A genetic basis for atrophy: dominant non-responsiveness and helicobacter induced gastritis in F₁ hybrid mice

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Abstract
Background—The importance of host factors in helicobacter induced gastritis has been shown in animal models. Infec-
tion of most mouse strains with Helicobacter felis results in a functional atrophic gastritis, while other strains remain gas-
tritis free.
Aims—To investigate these host factors further by using genetic crosses of res-
ponder and non-responder mice.
Methods—F₁ hybrids of the non-
responder CBA/Ca strain and three strains of mice known to develop H felis
induced gastritis were infected for three months with H felis. Gastritis was as-
essed by histopathology and serum antibody responses by ELISA.
Results—Infection of CBA/Ca mice and F₁
hybrids induced little or no gastritis. Analyses of the antibody responses in
these mice revealed virtually undetectable anti-helicobacter antibody levels despite
colonisation with high numbers of H felis. In contrast, infection of H felis responsive
strains induced gastritis and a significant humoral immune response.
Conclusions—The non-responsiveness of
CBA/Ca mice to H felis infection is domi-
nantly inherited. The lack of gastritis in
CBA mice and their offspring is probably
due to active suppression of the immune
response normally mounted against H felis. Investigation of these mechanisms
will provide important insights relevant to
induction of gastric atrophy and cancer in
humans.

Keywords: helicobacter; non-responsiveness; gastritis; F₁, hybrid; CBA

Helicobacter pylori is a Gram negative bacterium responsible for a large degree of morbidity and mortality in humans. Following infection of the stomach, H pylori colonises the gastric mucosa for the life of the host and by a variety of mechanisms, stimulates a chronic inflammatory reaction which is characterised by the infiltration of lymphocytes and neutrophils into the gastric mucosa.¹ In a small proportion of those infected, the chronic stimulation can lead to the development of gastric and duodenal ulceration and may also result in the develop-
ment of malignant disease such as mucosa associated lymphoid tissue lymphoma² and adenocarcinoma.³

There are many factors believed to contrib-
ute to the progression to helicobacter induced
diseases, including strain variation, dietary and
environmental differences, and host factors.
For example, some strains of H pylori express
virulence factors which are associated with the
development of more severe disease. Expres-
sion of the cag pathogenicity island, a collect-
on of over 30 genes, by some strains of bacte-
ria is associated with an increased chance of
developing the more serious complications of
helicobacter infection.⁴ Environmental factors
are also clearly important, with smoking being
associated with an increased incidence of ulcers⁵ and high levels of salt in the diet associ-
ated with an increased risk of cancer (reviewed
in Cohen and Röe⁶). In addition, treatment of
infected patients with acid suppressive drugs
leads to loss of bacterial colonisation in the
antrum and a reduction in antral gastritis, while the H pylori remains in the body of
the stomach and the body gastritis increases.⁷

Thus, acid levels can control both the location
of the infection and the extent of gastritis,
which has led to the proposal of a unifying
hypothesis linking H pylori infection, local acid
production, and gastroduodenal disease.⁸

Recently, evidence has arisen which indi-
cates that host genetic factors are also heavily
involved in the development of helicobacter
associated pathologies. In previous work, we
have shown that the development of helico-
bacter induced gastritis in a mouse model of H felis infection is host dependent, as infection of
different strains of mice with the same culture
of bacteria produced varying degrees of inflamma-
tory levels in the gastric mucosa.⁹ Infection
of C3H/HeJ, DBA/2, SJL, and C57BL/6 mice
induced a destructive gastritis in the body,
whereas the stomachs of infected BALB/c and
CBA/Ca mice had relatively normal histology

Abbreviations used in this paper: LPS,
lipopolysaccharide; MHC, major histocompatibility
complex; BHI, brain heart infusion.
Table 1  Assessment of colonisation with H felis

<table>
<thead>
<tr>
<th>Strain</th>
<th>Antrum</th>
<th>Antrum/body</th>
<th>Body</th>
<th>Body/cardia</th>
<th>Cardia</th>
</tr>
</thead>
<tbody>
<tr>
<td>CBA/Ca</td>
<td>3.2 (0.4)</td>
<td>2.8 (0.6)</td>
<td>0.5 (0.3)</td>
<td>2.1 (1.0)</td>
<td>1.9 (0.9)</td>
</tr>
<tr>
<td>C3H/He</td>
<td>2.7 (0.2)</td>
<td>2.4 (0.2)</td>
<td>1.6 (0.8)</td>
<td>1.9 (0.5)</td>
<td>1.2 (0.6)</td>
</tr>
<tr>
<td>C57BL/6</td>
<td>2.1 (1.0)</td>
<td>2.5 (0.8)</td>
<td>1.3 (0.7)</td>
<td>1.6 (0.8)</td>
<td>1.9 (0.6)</td>
</tr>
<tr>
<td>SJL</td>
<td>1.6 (0.8)</td>
<td>1.7 (1.0)</td>
<td>0.9 (0.5)</td>
<td>1.2 (0.8)</td>
<td>1.1 (0.8)</td>
</tr>
<tr>
<td>CBA×C3H/He</td>
<td>2.3 (0.8)</td>
<td>2.3 (0.7)</td>
<td>0.4 (0.3)*</td>
<td>0.7 (0.6)</td>
<td>0.7 (0.7)</td>
</tr>
<tr>
<td>CBA×C57BL/6</td>
<td>2.9 (0.5)</td>
<td>2.6 (0.5)</td>
<td>0.5 (0.4)*</td>
<td>1.8 (0.9)</td>
<td>1.3 (0.8)</td>
</tr>
<tr>
<td>SJL×CBA</td>
<td>2.3 (0.7)</td>
<td>2.9 (0.5)</td>
<td>0.7 (0.4)</td>
<td>1.5 (0.4)</td>
<td>1.2 (0.6)</td>
</tr>
</tbody>
</table>

Bacterial colonisation was assessed by light microscopic examination of May Graham-Giemsa stained sections. Scores are mean (SEM) grades of colonisation between 0 and 4, where 0 = no bacteria, 1 = 1–2 bacteria/crypt, 2 = 3–10 bacteria/crypt, 3 = 11–20 bacteria/crypt, 4 = >20 bacteria/crypt.

* CBA×C3H/He mice and CBA×C57BL/6 mice had a significantly reduced level of colonisation in the body compared with the C3H/He and C57BL/6 parent respectively (p<0.05).
corpus and antrum were evaluated. The intensity of the polymorphonuclear and mononuclear infiltration was graded from 0 (absent) to 3, where 3 indicated the most severe infiltrate observed. The inflammatory scores for both cells were considered separately for corpus and antrum, and then combined into a gastritis score for each of the two gastric compartments.

Lymphoid aggregates were counted and expressed as the total number seen in the combined sections from each animal.

The changes defined here as "functional atrophy" consisted of the apparent substitution of the parietal and chief cells of the corpus with mucous metaplasia consisting of larger, pale, globular cells that did not resemble the goblet cells found in intestinal metaplasia in the human stomach. The functional atrophy was also graded from 0 (absent) to 3. The highest score represented the most severe change seen in this group of mice (large areas of the corpus mucosa substituted by the metaplastic mucous cells). None of the animals showed complete replacement of the mucosa which would normally be defined as atrophy in humans.

MEASUREMENT OF ANTI-HELICOBACTER SERUM ANTIBODIES

An enzyme linked immunosorbent assay (ELISA) was used to measure anti-helicobacter antibody levels. Triplicate wells of microtitre plates (Dynatech, Chantilly, Virginia, USA) were incubated with \( H.\ felis \) lysate preparation (100 µg/ml) in carbonate buffer, pH 9.6. After washing with phosphate buffered saline (PBS)-0.5% Tween 20, the wells were blocked with PBS containing 2.5% non-fat dried milk and then incubated for one hour at 37°C with serial dilutions of sera. The wells were next incubated with biotinylated goat-antimouse IgA, IgG1, or IgG2a (Southern Biotechnology, Birmingham, Alabama, USA) and then with streptavidin-alkaline phosphatase (Calbiochem). Following addition of substrate (Sigma 104 phosphatase substrate tablets in diethanolamine buffer), the plates were read spectrophotometrically in an automated ELISA reader at a wavelength of 405 nm.

STATISTICS

The differences in \( H.\ felis \) colonisation and histopathology scores between different strains of mice were tested by non-parametric Kruskal Wallis (K-W) analysis. Only one stomach section from each animal was analysed. This raises the possibility of sampling error arising from only evaluating a small part of each stomach. However, 10 mice were studied per group, and any such effect should be minimal. Differences were considered significant at \( p<0.05 \).

RESULTS

EVALUATION OF GASTRITIS

To investigate the role of host factors in the generation of helicobacter induced gastritis, various strains and F1 crosses of mice (n=10) were infected with \( H.\ felis \). Three months following infection, stomach and serum samples were collected. Analysis of stained stomach sections for bacterial burden revealed that all strains challenged with \( H.\ felis \) were colonised, but that levels of colonisation varied between strains (table 1). The CBA/Ca parental strain and its F1 hybrid...
of F1 progeny had levels of gastritis which were not significantly different from the CBA strain, indicating that all the F1 strains had a helicobacter non-responsive phenotype (fig 1). All groups of mice were composed of 50% males and 50% females; no phenotypic variations were observed with respect to the sex of the mice.

**SERUM ANTIBODY RESPONSE**

The serum anti-\(H\) \(feli\) antibody response to infection in the various strains of mice was analysed by ELISA. There was a significant difference in the serum levels of anti-\(H\) \(feli\) IgA between the helicobacter responder strains of mice infected with \(H\) \(feli\) and the non-responder CBA mice and their F1 progeny (fig 2A; K-W \(p<0.001\)). Similarly, the IgG1 antibody response in CBA and the F1 hybrid strains was low relative to C3H/He and SJL mice, which had high and intermediate levels, respectively (fig 2B; \(p<0.001\)). The IgG2a antibody levels in sera from infected CBA and CBA \(\times\) C3H/He mice were very similar and significantly different from those found in C3H/He mouse sera which produced a high level antibody response (fig 2C; \(p<0.001\)). As C57BL/6 and SJL mice have a deletion of the IgG2a gene,15 anti-\(H\) \(feli\) IgG2a data are not shown. In summary, the sera from \(H\) \(feli\) infected CBA/CaH mice and the three F1 hybrids contained little or no anti-\(H\) \(feli\) IgG or IgA antibodies, in contrast to the responder C57BL/6, SJL, and C3H/He strains.

**Discussion**

Chronic infection with \(H\) \(pylori\) can cause a range of diseases including peptic ulcers and gastric cancer. The first studies which attempted to explain these differences postulated bacterial factors as being important. Certainly there are strains of the bacterium that cause more severe inflammation if they possess what is termed the “pathogenicity island”.4 However, we have previously challenged the simplistic view of the “ulcerogenic strain” as the sole explanation.1 Based on animal studies, we suggested that host factors are likely to be equally important in determining the outcome of disease. C57BL/6, C3H/He, DBA/2, and SJL mice all developed severe functional atrophy in the body mucosa with loss of parietal and chief cells after long term infection with \(H\) \(feli\), while BALB/c and CBA/Ca mice showed no remarkable lesions.3 We originally hypothesised that the lack of inflammation during \(H\) \(feli\) infection in BALB/c and CBA mice may have been due to one of two possibilities. Firstly, an inherent immunological defect in these strains of mice could prevent the development of gastritis. In support of this possibility, we have recently reported that C3H/HeJ mice, which have a genetic defect for LPS responsiveness,16 do not develop gastritis when infected with \(H\) \(feli\), in contrast to the LPS responsive C3H/He strain from which it arose.17 An alternative explanation was that the non-responder mice actively suppressed the immune response to the helicobacter antigens. The study reported here was designed to test this possibility. The \(H\) \(feli\) crosses had comparable colonisation levels in the antrum and the transitional zones, compared with C3H/He and C57BL/6 mice, but had significantly lower bacterial levels in the body (\(p=0.005\)). There was no significant difference in colonisation in the body of the SJL, CBA, and the three F1 hybrid strains. However, there were significant differences in the degrees of gastric inflammation observed for the various strains. Infection of C3H/He, C57BL/6, and SJL mice with \(H\) \(feli\) resulted in cellular infiltration (predominantly in the body but also in the antrum), the formation of lymphoid aggregates, and also what we now term functional atrophy (table 2; fig 1). In contrast, the extent of inflammation in CBA/Ca mice was significantly lower when compared with the three helicobacter responsive strains (\(p<0.015\)). The three strains
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The gastrointestinal tract has evolved an immune system which is primed to induce a state of non-responsiveness—a phenomenon termed oral tolerance. Delivery of antigens orally can generate immunity to non-responsiveness which prevents reactions against food antigens and commensals living in the gut (reviewed in Strobel and Mowat). In contrast to the normal non-responsiveness to other gut inhabiting commensals, helicobacter infection induces an inflammatory response in most strains of mice. One possible mechanism for the lack of response in some mice to *H felis* and its antigens may involve LPS. We have shown that LPS non-responsive mice lack gastritis and LPS may be involved in the induction of oral tolerance, although its role is unclear. Why a break in tolerance should occur during *H felis* infection, but not for many other Gram negative bacteria which also produce LPS is unknown. Perhaps it is due either to the unique location of the helicobacter, or to the biochemical and biological differences between helicobacter LPS and the LPS of other Gram negative bacteria. While mechanisms of tolerance induction in helicobacter infection have not been investigated, the finding of reduced antibody levels and gastritis raises the possibility that such processes may occur in *H felis* infected CBA mice and their F1 progeny.

It needs to be emphasised that the histopathological features observed in our mouse model do not completely mimic the human pathology. The characteristic antral chronic/active gastritis is missing. We have argued before that the lesions seen in mice represent a subset of the human pathology which may be particularly relevant to development of atrophy. We have suggested that atrophic changes may not necessarily be a direct consequence of long term active/chronic gastritis as has been hitherto assumed. In the human, subsets of atrophy and active/chronic inflammation cannot be distinguished, whereas in our mouse models they clearly are. Mucus metaplasia,
equivalent to that seen here, has been observed in some human specimens (Dixon, personal communication). We have also speculated that some type of induction, immunological effects may be responsible for the changes in the proliferative zone of the body glands and the disappearance of the chief and parietal cells. In summary, we have shown that CBA mice do not develop body gastritis when infected with *H. felis*, that this trait is dominantly inherited in three other strains of normally responsive mice, and that this non-responsiveness is associated with a lack of an antibody response suggesting suppression of the inflammatory response normally mounted against chronic helicobacter infection. Further investigation of the mechanism of this apparent suppression of the development of functional atrophy will provide important insights into aspects of the human disease which may be relevant to the induction of gastric atrophy and ultimately gastric cancer.

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