IBS

A polymorphism in *TNFSF15* is associated with susceptibility to IBS

The pathogenesis of IBS is poorly understood, although previous studies indicate that low-grade inflammation and immunological alterations may be relevant. A genetic component of IBS is also predicted from epidemiological research in twins and families—but studies thus far have failed to provide evidence of specific susceptibility genes.

Owing to the potential involvement of inflammation and innate immunity in IBS, Mauro D'Amato and colleagues decided to test their hypothesis that genes associated with the risk of IBD may also have a role in IBS.

“We selected 30 well-known IBD loci, and one DNA variant (allele) from each locus unambiguously associated with increased disease risk,” explains D'Amato. “We could then effectively test our hypothesis by simply studying the frequency of these predisposing alleles in IBS patients compared with healthy controls.”

1,992 individuals from two independent case-control cohorts were included in the study. The investigators discovered that a polymorphism in the *TNFSF15* gene is found much more frequently in patients with IBS, particularly those with constipation-predominant IBS, compared with controls.

“Our results provide further support for the role of immune activation in IBS, and pave the way for similar, more-detailed immunogenetic analyses,” says D'Amato. “Hundreds of risk loci have been identified in genome-wide association studies of many inflammatory diseases, and these represent ideal candidates to be tested in larger, multinational cohorts of IBS patients and controls.”

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