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IBD

GENETICS OF IBD IN ASIAN POPULATIONS

Genetic mutations found in patients with IBD and susceptibility genes for IBD seem to differ between Asians and Caucasians, a systematic analysis has revealed.

Current understanding of IBD genetics is mainly from European studies. "With the incidence of IBD increasing in Asia, large-scale genetic studies are required to improve our understanding of the variability of IBD genetics between different populations," says Siew Ng.

To this end, Ng *et al*. performed a systematic review and meta-analysis to compare the genetic variants associated with IBD in Asian and Caucasian populations. Studies conducted over 1950–2010 were included. Of the 477 abstracts found, data were extracted from 93 studies, comprising 17,976 patients with IBD from diverse Asian populations (including Han Chinese, Japanese and South Korean) in addition to 27,350 age-matched and sex-matched controls.

The researchers found that genetic variants associated with IBD differ between Asian and Caucasian populations. The major genetic variants associated with IBD in Caucasians —found in the genes encoding nucleotide oligomerization domain 2, interleukin 23 receptor and autophagy-related protein 16-like 1—were not detected in Asians. Interestingly, new polymorphisms within these same candidate genes were identified in Asian patients with IBD. "The finding that different polymorphisms in the same genes lead to IBD in different populations reinforces the concept that these genes have a key role in IBD pathogenesis," concludes Ng. Moreover, Asians had different susceptibility genes for IBD; polymorphisms in the gene encoding tumor necrosis factor superfamily member 15 had a strong risk association with IBD in Asians but only a modest risk association in Caucasians.

The authors plan to determine if IBD-associated genetic loci in populations of European origin are replicated in populations of non-European origin. Fine mapping and immunochip analysis of IBD-associated regions could help to determine IBD-associated genes and polymorphisms, and genome wide association analysis might identify new causal variants.

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Original article Ng S. *et al.* Genetics of inflammatory bowel disease in Asia: Systematic review and meta-analysis. *Inflamm. Bowel Dis.* doi:10.1002/ibd.21845