease in Scotland

The discovery of NOD2/CARD15 as the first susceptibility gene in Crohn’s disease has contributed significantly to a fundamental change in the direction of basic research in inflammatory bowel disease (IBD), triggering renewed interest in the integrity of the innate immune response in IBD and appropriate orchestration of a subsequent adaptive immune response. More widely, in all complex diseases this finding in 2001 provided a much welcomed and needed proof of principle for non-parametric linkage analysis. Another study with major implications for the pathogenesis of Crohn’s disease as well as for investigation of all complex disorders has recently been published. The North American consortium performed an association study testing 308 332 markers spanning the entire genome in 567 patients with ileal Crohn’s disease and 571 controls of non-Jewish European ancestry. Of the three markers reported to reach genome-wide significance after stringent Bonferroni correction, two were located in the NOD2/CARD15 gene. The third marker (rs11209026) was a non-synonymous variant in the interleukin-23 receptor (IL23R) gene on chromosome 1p31. Replication was obtained in the index paper in a Jewish ancestry case-control analysis of patients with Crohn’s disease by transmission disequilibrium testing in 883 families with offspring affected by IBD and in a combined case-control analysis of these three cohorts (IBD, p = 6.62E−19).

IL-23 is a pivotal cytokine in the differentiation of helper T cells, especially their differentiation into Th17 T cells. Although the Th17 T cell subset has been shown to mediate chronic and autoimmune inflammatory conditions in animal models, clear evidence exists for the central role of IL-23 in the development of intestinal disease. Both Crohn’s disease and ulcerative colitis commonly first present during childhood and adolescence and are associated with high disease-related and treatment-related morbidity in these young patients. Disease incidence is high in our population, and in others in Northern Europe in whom the NOD2/CARD15 contribution is small. These considerations, together with well established epidemiological data suggesting that early-onset disease has a strong genetic basis, provide a clear scientific rationale for performing molecular studies in this group.

Our aim was to assess the contribution of the Arg381Gln variant (rs11209026) of IL23R in determining susceptibility and phenotype in childhood onset IBD in Scotland. We also sought to investigate the interaction between carriage of any of the three common NOD2/CARD15 variants and carriage of this IL23R variant in determining susceptibility to Crohn’s disease. A total of 1294 subjects comprising 358 with IBD aged <17 years at diagnosis (table 1), 594 parents and 342 controls were genotyped for rs11209026 GA using TaqMan (7900HT sequence detection system; Applied Biosystems, Foster City, California, USA). Allelic and genotypic frequency comparisons between cases and controls using χ² and transmission disequilibrium testing were applied to assess the association of IL23R rs11209026 with IBD. The three common NOD2/CARD15 variants were genotyped as previously described.10 In cases and controls, rs11209026 was in Hardy-Weinberg equilibrium. The allelic frequency of rs11209026A differed significantly between IBD/Crohn’s disease cases and controls (2.9%/3.0% vs 5.5%, p = 0.01, OR 0.51 (95% CI 0.30 to 0.88) and p = 0.04, OR 0.53 (95% CI 0.28 to 0.98); table 2).

The GG genotype was associated with an increased risk of IBD/Crohn’s disease (p = 0.01, OR 2.01 (95% CI 1.15 to 3.49) and p = 0.03, OR 1.96 (95% CI 1.03 to 3.70)). Analysis by transmission disequilibrium testing showed significant overtransmission of the G allele for IBD (p = 0.004) and Crohn’s disease (p = 0.04), with a trend towards significance in ulcerative colitis hindered by a small number of informative families with ulcerative colitis (table 3).

In Crohn’s disease there was no difference (p = 0.94) in allelic frequency between NOD2/CARD15 wild type and NOD2/CARD15 variant-carrying patients. However, owing to the small numbers of cases and controls carrying this IL23R variant, our study was not adequately powered to formally assess epistasis with NOD2/CARD15. Genotype-phenotype analysis in Crohn’s disease and ulcerative colitis based on the Montreal classification did not demonstrate any significant effect of IL23R rs11209026 specifically, we were not able to show a protective effect against ileal Crohn’s disease (p = 0.21). The successful identification of IL23R as a novel IBD susceptibility gene has provided proof of principle for the applicability of genome-wide association studies in the genetics of complex diseases. We show for the first time that IL23R variation influences susceptibility to IBD and Crohn’s disease, but not phenotype, in an exclusively paediatric IBD cohort. The data complement the results of the initial North American study and the replication studies currently underway in the UK adult population. However, the contribution of this IL23R allele to IBD is not sufficiently strong to explain the high incidence of childhood IBD in our or other populations with a low NOD2/CARD15 contribution. Other determinants are likely to be involved in Northern Europe.13,14 Genome-wide association scanning has already provided other candidates requiring rigorous analyses.15,16

Acknowledgements

The authors acknowledge the contribution of staff at the Medical Research Council Human Genetics Unit Edinburgh, the Wellcome Trust Clinical Research Facility Edinburgh and the referring physicians from Scottish Gastrointestinal Medicine and Surgery services. They also acknowledge the help of all patients and parents who participated in the study together with the specialist nurses, dieticians and secretaries.

**Table 1** Demographic data and inflammatory bowel disease (IBD) phenotype in patients diagnosed with IBD at <17 years of age based on Montreal guidelines for classification of Crohn’s disease/ulcerative colitis

<table>
<thead>
<tr>
<th>N</th>
<th>M/F</th>
<th>Median age at diagnosis (Q1–Q3)</th>
<th>CD/UC/IBD type</th>
<th>OR</th>
<th>p Value</th>
<th>OR</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>358</td>
<td>205/153</td>
<td>(6.6–12.9)</td>
<td>239/88/31</td>
<td>2.01</td>
<td>0.01</td>
<td>0.51</td>
<td>0.01</td>
</tr>
</tbody>
</table>

**Table 2** Interleukin-23 receptor (IL23R) rs11209026G/A (Arg381Gln) genotype and allelic frequencies in controls and patients with inflammatory bowel disease (IBD), Crohn’s disease (CD) and ulcerative colitis (UC) diagnosed <17 years of age

<table>
<thead>
<tr>
<th>Allele</th>
<th>CD</th>
<th>UC</th>
<th>IBD</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>HWE</td>
<td>0.73</td>
<td>0.73</td>
<td>0.73</td>
<td>0.73</td>
</tr>
<tr>
<td>GG</td>
<td>0.08</td>
<td>0.08</td>
<td>0.08</td>
<td>0.08</td>
</tr>
<tr>
<td>GA</td>
<td>0.06</td>
<td>0.06</td>
<td>0.06</td>
<td>0.06</td>
</tr>
<tr>
<td>AA</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
<td>0.04</td>
</tr>
<tr>
<td>Allele E</td>
<td>6.17</td>
<td>6.17</td>
<td>6.17</td>
<td>6.17</td>
</tr>
</tbody>
</table>

| Hardy-Weinberg equilibrium (HWE) p values are given. |
Table 3  
Interleukin-23 receptor (IL23R) rs11209026G/A (Arg381Gln) transmission disequilibrium testing in trios with childhood onset IBD

<table>
<thead>
<tr>
<th>rs11209026G/A</th>
<th>Arg381Gln Arg381Gln</th>
<th>Informative families (n)</th>
<th>Transmissions observed</th>
<th>Transmissions expected</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>IBD</td>
<td>34</td>
<td>59</td>
<td>50.5</td>
<td>0.004</td>
<td></td>
</tr>
<tr>
<td>CD</td>
<td>23</td>
<td>39</td>
<td>34</td>
<td>0.04</td>
<td></td>
</tr>
<tr>
<td>UC</td>
<td>9</td>
<td>16</td>
<td>13.5</td>
<td>0.09</td>
<td></td>
</tr>
</tbody>
</table>


IBD, inflammatory bowel disease; CD, Crohn’s disease; UC, ulcerative colitis.

Competing interests: None.

References


JAK V617F missense mutation is absent in pancreatic cancer

Ablant constitutive activation of STAT3 (signal transducer and activator of transcription) leads to cellular transformation and aids tumorigenesis in pancreatic cancer and its inhibition can lead to growth arrest.4,4 The exact mechanism of this constitutive activation has not been elucidated, although downstream mediators may include ERK and p21 signaling.4,4 Blocking JAK2 (Janus Kinase), a known upstream activator of STAT3, by AG490, a tyrophitin inhibitor, reduced phosphorylation of STAT3 and produced comparable in vitro effects, suggesting a role for JAK2 in pancreatic carcinogenesis.6 JAK2 V617F mutation has recently been shown by several independent groups to play an important role in myeloproliferative disorders as well as prothrombotic states such as Budd-Chiari syndrome (which may be due to latent myeloproliferative disorders).4,4 We propose that JAK2 V617F mutation may play a role in pancreatic cancer, in which the prothrombotic state is well recognised.

We analysed genome DNA (all from unstained slides of representative surgical specimens) from 26 patients undergoing surgery for various pancreatic diseases (table 1) along with genomic DNA from 10 cell lines (Panc1, Paca3, MiaPaCa2, Capan1 and 2, Suti2, AsPC1, 818,4, Hpa2, H766T) for JAK2 V617F mutation using phenol-chloroform extraction with ethanol precipitation, using appropriate positive and negative controls as previously described.4 Briefly, all cells (>70% tumour cell nuclei in cancer specimens, no microdissection) were scraped from unstained slides into high salt buffer and samples were made up to 200 μl with protease K, RNase A and sodium dodecyl sulfate, incubated at 37°C overnight before phenol extraction and ethanol precipitation. Genomic DNA from cell lines was extracted from 70% confluent million cells using Trizol (Invitrogen Ltd, Paisley, UK) reagent digestion followed by ethanol precipitation. A highly sensitive allele-specific PCR was used to detect the JAK2 V617F mutation in 14 of JAK2 (corresponding to amino acid position 617) as previously described.6 Briefly, a three primer PCR was performed which, in the absence of a mutation, produces an internal amplification control band. Where a mutation is present, an additional band is also amplified and is specific to the mutant sequence. The sensitivity of the assay is 1 cell in 100, determined by mixing positive control genomic DNA (extracted from HEL cells) with non-mutated genomic DNA. We have previously validated this methodology by conventional Sanger sequencing and pyrosequencing.6 No such mutations were detected at the JAK2 617 codon for pancreatic cancer or cell samples.

We propose that STAT3 activation, as previously described in pancreatic cancer,4,4 by mechanisms other than constitutive activation of JAK2 by missense mutation at the V617F site. Similarly, while JAK2 mutation is absent in acute myeloid leukaemia, STAT3 activation is common and is being explored.11 in glioblastoma, for example, it has been suggested that STAT3 is activated by exogenous interleukin (IL-4).11 IL-4 interacts with IL-13R2 receptor and, although IL-13R2 does not bind with STAT3 directly, it blocks STAT6 activation and excludes this downstream event. Thus, IL-4 can have an anti-apoptotic effect in glioblastoma cells via STAT3 signalling. Conversely, deletion of the SOC3 (suppressor of cytokine signalling 3) gene in liver cancer12 and silencing of the SHP1 gene (by methylation) in lymphoma12 can activate STAT3 signalling. It has recently been suggested that there may be novel mutations in cancer in which JAK2 V617F mutation may contribute for a minority of patients with polycythemia vera and idiopathic erythrocytosis, who are