# More than 200 genes identified for Crohn's Disease

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More than two hundred gene locations have now been identified for the chronic bowel condition Crohn's Disease, in a study that analysed the entire human genome.

Published today in *The* American Journal of Human Genetics, scientists at UCL have devised a new method for identifying and mapping gene locations for complex inherited diseases. Using this method, they have been able to identify a large number of additional genes for Crohn's Disease, making a total of more than 200, which is more than have been found for any other disease. For example, there are just 66 known gene-regions for type 2 diabetes.

Crohn's Disease, a type of Inflammatory Bowel Disease, is a chronic illness of complex origins affecting approximately 100 to 150 people per 100,000. Understanding the genetic component of such complex diseases is central to explaining patients' symptoms and improving treatment.

Despite Crohn's having a large genetic component, this has been hard to dissect. This is partly due to the large number of genes involved, their complex interactions with environment and the spectrum of clinical presentations. As a result, many scientists have been focusing on ever larger cohorts of patients under the impression that larger data sets data will give better results.

This study shows how studying smaller but better defined groups can

lead to a better understanding of how complex diseases are inherited, and paving the way for personalised treatment.

Dr Nikolas Maniatis, senior author from the UCL Research Department of Genetics, Evolution and Environment, said: "The discovery of so many gene locations for Crohn's Disease is an important step forward in understanding the disease, which has a very complicated genetic basis. We hope that the method we have used here can be used to identify the genes involved in other diseases which are similarly complex, for example different cancers and diabetes."

The research team used UK data provided by the Wellcome Trust Case Control Consortium (WTCCC), which includes genetic information of 1698 CD patients. The team's results were also replicated using independent US data provided by the American National Institute of Diabetes and Digestive and Kidney Diseases (NIDDK), which contains genetic information of 813 patients with CD.

Dr Maniatis said: "The discovery of so many additional genes for Crohn's and much more precise locations within the gene-regions was partly because of the highly informative genetic maps of the human genome that we have used in our approach to locating the genes involved."

He added: "The success of our work was also attributable to the fact that we were able to subdivide patients by disease presentation. Data stratification can help sort out the genetics, and before long genetics will be able to sort out patients".

The team have provided the first clear evidence that some clinical sub-groups of patients are likely to carry different risk genes and their study shows how with a sufficiently powerful method more genes can be found in small groups of patients.

Professor Dallas Swallow, a collaborator and co-author also from the UCL Research Department of Genetics, Evolution & Environment, said: "Some genes are likely to have a large effect and some small, but not all genes will act the same way in all patients. We can combine all this information with that obtained by others from examining cellular and molecular changes to sort this out. This will ultimately lead to more personalised strategies for treatment".

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