Schizophrenia:
genes under the microscope to identify molecular triggers

An international group of researchers is working to decipher the molecular mechanisms behind the disease. The University of Trento is part of the “CommonMind Consortium” with Enrico Domenici of CIBIO. The first results of their studies have been published in “Nature Neuroscience”

Trento, 5 October 2016 – (e.b.) Different genes might be associated with schizophrenia, but recent studies point in the direction of at least three genes, and some other factors, that make us vulnerable to this disease. In the near future, this discovery might lead to the development of new treatments.

Looking into the microscope is an international group of researchers and one of them is Enrico Domenici of CIBIO, the Center for Integrative Biology of the University of Trento.

«Thanks to recent advances in genomics – says Domenici (Laboratory of Neurogenomic Biomarkers, CIBIO) – we now know that there are many subtle variations, in over 100 different genomic regions, that may increase a person’s risk of developing this highly disabling disorder in their life. But very little is known on how these variations exert their effects».

The researchers’ work started four years ago with the establishment of the CommonMind Consortium, an international consortium made up of scientists from nine institutions and four different countries, thanks to public and private funds. The aim of the consortium was to decipher the molecular mechanisms at play in the brain of patients with mental disorders and make this data broadly available to the scientific community. “Nature Neuroscience” has recently published an article on the first steps towards the identification of the genes that might explain disease vulnerability.

Domenici explains: «We started from the analysis of post mortem brain tissue from over 600 schizophrenic patient and healthy donors. Thanks to advanced sequencing and data analysis technologies, we were able to identify, in the 100 different genomic regions, a series of genetic variants responsible for changes in cerebral processes at molecular level. With more accurate analysis, we have finally identified five suspect genes and by testing them in cellular and animal models, we found that three of them induced deficits that are similar to those found in tissues from schizophrenic patients. This achievement opens new perspectives to understand the genetic mechanisms that, together with other factors, contribute to the development of schizophrenia. The research work continues: by further investigating the role of these genes we hope to set the basis for the development of new therapeutic treatments».
The article, “Gene Expression Elucidates Functional Impact of Polygenic Risk for Schizophrenia”, published on 26 September in “Nature Neuroscience”, is available at:

http://www.nature.com/neuro/journal/vaop/ncurrent/full/nn.4399.html

Photo reportage by Giovanni Cavulli for the University of Trento

In the pictures, Enrico Domenici with his team at Cibio (Laboratory of Neurogenomic Biomarkers, CIBIO). From left to right, at the table: Roberto Visintainer - Daniela Calini - Enrico Domenici - Michele Filosi.