Synopsis of Original Research Paper

Exploration of biomarkers of schizophrenia using hair follicles

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Biomarkers at the substance level are needed as objective evidence to elucidate the pathophysiology of schizophrenia. We have been focusing on "hair follicles," which are derived from the same ectoderm as the brain, as a biological sample useful for stratifying psychiatric disorders. In this study, we compared gene expression patterns in follicle cells from schizophrenia and healthy controls and found that 241 genes were up-regulated, and 28 genes were down-regulated in the schizophrenia group (FDR < 0.1, |fold change| > 1.2). The Gene Ontology (GO) Biological Process pathway was found to be enriched in a pathway related to "prepulse inhibition", a known intermediate phenotype of schizophrenia, a "microglial pathway", and an "MHC class II pathway" involved in antigen presentation by immune system cells. In addition, the GO Cellular Component pathway was enriched in pathways related to "ribbon synapses" in the active zone of synapses and pathways related to "astrocyte projection", which have attracted attention for their association with brain function. It is very significant that we found these results by conducting hypothesis-free gene expression analysis of hair follicles. Based on the results of this study, we intend to pursue the possibility that the expression of these biomarker genes may be useful in the early detection of schizophrenia patients, therapeutic evaluation, and drug discovery.