The role of adherent-invasive \textit{E. coli} (AIEC) in Crohn disease (CD) has been in debate for decades. AIEC bacteria are found in the small intestine of patients with chronic CD, but it has remained unclear whether this infection is causal or secondary to underlying immune deficiencies in CD patients. In this issue of the \textit{JCI}, Chassaing and colleagues demonstrate that AIEC bacteria express an adherence factor called long polar fimbrae (LPF) that aids in the binding of these bacteria to M cells overlying Peyer’s patches and subsequent entry into lymphoid tissue. These findings provide a mechanism of AIEC penetration but do not prove that AIEC is causing a primary infection in the Peyer’s patches that is necessary for the initiation or persistence of CD inflammation.
could also speculate that the activation of vFLIP (with or without other latent viral transcripts) at a more mature stage of B cell differentiation, such as in post-GC B cells, will permit completion of the GC reaction and better recapitulate KSHV-lymphoproliferation development. These three studies are opening up new avenues to explore the immunobiology of KSHV as it relates to its principal reservoir, B lymphocytes.

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Adherent-invasive E. coli in Crohn disease: bacterial “agent provocateur”

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The role of adherent-invasive E. coli (AIEC) in Crohn disease (CD) has been in debate for decades. AIEC bacteria are found in the small intestine of patients with chronic CD, but it has remained unclear whether this infection is causal or secondary to underlying immune deficiencies in CD patients. In this issue of the JCI, Chassaing and colleagues demonstrate that AIEC bacteria express an adherence factor called long polar fimbriae (LPF) that aids in the binding of these bacteria to M cells overlying Peyser’s patches and subsequent entry into lymphoid tissue. These findings provide a mechanism of AIEC penetration but do not prove that AIEC is causing a primary infection in the Peyser’s patches that is necessary for the initiation or persistence of CD inflammation.

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Proposed role of AIEC in the pathogenesis of CD. Left: CD is initiated by a genetically determined (AIEC-independent) mucosal immune response to components of the resident gut microflora; this includes the production of proinflammatory cytokines such as IL-12p70 and IFN-γ. Middle: The inflammatory response leads to increased expression of an epithelial binding site, CEACAM6, on polarized epithelial cells and thus sets the stage for the selective proliferation of preexistent E. coli with an AIEC phenotype. Right: AIEC bacteria enter the Peyer’s patches via binding of LPF to GP2 on the surface of M cells overlying the patches; within the patches, they can exacerbate inflammation by inducing innate immune responses of patch macrophages; AIEC can also enter the lamina propria, probably via ulcerations resulting from the inflammation, and exacerbate inflammation at this site as well.

Figure 1

AIEC (ExPEC) strains, but contains genes derived from Salmonella and Yersinia organisms as well; however, while it contains several pathogenicity islands encoding a variety of virulence factors, it lacks most of the virulence genes found in ExPEC strains and thus stops short of being a virulent, acute disease–inducing agent (7).

In the current issue of the JCI, Chassaing et al. (the Darfeuille-Marchaud group) shed new light on the nature of AIEC (8). Previous studies by Hase et al. had shown that pathologic organisms express an operon encoding long polar fimbriae (LPF) that facilitates binding of the organism to a glycoprotein (GP2) on the surface of M cells (specialized epithelial cells on the surface of Peyer’s patches through which organisms and molecules gain entry into the underlying lymphoid tissue); in addition, they showed that such binding allows entry of the bacteria into the Peyer’s patches, followed by initiation of immune responses at this lymphoid site (9). In these new studies, Chassaing et al. show that AIEC bacteria express LPF and that LPF+ AIEC bacteria bind to M cells and gain entry into the Peyer’s patches, whereas mutant LPF− AIEC bacteria (which still have type 1 pili) do not bind to M cells or gain entry. In contrast, LPF expression is not necessary for AIEC binding to polarized enterocytes (which depends solely on CEACAM6). Turning to studies of CD patients, the authors showed that 47% of 55 CD patients harbored E. coli expressing an LPF with either a Shigella or E. coli (LF82) sequence, compared with 17.2% of 29 control patients. Finally, these authors showed that mice deficient for NOD2 (an intracellular sensor of a bacterial wall peptide encoded by a gene associated with increased risk for CD) express increased amounts of GP2 on M cells and thus had increased numbers of LPF+ AIEC bacteria. Nevertheless, this was not associated with induction of colitis.

While previous studies had shown that one can find AIEC bacteria in the lamina propria, it was not clear that such entry was a primary event occurring before an inflammatory process had caused ulceration of the mucosa (10). The significance of these new findings is that they provide a mechanism of AIEC penetration, albeit into the Peyer’s patches rather than into the lamina propria. However, this does not prove that AIEC is causing a primary infection in the Peyer’s patches that is necessary for the initiation or persistence of CD inflammation. If this were the case, it would be hard to explain disease in the large intestine in all cases or in the small intestine in most cases despite the absence of AIEC. A more conservative interpretation of the findings is that the inflammatory conditions in the small intestine during the initiation of CD favors the selection and expansion of AIEC bacteria, which may then intensify the preexisting inflammation. The fact that inflammatory cytokines can induce the expression of CEACAM6 (3) supports
this view, since provision of an epithelial binding site to an organism is likely to lead to selective proliferation of small numbers of preexisting organisms with an AIEC phenotype. Similarly, loss of the antibacterial function of Paneth cells in the terminal small intestine, a known consequence of CD, could also be contributing to the emergence of AIEC (11). Finally, the view that AIEC bacteria appear in the terminal ileum as an effect rather than as a cause of the inflammation is also supported by a recently described murine model of experimental colitis occurring in T-bet/RAG2-deficient mice (so-called TRUC mice), which exhibit excessive TNF-α production and develop a “colitogenic” intestinal microflora that can transmit colitis to co-housed or cross-fostered normal mice (12). Analysis of the intestinal microflora of these TRUC mice revealed that increased colonization by Klebsiella pneumoniae and Proteus mirabilis correlated with the presence of colitis, and while these organisms by themselves did not cause colitis in germ-free mice, they did cause colitis in mice with a specific pathogen–free flora (13). More to the present point, treatment of the colitis by administration of anti–TNF-α or suppressor T cells (which were absent in the RAG-deficient hosts) led to amelioration of colitis associated with either a decrease in the levels of the two implicated bacteria (anti–TNF-α treatment) or no change in these levels (suppressor cell treatment), suggesting that the inflammatory environment was causing either quantitative or qualitative alterations in the behavior of these and perhaps other organisms (13). In either case, it was apparent that the maintenance of a colitogenic microflora required the presence of an underlying (and preexisting) mucosal immune abnormality. In light of these studies, it would be interesting to determine whether AIEC persisted in the small intestine of patients successfully treated with anti–TNF-α despite amelioration of disease.

**Host factors that might license AIEC pathogenesis**

Since AIEC infection occurs in a substantial number of normal individuals without disease, the need for an underlying immune abnormality for the development of AIEC infection (as indicated above) may be accompanied by a similar need to license AIEC to exert pathogenic effects. One possibility here is that CD patients harbor a genetically determined immunodeficiency that renders them unable to clear organisms gaining entry to the lamina propria (such as AIEC), and the latter thus persist at this site and evoke chronic inflammation. This seems doubtful, however, given the fact that this same immunodeficiency (if it exists) doesn’t cause an increased incidence of infection with true gastrointestinal pathogens such as *Shigella*, an organism that also expresses LPF that would enable it to enter the Peyer’s patch; and, in fact, there is no evidence that such pathogens cause CD. Another piece of evidence against this possibility is that while NOD2-deficient mice exhibit increased entry of AIEC into Peyer’s patches owing to higher numbers of GP2-expressing M cells and, in general, manifest decreased epithelial barrier function, these mice do not develop colitis upon challenge with AIEC (14). This finding relates to the possibility that an underlying immunodeficiency enables AIEC-induced inflammation, because NOD2 deficiency has been associated with decreased capacity to kill intracellular organisms due to defective autophagy and that AIEC bacteria manifest enhanced proliferation in cells with a defect in autophagy due to ATG16L1 deficiency (15, 16). Thus, the failure of AIEC to cause colitis in NOD2-deficient mice suggests that subtle immunodeficiency such as that possibly caused by NOD2 dysfunction does not predispose to an AIEC-mediated colitis.

**A consensus model of CD**

Another underlying genetically determined abnormality (or class of abnormalities) that could increase the potential of AIEC to induce inflammation relates to the now dominant hypothesis of CD pathogenesis, alluded to above, that holds that the disease is due to a genetically determined hyperreactivity to normal commensal microflora in the gastrointestinal tract. The very powerful evidence in favor of this concept includes the fact that colitis can be induced in mice with a specific pathogen–free microflora and not in the absence of a microflora (17). In addition, the best-characterized genetically determined risk factors now identified through genome-wide searches, the aforementioned NOD2 polymorphism, is thought to act by inactivation of a normal brake on innate (TLR-induced) enhancement of mucosal immune responses (18, 19). Finally, and perhaps most importantly, extensive studies of the colonial bacterial flora in CD have not revealed the presence of potentially pathogenic organisms; on the contrary, they have revealed deletions of certain bacterial groups that could result in loss of organisms that ordinarily induce suppressor or inhibitory responses so that, again, the microfloral changes encourage immunologic hyperresponsiveness (20, 21). In conclusion, therefore, the most likely scenario for AIEC activity is that CD is initiated by a dysregulated response to normal intestinal organisms and this creates an inflammatory milieu that favors expansion and invasion of AIEC in some patients; the latter then contribute to the inflammation by serving as an organism that has a prominent role in feeding the underlying immune hyperresponsiveness (Figure 1).

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RAS signaling pathway modifications and hypertrophic cardiomyopathy: getting into and out of the thick of it

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In this issue of the JCI, Wu et al. and Marin et al. describe two new mouse models of inherited disorders of the RAS/MAPK signal transduction pathway that display hypertrophic cardiomyopathy (HCM); the model from the former paper was from a gain-of-function Raf1 mutation, and the model from the latter paper was from a protein tyrosine phosphatase, non-receptor type 11 (Ptpn11) mutated allele encoding Shp2 with impaired catalytic function. The two groups show that HCM arises from increased signaling through Erk1/2 and the mTor complex 1, respectively, and that those cardiac issues can be prevented or reversed with small-molecule therapies inhibiting the appropriate pathway. Aside from being the first studies of treatment for Noonan syndrome and related disorders in a mammalian system, these papers provide important insights into the role of RAS signaling in cardiac hypertrophy and suggest the complexity in developing meaningful therapy for individuals with these RASopathies.

Signaling initiated by extracellular ligands, such as growth factors and cytokines, that is transduced through RAS proteins to multiple effectors, including the MAPKs, is central to cell proliferation, survival, differentiation, metabolism, and migration. The paradigmatic RAS/MAPK pathway (Figure 1) involves RAF proteins, particularly RAF1 and BRAF, which are MAPK kinase kinases that are activated after binding to RAS-GTP and then activate MAPK kinases, MEK1 and MEK2, which, in turn, activate the MAPKs, ERK1 and ERK2. Since its discovery nearly 30 years ago (1), the enormous role of perturbed RAS/MAPK signaling in cancer biology has become evident. Specifically, more than 30% of human cancers include mutations in genes encoding proteins in this pathway, particularly RAS proteins and BRAF. The vast majority of these genetic defects are acquired and result in increased activation of ERK1/2, often through gain-of-function alterations of the mutant proteins.

The importance of increased RAS/MAPK signaling in cancer spurred efforts to develop novel therapies that can reduce it (2). One strategy is to inhibit the mutant protein specifically. The best example of that approach is the ongoing work with PLX4032 (also known as RO5185426), which targets the BRAFV600E, the most common oncprotein implicated in melanoma (3). Successful phase I and II clinical trials with malignant melanoma have been completed, and a phase III trial is ongoing (4). However, the more common approach has been to develop small molecules that inhibit RAS/MAPK signaling broadly. Products of this track have included the farnesytransferase inhibitors, which are intended to reduce RAS translocation to the cell membrane, a necessary step for signaling, and inhibitors of RAF and MEK activities. To date, these efforts have been less successful (5). Since RAS/MAPK signaling is present in a wide array of normal cells and RAS proteins control multiple cellular processes and have several downstream effectors, titrating the right level of inhibition to provide therapeutic efficacy without incurring intolerable side effects is challenging. Indeed, clinical trials with PD325901, which is a highly specific MEK inhibitor, were terminated early due to ophthalmologic and neurologic toxicity, despite the fact that MEK1/2 are downstream in the RAS pathway and are only known to activate ERK1/2 (6).

After the discovery of the RAS/MAPK pathway, studies with model organisms like Drosophila melanogaster and Caenorhabditis elegans elaborated its central role in organismal development (7, 8). Subsequent experiments with loss-of-function alleles and cancer-related gain-of-function mutations, particularly in mouse models, generally produced one of two outcomes. For some genes

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