GENETICS

FINDING NEMO

17.04.2007

ATG16L1 is now confirmed as a candidate gene for Crohns disease:

> Specifically, the LD structure and association mapping around the most associated SNP […] rs2241880 implicated a region on chromosome 2q37.1 containing a single gene known as ATG16 autophagyâ€“related 16-like 1 (ATG16L1) […] Logistic regression analyses conditional on A197T in the family-based samples indicated that this coding variant can fully explain the association signal to this locus; thus, we consider this to be the causal risk variant.

Excellent to have this replication, although the argument above cannot convince me that this already a causal variant.
ATG16L1 seems to be most abundant in CD4+ and CD8+ cells and knockdown of the gene will lead to loss of S. typhimurium autophagy. Does rs2241880 really induce a loss of function and how does it relate to TLR7 and NOD2/CARD15 signalling?
The authors of another Nature paper believe that there is a primary NF-kB signalling defect in the Toll-like receptor activation by intestinal bacteria – see also KEGG pathways.
It will be much easier now to ask the right questions.