Study shows epigenetic changes in children with Crohn's disease

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A new study finds a wide range of epigenetic changes—alterations in DNA across the genome that may be related to key environmental exposures—in children with Crohn's disease (CD), reports *Inflammatory Bowel Diseases*, official journal of the Crohn's & Colitis Foundation of America (CCFA).

The study provides "compelling evidence" of alterations of DNA in several regions of the genome in children with CD, according to Professor Jack Satsangi of University of Edinburgh and colleagues. In addition to providing new insights into how genes and the environment interact, the results may have early implications for clinical management of CD.

Epigenetic Changes in Childhood-Onset Crohn's Disease

The researchers performed a "genome-wide" study in children with newly diagnosed CD, before any treatment, to look for possible epigenetic changes that may affect gene behavior. Epigenetic changes reflect the impact of a wide range of environmental factors on genes.

The results showed strong evidence of such changes at 65 different sites across the genome. Nineteen sites showed clustering of epigenetic changes, pointing at genetic pathways that might be relevant to CD development.

Similar patterns were present in a separate group of children who had been treated for CD, as well as in a group of treated adults.

The study highlighted "highly significant" changes in two specific gene locations (loci), which include genes responsible for immune and cellular functions that could contribute to the development of CD. Two probes for these loci were highly accurate in predicting which children would have CD, providing a potentially useful "biomarker" for use as a diagnostic test.

'Exciting and Immediate Implications' for Clinical Management

One specific gene location seemed particularly important, as it has been implicated in a number of different cancers, including colorectal cancer. The same area has a known role in the development of T-cells, a key type of immune cell.

The study also identified a number of other loci that might play a role in the development of CD, warranting further study.

The new research adds to the growing body of evidence of epigenetic changes in diseases such as rheumatoid arthritis, multiple sclerosis, type 2 diabetes, and obesity. The findings highlight the importance of combining information on DNA changes, genes, and gene expression in future studies of these and other complex diseases, Dr Satsangi and colleagues believe.

Crohn's disease is a painful, medically incurable illness that may attack anywhere along the digestive system. Crohn's disease and ulcerative colitis, which involves only the large intestine (colon), are the two main types of inflammatory bowel disease. Some 1.4 million American adults

and children suffer from CD or ulcerative colitis.

Although much more research is needed to understand the epigenetic changes, the investigators believe their findings could lead to advances in clinical management of childhood-onset CD in the near future. They write, "There are exciting and immediate implications for early clinical translation; the discovery of easily accessible biomarkers in peripheral blood to predict disease susceptibility, progression or response to therapy and the potential for new therapeutic targets."

More information: Click here to read "Two-stage Genome-wide Methylation Profiling in Childhood-onset Crohn's Disease Implicates Epigenetic Alterations at the VMP1/MIR21 and HLA Loci."

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