Genomic, epigenetic and proteomic biomarkers in psychosis: a translational approach including high-risk individuals, patients with schizophrenia and animal models (GEPI-BIOPSY)

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Our project aims to identify prognostic biomarkers associated with the psychotic phenotype using an integrative dataset and a machine-learning approach. We will study genetic (polygenic risk scores for schizophrenia), epigenetic (genome-wide DNA methylation) and proteomic (quantitative high-throughput information of 100s to 1000s of proteins) biomarkers in the blood of individuals with and without psychotic experiences and in patients with schizophrenia at different stages of the illness in order to assess the progression of these biomarkers. We will also use an animal model of schizophrenia (prenatal maternal immune activation [MIA] with the viral mimic polyinosinic-polycytidylic acid) in order to determine the pathological value of the same biomarkers (epigenetic and proteomic signatures) in blood and brain tissue as well as the relationship between DNA methylation and proteomic patterns in peripheral vs brain tissue. Similar behavioural measures (pre-pulse inhibition, cognitive function, social interaction, and anhedonia) will be also studied under a translational approach in both, adolescents (with and without psychotic experiences) and rats (MIA vs controls), in order to correlate them with genomic, epigenetic or proteomic signatures in blood. Machine learning methods will be used for identifying potential clusters or subtypes in terms of behavioural data and complimentary biomarkers at the genomic, epigenetic and proteomic level.