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First genetic map of Attention Deficit Hyperactivity Disorder

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Summary: An international study, focused on the analysis of the genome of more than 50,000 people worldwide, has identified twelve specific fragments of DNA related to the vulnerability of the attention deficit hyperactivity disorder (ADHD).

FULL STORY

An international study, focused on the analysis of the genome of more than 50,000 people worldwide, has identified twelve specific fragments of DNA related to the vulnerability of the attention deficit hyperactivity disorder (ADHD). The study, published in the journal *Nature Genetics*, involves more than eighty authors among which are several Catalan researchers such as Bru Cormand, researcher of the University of Barcelona, the Institute of Biomedicine of the UB (IBUB), the Research Institute Sant Joan de Déu (IRSJD) and the Rare Diseases Networking Biomedical Research Center (CIBERER); Josep Antoni Ramos Quiroga, Marta Ribasés, Miquel Casas and Cristina Sánchez Mora (University Hospital Vall d'Hebron and CIBERSAM), Amaia Hervás (University Hospital Mutua Terrassa) and Jordi Sunyer (Barcelona Institute for Global Health, ISGlobal), among others.

First global ADHD study at genomic scale

ADHD is one of the most common psychiatric disorders in children and adolescents: it affects about 5 % of the kids and 2.5 % in adults. It is represented by attention deficit, hyperactivity and impulsive behaviour, and it limits the personal and social skills of those with the disorder. With quite and unknown origin, everything points out that ADHD is the result of the combination of environmental factors (toxicological, psychological and social, etc.) with a polygenic hereditary basis (which would explain about 75 % of the disorder).

The study now published by *Nature Genetics* is the largest one at a genomic scale on ADHD so far, and it focuses on the role of common genetic variants in general population. The study is led by the experts Benjamin M. Neale, (Harvard Medical School, United States), Anders D. Børglum (University of Aarhus, Denmark), and Stephen V. Faraone (the State University of New York, United States), with the support from international platforms like the Psychiatric Genomics Consortium (PGC), the Early Genetics and Lifecourse Epidemiology (EAGLE Consortium) and the Roadmap Epigenomics Mapping Consortium.

Pursuing ten million loci in the human genome

The international team has analysed about ten million positions (loci) of the genome in more than 50,000 people -patients and controls- from different countries in Europe, the United States, Canada and China. Through the whole genome association study (WGAS), they analysed the changes in a DNA nucleotide (SNP), the most common in the human genome.

The study reveals these common genetic variants "weight a 21 % of the total ADHD genetics," says Bru Cormand, head of the Research Group on Neurogenetics at the Faculty of Biology of the UB. "In addition -adds the expert-, most genetic alterations that were identified are found in regions of the genome that are kept along evolution, which highlights its functional relevance."

In particular, the international research study identifies twelve genomic segments -most of them corresponding to specific genes- that provide the ADHD with vulnerability. Specifically, many of the genetic changes that are related to this disorder affect regulating elements of the gene expression in the brain.

FOXP2 gene: the genetic bases of language in humans

Among the identified fragments is the gene FOXP2- one of the most studied genes regarding language development in humans-, which encodes a protein with a distinguished role in the creation of neural synapse and learning. FOXP2 had been regarded as the candidate gene to ADHD in a previous study (Psychiatric Genetics, 2012), in which some Catalan authors who participate in the new study were involved too. At the moment, this is one of the few cited genes in the scientific bibliography that appears again the genetic map of the ADHD, published in *Nature Genetics*.

Another identified gene -DUSP6- is involved in the control of dopaminergic neurotransmission, a target process for the most common ADHD pharmacological treatments. Also, the SEMA6D gene, expressed in the brain during the embryonic development, could play an important role in the creation of neural branches.

The international study reviews the potential genetic basis shared between ADHD and more than two-hundred phenotypes (psychiatric and non-psychiatric). According to Cormand, "results reveal a genetic overlap between ADHD and major depression, anorexia, level of education, obesity, reproductive success, smoking or insomnia, among others."

Several previous studies that were conducted on twins proved that 75 % of the disorder can be explained with genetic factors. This new study starts defining in a more specific way the genetic landscape of ADHD, identifying around ten specific genes that contribute to the vulnerability of the disease. According to the researcher, "this study reinforces, against deniers, the idea that ADHD is a disorder with a solid biological basis, where genetics mean a lot."

Scientific consortiums: large-scale international science

This first genetic map of the vulnerability of ADHD places the research effort of experts from more than seventy institutions around the world, and joins the scientific progress to improve the diagnosis of psychiatric disorders with genetics. "These results show the importance of promoting large scale-studies -- which is only possible through big international consortiums -- to explore the genetic basis of complex brain diseases," concludes Bru Cormand.

Story Source:

Materials provided by **University of Barcelona**. *Note: Content may be edited for style and length.*

Journal Reference:

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