

FROM GENE EXPRESSION VARIATION TO DEFINITION OF BIOMARKERS IN DEPRESSION

R. Belzeaux¹, E.C. Ibrahim²

¹Psychiatrie Universitaire, AP-HM, ²CRN2M, Aix Marseille Universitaire, Marseille, France

Several studies examined gene expression variations in depressive patients compared to control subjects in post-mortem samples as well as in fresh peripheral tissues.

Our aim has been investigate gene expression variations during Major Depressive Episode (MDE) in peripheral blood mononuclear cells (PBMCs). We collected PBMCs from two different cohorts of severe MDE patients (n=11 and n=13) and compared gene expression between patients and matched-control subjects. Moreover, in a 64 weeks prospective study, we had the opportunity to investigate what happens when a healthy subject gets his first MDE. We analysed gene expression variations accross time in both patients and controls and used both pan-genomic microarray and RT-qPCR strategies for RNA quantification. Finally, to compare gene expression variations in blood tissue and in post-mortem, we benefited from transcriptome databases to reanalyze, with uniform filtering and quantification procedures, gene expression in a large set of samples collected from other groups.

We found several genes whose expression vary significantly between patient and control subjects as well as between the severe acute MDE phase and the following therapeutic response or remission phases occuring several weeks and months later, respectively. Beyond then, both well-known candidate genes, such as 5HTT, TPH1 or NRG1, and new genes (HIST1E1, PPT1) could be proposed for biomarkers development in MDE.

Our results demonstrate that gene expression variation in PBMCs could be relevant as biomarkers for depression. The convergence of our data and other studies will be discussed as well as the comparability between brain and blood gene expression.