

Scientists uncover further steps leading to celiac disease

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Scientists who last year identified a new genetic risk factor for coeliac disease, have, following continued research, discovered an additional seven gene regions implicated in causing the condition.

The team, lead by David van Heel, Professor of Gastrointestinal Genetics at Barts and The London School of Medicine and Dentistry, have further demonstrated that of the nine coeliac gene regions now know, four of these are also predisposing factors for type 1 diabetes. Their research sheds light not only on the nature of coeliac disease, but on the common origins of both diseases. It is published online today (2 March 2008) in *Nature Genetics*.

Professor van Heel and his team, including collaborators from Ireland, the Netherlands, and the Wellcome Trust Sanger Institute, first performed a genome wide association study in coeliac disease. Genetic markers across the genome were compared in coeliac disease subjects versus healthy controls. They then assessed around 1,000 of the strongest markers in a further ~ 5,000 samples. Their results identified seven new risk regions, six of which harbour important genes critical in the control of immune responses, highlighting their significance in the development of the disease.

Coeliac disease is common in the West, afflicting around 1 per cent of the population. It is an immune-mediated disease, triggered by intolerance to gluten (a protein found in wheat, barley and rye containing foods), that prevents normal digestion and absorption of nutrients. If

undetected it can lead to a number of often severe problems among them anaemia, poor bone health, fatigue and weight loss. Currently only a restricted diet can diminish symptoms.

Professor van Heel said: “So far our findings explain nearly half of the heritability of coeliac disease - now studies with many more samples from individuals with coeliac disease are needed to identify the precise causal genetic variants from each region, and understand how these influence biological processes.”

Source: Queen Mary, University of London

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