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Analyses of IPSC-derived dopaminergic neurons from Parkinson disease

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Parkinson disease (PD) is a neurodegenerative disorder associated with the progressive loss of dopaminergic neurons (DAn) in the substantia nigra pars compacta (SNpc). Although most cases are sporadic, around 5-10% encompasses monogenic forms caused by pathogenic mutations in PD-associated genes like the leucine-rich repeat kinase 2 (LRRK2) which is clinical and neuropathologically undistinguishable from sporadic PD (sPD). To explore molecular alterations in these cell models of PD, we analyzed the DNA methylome and RNA transcriptome in induced pluripotent stem cells (IPSC)-derived DAn generated from keratinocytes of L2PD and sPD patients, and age-matched healthy subjects, using high-density arrays. Differentially methylated CpG sites (DMCpGs) were annotated to nearby genes, quantifying the relative distribution of DMCpGs across different gene-related regions, and statistically correlating them with their corresponding transcripts expression values. Associated pathways and gene ontology terms were determined by Gene Enrichment Analysis. Overall, extensive in silico data analysis were performed in order to go deep into the molecular processes involved in genetic and sporadic forms of PD.

Biography

Mario Ezquerra after receiving his PhD in 2000 from the University of Barcelona, performed Postdoctoral training in the field of genetics of neurodegenerative diseases in the Institute Pasteur of Lille (2000-2001, France), and from 2001 to 2007 at the Fundacio Clinic de Barcelona. In late 2007, he joined the Institut d'Investigacions August Pi y Sunyer (IDIBAPS), and he currently enjoys a Miguel Servet fellowship in the position of Researcher at the Laboratory of Neurodegenerative diseases. He is a member of the Center for Networked Biomedical Research on Neurodegenerative Diseases (CIBERNED). He has published more than 50 papers in international peer review journals.

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