INFLAMMATORY BOWEL DISEASE

Genetic basis for increased intestinal permeability in families with Crohn’s disease: role of CARD15 3020insC mutation?

S Buhner, C Buning, J Genschel, K Kling, D Herrmann, A Dignass, I Kuechler, S Krueger, H H-J Schmidt, H Lochs

Background and aim: A genetically impaired intestinal barrier function has long been suspected to be a predisposing factor for Crohn’s disease (CD). Recently, mutations of the caspase recruitment domain family, member 15 (CARD15) gene have been identified and associated with CD. We hypothesise that a CARD15 mutation may be associated with an impaired intestinal barrier.

Methods: We studied 128 patients with quiescent CD, 129 first degree relatives (CD-R), 66 non-related household members (CD-NR), and 96 healthy controls. The three most common CARD15 polymorphisms (R702W, G908R, and 3020insC) were analysed and intestinal permeability was determined by the lactulose/mannitol ratio.

Results: Intestinal permeability was significantly increased in CD and CD-R groups compared with CD-NR and controls. Values above the normal range were seen in 44% of CD and 26% of CD-R but only in 6% of CD-NR, and in none of the controls. A household community with CD patients, representing a common environment, was not associated with increased intestinal permeability in family members. However, 40% of CD first degree relatives carrying a CARD15 3020insC mutation and 75% (3/4) of those CD-R with combined 3020insC and R702W mutations had increased intestinal permeability compared with only 15% of wild-types, indicating a genetic influence on barrier function. R702W and G908R mutations were not associated with high permeability.

Conclusions: In healthy first degree relatives, high mucosal permeability is associated with the presence of a CARD15 3020insC mutation. This indicates that genetic factors may be involved in impairment of intestinal barrier function in families with IBD.
CARD15 mutation and intestinal barrier in Crohn’s disease

A total of 128 patients with a confirmed diagnosis of CD were included in the present study (85 females, 43 males; median age 36 years (range 16–63)). Patients were recruited from Charité University Hospital (Berlin, Germany). Diagnosis of CD was based on standard clinical, radiological, endoscopic, and histological criteria. The disease was located in the terminal ileum in 37 patients (30%), the colon in 20 patients (16%), the ileocolon in 53 patients (40%), and the upper gastrointestinal tract in 18 patients (14%). Ninety patients were currently taking mesalamine, 31 oral prednisolone (n = 19 <10 mg), 19 oral budesonide, five sulfasalazopyridine containing compounds, and 21 patients had no current medication. All patients were in clinical remission; mean CD activity index was 82 (range 5–148). None of the patients was taking antibiotics or tumour necrosis factor α (TNF-α) antibodies.

First degree relatives (CD-R)
A total of 129 first degree relatives of patients with CD were studied (83 females, 46 males; median age 43 years (range 15–82)), including 62 parents, 27 siblings, and 40 children of CD patients. Forty eight of the CD-R had been living in the same household with CD patients, at least since the time of diagnosis (CD-R household members).

Non-relatives (CD-NR)
Sixty six non-blood relatives of CD patients were included in the present study (23 females, 43 males; median age 38 years (range 20–68)). Except for one person (the stepfather of a CD patient), all CD-NR were the partners of the patients. All lived in the same household with the patient, the majority (n = 51) since the time of CD diagnosis.

Healthy controls
A total of 96 healthy volunteers (56 females, 40 males; median age 32 years (range 19–65)) were used as controls. They were predominantly recruited in cooperation with the Department of Transfusion Medicine of Charité University Hospital.

Predetermined exclusion criteria
Predetermined exclusion criteria were any (for CD patients: concomitant) gastrointestinal or hepatobiliary disease, severe neurological, endocrine, cardiovascular, pulmonary, or renal disease, gastrectomy, colecystectomy, or extensive resection of the small bowel, cancer, rheumatoid based diseases, acute infections, acute urticaria, or pregnancy. Alcohol and non-steroidal anti-inflammatory drugs (NSAID) were forbidden for at least 48 hours before the test. CD family members (CD-R and CD-NR) and controls showing any signs or symptoms of IBD-like recurrent diarrhoea, flatulence, gastrointestinal pain, or blood in the stool, or any other chronic illness, were excluded from the study. Additionally, drug intake, including glucocorticosteroids, antimicrobial agents, immunosuppressives, and regular consumption of NSAIDs (for example, for arthropathies) was not allowed for family members or controls. Persons with any previous gastrointestinal or colorectal surgery were excluded. In general, no drugs influencing gut functions, including laxatives and antidiarrhoeal agents, were allowed for 24 hours before the onset of the test. Finally, smoking was strictly forbidden in the morning before the test and during the test. Moreover, every participant was asked to record alcohol and cigarette consumption and medicine intake for one week before the test.

Study regimen
The intestinal permeability test was carried out at home by all persons. Blood samples for genetic analysis were taken in a subgroup of study participants, either at the outpatient department of the clinical centres involved or at their family doctors. A standardised questionnaire was used for data inquiry.

Intestinal permeability
Intestinal permeability was assessed using a sugar drink test, as previously described in detail. The test is based in principle on measurement of urinary excretion of an orally administered non-metabolised sugar probe molecules; the lactulose/mannitol ratio (permeability index, PI) served as a marker for intestinal permeability. After an overnight fast, each subject provided a pre-test urine sample. Then they drank a solution containing 10 g lactulose and 5 g mannitol dissolved in 100 ml water. Urine was collected over five hours with sodium azide as preservative. Subjects went without food during the test but were allowed to drink water after two hours. Total urine volume was recorded on completion of the test and a 10 ml aliquot was stored at −20°C until analysis.

For sample preparation the protein was removed with sulfoalicylic acid and urine was desalted with Amberlite MB-3 resin in acetate form. Using meso-erythritol and turanose as internal standards, the sugars were separated, analysed, and quantified by high performance liquid chromatography with pulsed electrochemical detection ( Dionex, Idstein, Germany); chromatography module 250 × 40 mm Carbopac

![Figure 1](https://www.gutjnl.com)
PA-1 column (Dionex); eluent 150 mmol NaOH; flow 1 ml/min. Results were expressed as percentage recovery of the ingested dose of the sugars.

**Gene analysis**
All methods used for gene analysis have been described previously in detail. Briefly, genomic DNA was prepared from peripheral blood using commercially available extraction columns (QIAamp Blood Kit; Qiagen, Hilden, Germany). After amplification of exon 11 of the CARD15 gene and cycle sequencing using an ABI 310 automatic sequencer (Applied Biosystems, Weiterstadt, Germany), genotyping of the three CARD15 polymorphisms (R702W, G908R, and 3020insC) was performed using the fluorogenic 5'-nuclease assay. Primers and probes were the same as previously described.

**Statistics**
Differences in permeability data between the study groups were analysed using the Kruskal-Wallis test and, in case of significance, the Mann-Whitney U test. The level of significance ($\alpha$) was chosen at 5%. An $\alpha$ adjustment was applied by Bonferroni procedure. Differences between incidences were tested by cross tables and $\chi^2$ statistics.

The upper limit of normal intestinal permeability was defined as mean value $+2SD$ of the control group ($=0.03$), as previously described.

**Ethics**
The study was approved by the ethics commission of the Charité University Hospital and informed consent was obtained from each participant.

### RESULTS

#### Intestinal permeability

Intestinal permeability was significantly increased in CD patients and in CD-R compared with controls and CD-NR (fig 1). Values above the normal range were seen in 44% of CD patients and in 26% of CD-R, but in only 6% of CD-NR and in none of the controls. This already refutes the role of an environmental factor being predominantly responsible for barrier dysfunction. To further differentiate between genetic and environmental factors, we concentrated on the group of CD first degree relatives and used the household community with the CD patients to investigate the influence of environmental factors on intestinal permeability. Thirty seven per cent ($n=48$) of CD-R lived in the same household with the patient since the time of CD diagnosis (CD-R household members). Forty seven per cent ($n=61$) of CD-R lived in a different household than the patient, both at the time of CD diagnosis and at the time of the test (CD-R non-household members). As seen in table 1, intestinal permeability did not differ between these two groups, indicating that household community, as an environmental factor, does not explain the general differences in intestinal barrier function described above.

We further analysed the effect of smoking habits in each group. The proportion of smokers showing a PI above the normal limit was higher compared with non-smokers (61% vs 37%; $p=0.019$, Fisher’s exact test) in CD patients but in none of the other groups (CD-R, $p=0.602$; CD-NR, $p=0.563$). Median values for intestinal permeability did not differ between smokers and non-smokers in any of the groups. Additionally, a slight gender disproportion in the CD-R and

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Control</th>
<th>CD</th>
<th>CD-R</th>
<th>CD-NR</th>
</tr>
</thead>
<tbody>
<tr>
<td>3020insC</td>
<td>(n=62)</td>
<td>(n=121)</td>
<td>(n=106)</td>
<td>(n=50)</td>
</tr>
<tr>
<td>Wild-type</td>
<td>98% (61)</td>
<td>78% (94)</td>
<td>77% (82)</td>
<td>88% (44)</td>
</tr>
<tr>
<td>Heterozygous mutant</td>
<td>2% (1)</td>
<td>18% (22)</td>
<td>22% (23)</td>
<td>10% (5)</td>
</tr>
<tr>
<td>Homozygous mutant</td>
<td>4% (5)</td>
<td>1% (1)</td>
<td>2% (1)</td>
<td></td>
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<tr>
<td>$p&lt;0.0005$</td>
<td>$p&lt;0.0005$</td>
<td>$p=0.044$</td>
<td></td>
<td></td>
</tr>
<tr>
<td>R702W</td>
<td>(n=62)</td>
<td>(n=120)</td>
<td>(n=106)</td>
<td>(n=50)</td>
</tr>
<tr>
<td>Wild-type</td>
<td>94% (58)</td>
<td>83% (100)</td>
<td>84% (89)</td>
<td>88% (44)</td>
</tr>
<tr>
<td>Heterozygous mutant</td>
<td>6% (4)</td>
<td>14% (17)</td>
<td>15% (16)</td>
<td>12% (6)</td>
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<tr>
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<td>3% (3)</td>
<td>1% (1)</td>
<td>2% (1)</td>
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<tr>
<td>$p=0.06$</td>
<td>$p=0.091$</td>
<td>$p=0.337$</td>
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<tr>
<td>G908R</td>
<td>(n=62)</td>
<td>(n=120)</td>
<td>(n=105)</td>
<td>(n=50)</td>
</tr>
<tr>
<td>Wild-type</td>
<td>97% (60)</td>
<td>92% (110)</td>
<td>98% (103)</td>
<td>98% (49)</td>
</tr>
<tr>
<td>Heterozygous mutant</td>
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<td>8% (10)</td>
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<td>2% (1)</td>
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<tr>
<td>$p=0.343$</td>
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<td>$p=1.000$</td>
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</tr>
<tr>
<td>Overall</td>
<td>(n=62)</td>
<td>(n=121)</td>
<td>(n=106)</td>
<td>(n=50)</td>
</tr>
<tr>
<td></td>
<td>11% (7)</td>
<td>43% (52)</td>
<td>37% (39)</td>
<td>24% (12)</td>
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</tbody>
</table>

CD, Crohn’s disease; CD-R, first degree relative of a patient with CD; CD-NR, non-related household member living with a patient with CD. Overall, number of persons carrying at least one mutation. $p$ values for differences in frequency distribution of CARD15 mutations between CD groups and controls (Fisher’s exact test).

Number of cases in parentheses.
Three major polymorphisms within the coding region of the CARD15 gene (3020insC, R702W, and G908R) have been described in Crohn’s disease patients. Genetic analysis of these polymorphisms in family members of patients with Crohn’s disease has revealed interesting findings.

Firstly, the prevalence of these mutations was significantly increased in CD patients compared with controls. The proportion of the heterozygous plus homozygous mutations was 22%, being similar to that found in the CD-R group (23%). In the CD-NR group, the corresponding value was 12%. A similar tendency was obvious for the R702W mutation while data for the G908R did not differ between the study groups.

Intestinal permeability did not differ between CD-R subgroups. CD-R household members were living in the same household with patients at the time of diagnosis and at the time of the test; CD-R non-household members were living on their own during the whole period.

**Genetic analysis**

Three major polymorphisms within the coding region of the CARD15 gene (3020insC, R702W, and G908R) have been associated with CD. The results of the present study are illustrated in Table 2. A significantly higher prevalence of the frameshift mutation 3020insC was found in CD patients and their first degree relatives compared with controls. The frequencies of elevated permeability were 44% and 52%, respectively. In contrast, in healthy CD first degree relatives, high mucosal permeability was similar in first degree relatives and CD patients and higher compared with controls.

CD-NR groups had no significant effect on intestinal permeability values (data not shown). The same was true for the CD-R subgroup, where intestinal permeability values were similar to those found in the CD-R group.

**DISCUSSION**

In the present study there were three main findings. Firstly, healthy first degree relatives of patients with Crohn’s disease showed increased intestinal permeability in contrast with unrelated household members and controls. Secondly, the prevalence of the CARD15 3020insC mutation was similar in first degree relatives and CD patients and higher compared with controls. Thirdly, in healthy first degree relatives, high mucosal permeability and the presence of a CARD15 3020insC mutation were significantly associated.

Looking for a possible link between the prevalence of the CARD15 mutation and intestinal barrier function, individual study groups were divided into subgroups according to the occurrence of a mutation (Table 3). In CD-NR, all of the mutation carriers had increased intestinal permeability. In CD wild-types and patients with the 3020insC mutation, the frequencies of elevated permeability were 44% and 52%, respectively. In contrast, in healthy CD first degree relatives, high mucosal permeability was significantly higher in CD-R with the 3020insC mutation compared with CD-R wild-types (Fig 2). In four CD-R, combined mutations (3020insC and R702W) occurred; three of them also had increased permeability. In contrast, neither R702W nor G908R alone showed a clear association. In CD-NR, all of the mutation carriers had normal permeability (Table 3).
PI above the normal level. However, data in the literature appear contradictory. Some studies documented high baseline permeability not only in related 1 4–6 but also in unrelated household members (spouses) of CD patients. 7 8 12 These reports were partly limited by sample size and some used a lower “upper limit of normality” for permeability values than those used in our study (for example, 0.0195 and 0.0170), which may have had a slight effect on the frequency distribution of the data. However, under close scrutiny, they also revealed clear evidence that epithelial hyperpermeability of the intestine, in response to insults causing barrier dysfunction, was restricted to CD first degree relatives and was not seen in spouses. 4 In summary, data indicate a genetic rather than an environmentally induced background for intestinal barrier dysfunction in CD.

Our results add further support to the role and value of intestinal barrier function as a subclinical marker in families with CD. The question of whether increased intestinal permeability may be a primary or causative factor in disease development cannot be answered from the present data. It is assumed by some authors that slight inflammation may be a primary event preceding barrier disruption. A recent study using faecal calprotectin concentration for detection of intestinal inflammation reported 88% (n = 43) of CD patients, 49% (n = 74) of CD first degree relatives, and 13% (n = 2) of CD spouses with abnormally high values. 24 The authors proposed a genetic basis for subclinical inflammation representing a risk factor for CD. Others reported a relationship between faecal calprotectin and intestinal permeability. 25 It could be that subclinical inflammation may precede barrier disruption. However, a definition of causality is difficult in this case because both factors present at the same time as secondary factors, perpetuating and worsening the processes in the intestinal mucosa. In our opinion neither method (faecal calprotectin detection nor in vivo permeability measurement) provides sufficient sensitivity to answer this question. Analysis of mucosal tight junction components and metabolisms in CD first degree relatives, for example, may be more useful. However, the results of Thjodleifsson and colleagues 25 stress the importance of a genetic basis of CD and support the role of subclinical markers.

A possible genetic mechanism involved in barrier dysfunction in healthy family members is unknown. An interesting candidate for such a genetic factor is the CARD15 gene, or rather its mutations associated with CD. In accordance with the main findings in European, Canadian, and US Caucasian populations, 13 14 15–17 our gene analysis revealed a significantly higher prevalence of the CARD15 3020insC mutation in CD patients compared with controls. Interestingly, this was also true for CD first degree relatives. Values were similar to those of patients and, in contrast with non-blood relatives, significantly higher compared with controls. Obviously, there was transmission of the polymorphisms within genetically related persons, which supports recent data. 22 However, the striking finding of the present study was that healthy first degree relatives carrying a 3020insC mutation were more often characterised by high intestinal permeability than wild-types. Eighty five per cent of CD-R wild-types had normal permeability, and a high risk of postoperative relapse and reoperation. 16 17 19 20 3020insC may therefore characterise a subgroup or subtype of CD associated mainly with ileitis. Regarding a possible link with intestinal barrier function, the physiological consequences of a CARD15 mutation are crucial. As already mentioned, the CARD15/NOD2 protein is an intracellular receptor for muramyl dipeptide, a conserved structure in bacterial peptidoglycan. 20 21 In human intestinal tissue the protein is expressed predominantly in Paneth cells in the crypts of the terminal ileum. 22 Clear functional consequences have been demonstrated, mainly for the frameshift mutation 3020insC. 3020insC results in diminished bacterial recognition and hyporesponsiveness to bacterial muramyl dipeptide showing attenuated or complete loss of NFκB activation. A signalling defect of the innate immunity was indicated. 18 20 22 23 24 Studies in mice 25 and humans 26 reported a 3020insC associated diminished expression of antimicrobial peptides such as defensins in intestinal Paneth cells. The authors speculated that defensin deficiency may lead to impaired mucosal barrier and susceptibility to bacterial invasion which could trigger inflammation and loss of tolerance against the luminal flora. 27 A direct effect of bacterial products on tight junction integrity 28 or a secondarily exaggerated local inflammatory response of the adaptive immune system (that is, high TNF-α or NFκB production) 29 may cause or facilitate barrier break. Both of these pathways are possible and may play a role. They might gain special importance, representing an early event, probably pointing towards a subgroup of persons. Interestingly, an older study reported abnormal faecal flora in patients with CD and their first degree relatives. 30

However, if there is an association between the CARD15 mutation and impaired barrier function, why is this association not obvious in CD patients but only in a subgroup of healthy first degree relatives of CD patients? These are two completely different situations. One is the healthy first degree relative of a CD patient. This person has no clinical symptoms of CD but has a CARD15 mutation and impaired barrier function which may bear a risk but which may not develop any clinical relevance. The other situation is a confirmed diagnosis of a chronic inflammatory bowel disease (that is, CD). In our study, 44% of CD patients without any CARD15 mutation (that is, wild-types) showed pathologically high permeability values. In current CD, various factors, including the dynamism of the inflamed disturbed barrier itself, influence barrier function. Early events could be easily masked. These factors are mainly drugs such as prednisolone or mesalazine, 32 or the effects of mal- and dysnutrition, 33 stress, 34 or changes in luminal bacterial load and composition, 35 which are all associated with CD and which are accompanied by reinforcement or impairment of the intestinal barrier.

In summary, the present data indicate a genetic rather than an environmental basis for the intestinal barrier dysfunction in CD. From our data, we speculate that the CARD15 3020insC mutation could be one genetic factor involved in impairment of intestinal barrier function. However, it is obvious that this is not the only factor. Association between the CARD15 gene mutation and intestinal hyperpermeability in healthy first degree CD relatives may be one step towards the identification of other target genes involved in similar processes or possibly interacting with the CARD15 gene, as recently discussed 33 and proposed for the DLG5 gene. 44 Our data point towards a very early step in the disease process. Considering the high intestinal bacterial load in CD patients compared with controls, 41 early barrier dysfunction gains special significance with respect to the pathogenesis of CD. However, longitudinal studies in CD families are necessary to investigate which additional factors may lead to the outbreak of the disease.
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Authors’ affiliations

S Buhner, C Buning, J Genschel, D Herrmann, S Krueger, H H-J Schmidt, H Lochs, Department of Gastroenterology, Hepatology, and Endocrinology, Campus Charité Mitte, Charité-Universitätsmedizin Berlin, Germany

A Dignass, Department of Gastroenterology and Gastroenterology, Campus Virchow Klinikum, Charité-Universitätsmedizin Berlin, Germany

I Kuechler, Institute of Medical Biometry, Campus Charité Mitte, Charité-Universitätsmedizin Berlin, Germany

Conflict of interest: None declared.

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