Celiac disease and Crohn's disease share part of their genetic background

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An investigation has found that celiac disease and Crohn's disease, both inflammatory diseases of the gastrointestinal tract, share at least four genetic risk loci. Together, researchers from the University of Groningen, The Netherlands; the Broad Institute, USA; the Université de Montréal and Montreal Heart Institute in Canada performed a combined meta-analysis of genome-wide data for celiac disease and Crohn's disease. This meta-analysis, published in the open-access journal *PLoS Genetics* on January 27, has identified two new shared risk loci and two shared risk loci that had previously been independently identified for each disease.

The pathogenesis of both celiac disease and Crohn's disease is only partly understood, although it is known that they are affected by both genetic and environmental risk factors. At least one in every hundred individuals in the Western world develop celiac disease; Crohn's disease is much less common but can be accompanied by more severe symptoms as it can affect the whole gastrointestinal tract. Celiac patients develop an inflammation of the small bowel in reaction to gluten, whereas there is no specific known autoantigen for Crohn's disease. However, the primary cause of Crohn's disease is thought to be a dysregulated immune response to gut bacteria. In order to gain a better understanding of the pathogenesis and to aid in developing therapies against these disorders, knowledge of the genetic background of the diseases is vital.

As it has previously been shown that celiac patients are at a higher risk of developing Crohn's disease than non-sufferers, it had been thought that the two illnesses would share genetic risk loci. This study combined the results from the genetic investigations into both diseases to show that part of the genetic background of Crohn's disease and celiac disease is shared, which confirms a common pathogenesis for these disorders. Although additional studies will be necessary to understand the mechanisms by which these variants influence both Crohn's disease and celiac, the current study provides a proof of principle that risk factors shared across related diseases can be identified by directly combining genetic data from clinically distinct diseases.

More information: Festen EAM, Goyette P, Green T, Boucher G, Beauchamp C, et al. (2011) A Meta-Analysis of Genome-Wide Association Scans Identifies IL18RAP, PTPN2, TAGAP, and PUS10 As Shared Risk Loci for Crohn's Disease and Celiac Disease. PLoS Genet 7(1): e1001283. doi:10.1371/journal.pgen.1001283

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