New IBD genes?
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New reports of potential novel inflammatory bowel disease (IBD) genes further advance our understanding of the genetic basis of IBD

Crohn’s disease (CD) and ulcerative colitis result from an inappropriate response of the mucosal immune system to the normal enteric flora in a genetically susceptible individual. The importance of genetic predisposition was firmly established in 2001 by the identification of the first CD susceptibility gene NOD2 (CARD15) on chromosome 16q12 (IBD1). It is now clear that NOD2 variants contribute only a small part to genetic susceptibility, suggesting the existence of other, as yet unidentified, genes. Although these have remained elusive, linkage studies have provided important clues to their location, implicating at least seven other regions of the human genome.

Two recent studies report the cloning of potential novel inflammatory bowel disease (IBD) genes within linkage areas on chromosomes 5 and 10. Linkage between CD and chromosome 5q31-33 (IBD5) was first demonstrated in 1999 and further characterisation of this locus refined the region to a highly conserved 250 kb haplotype. Identifying the IBD5 causation(s) has been hampered by the degree of linkage disequilibrium and the density of immunoregulatory genes on this haplotype. A Canadian group now suggest that the true IBD5 disease causing mutations occur in SLC22A4 and SLC22A5, encoding OCTN1 and OCTN2 respectively, members of the organic cation transporter subfamily. These proteins are involved in the elimination of toxins and the uptake of various physiological substrates, including carnitine (required for oxygen burst mediated pathogen killing). OCTN1 and OCTN2 are widely expressed, including in intestinal epithelial cells, macrophages, and T cells. Two putatively functional single nucleotide polymorphisms (SNPs), one in SLC22A4 and the other in SLC22A5, form a risk haplotype enriched in individuals with CD. The L503F (leucine to phenylalanine at codon 503) polymorphism maps to a region of SLC22A4, important for cellular transport, and functional data presented by the authors suggest the variant allele may affect uptake of carnitine, various xenobiotics, and toxins. The SLC22A5 SNP is located in the gene promoter where it appears to disrupt a predicted heat shock element required for the binding of heat shock transcription factors. Possession of the risk haplotype is associated with a 3–4-fold risk of disease, similar to that for possession of CARD15 mutations. Interestingly, the risk was much greater in the presence of both the risk haplotype and CD associated CARD15 alleles, consistent with an interaction between IBD5 and CARD15. The strong linkage disequilibrium across IBD5 makes interpretation of association data from individual SNPs difficult. This region is rich in genes, many of which are attractive candidates for disease pathogenesis. It therefore remains possible that other “functional” SNPs, expressed in tissues relevant to IBD, exist on this haplotype. Precisely how these SNPs might interact with NOD2 to increase the risk of CD remains unclear. However, tantalising clues are provided by the suggestion that α-defensins are potential substrates of OCTN1 and 2, and by a recent report suggesting that NOD2 variants may actually increase susceptibility to CD, through a defect in α-defensin production. The same group has published a study in an independent cohort confirming their findings. Analyses in this cohort have revealed particular association with ileal CD in contrast to a previous study suggesting an association between IBD5 and perianal CD.
A second study reports an association between SNPs in DLG5, a member of the membrane associated guanylate kinase gene family, and IBD. A German group performed linkage disequilibrium mapping of a locus on chromosome 10 and demonstrated association with variants in DLG5. Four common haplotypes across DLG5 were identified. Haplotype D (containing the unique SNP 113A) conferred a modest risk of CD while haplotype A was protective. The results were replicated in a case control study and once again possible interaction with the CD associated CARD15 alleles was noted. DLG5 is expressed in the colon and small intestine where it acts as a multifunctional adapter and scaffold protein involved in the regulation of epithelial cell growth, shape, and polarity. Computer prediction programs suggest that the IBD associated DLG variants may impair this scaffolding function, but at present supportive data from functional experiments are not available. One published study has confirmed the association between CD and SNP113A (but not with the common haplotype) although two other studies have not been able to confirm CD association with DLG5.

Further large adequately powered studies in different populations are now required to assess the probable moderating effect of this gene in CD susceptibility.

The rapid advances in our understanding of the genetic basis of IBD are yet to impact on routine clinical practice although recent discoveries have provided considerable insights for investigators. There is considerable optimism that as IBD genes are identified and their environmental interactions unravelled that we may be able to better define the heterogeneous group of patients with IBD, aid understanding of the molecular mechanisms specific to subgroups of disease, and provide a framework to predict clinical phenotype and response to therapy. These novel findings reported by the Canadian and German make an important contribution towards this goal.

**REFERENCES**