What is the association between ATG16L1 and inflammatory bowel disease?

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Inflammatory bowel disease, including Crohn's disease (CD) and ulcerative colitis (UC), are chronic relapsing disorders of the gastrointestinal tract, which have a complex genetic background. A recent meta-analysis research from China suggests that the mutation of ATG16L1 increases the risk for CD and UC in adults, but is different in children.

The ATG16L1 gene is located on chromosome 2 and encodes a protein involved in the formation of autophagosomes during autophagy. Autophagy is a cytoplasmic process that keeps a cell stable. Hampe et al first identified ATG16L1 as a Crohn's disease (CD) susceptibility gene in 2007, and many other studies have arisen since then. However, the definite relationship of variants of ATG16L1 with IBD remains unclear.

A research article to be published on March 14 , 2010 in the World Journal of Gastroenterology addresses this question. This meta-analysis, led by Jia-Fei Cheng and his colleagues selected publications that addressed the relationship between rs2241880/T300A polymorphism of ATG16L1 and inflammatory bowel disease (IBD). Forty-one papers were found through the literature search, and 25 of them were included in the final analysis according to strict exclusion criteria. Each of the 25 studies included cases of CD, with various subsets of papers that considered different ethnic populations. Fourteen papers included both CD and UC cases. As to children, seven of the included studies explored the relationship between the incidence of the variant of ATG16L1 and CD, while only two studies reported cases of child-onset UC.

The researchers found that the variant of ATG16L1 was associated a higher risk for CD and UC. For child-onset IBD, this variant was related to CD but not UC. These findings suggest a role for autophagy in the development of IBD, although the exact role that ATG16L1 plays in IBD etiology is unknown. Until recently, autophagy was considered to be only a cell maintenance mechanism. However, recent research has uncovered a role for autophagy in innate and adaptive immunity, which sheds light on the potential mechanism of the correlation between this gene mutation and an increased risk for IBD.

Further exploration of the molecular and cellular basis for the observed association between ATG16L1 and IBD may expand our understanding of the pathophysiology that underlies the development of IBD.

More information: Cheng JF, Ning YJ, Zhang W, Lu ZH, Lin L. T300A polymorphism of ATG16L1 and susceptibility to inflammatory bowel diseases: A meta-analysis. World J Gastroenterol 2010; 16(10): 1258-1266 www.wjgnet.com/1007-9327/full/v16/i10/1258.htm

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