

# Transcriptome Meta Analysis to Identify Novel Pharmacological Targets in Parkinson's Disease

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The understanding of the genetic basis of the Parkinson's disease (PD) and the correlation between genotype and phenotype has revolutionized our knowledge about the pathogenetic mechanisms of neurodegeneration, opening up exciting new therapeutic and neuroprotective perspectives. Genomic knowledge of PD is still in its early stages and can provide a good start for studies of the molecular mechanisms that underlie the gene expression variations and the epigenetic mechanisms that may contribute to the complex and characteristic phenotype of PD. In this study we used the software TRAM (Transcriptome Mapper) to analyse publicly available microarray data of a total of 151 PD patients and 130 healthy controls substantia nigra (SN) samples, to identify chromosomal segments and gene loci differential expression. In particular, we separately analyzed PD patients and controls data from post-mortem snap-frozen SN whole tissue and from laser microdissected midbrain dopamine (DA) neurons, to better characterize the specific DA neuronal expression profile associated with the late-stage Parkinson's condition. In particular, the default "Map" mode and single gene level analysis resulted in 4 segments mapping on 4 different chromosomes and 759 significative single transcripts, respectively, for DA neurons. In conclusion, TRAM software allowed us to **emphasize** the deregulation of some genomic regions and loci involved in key molecular pathways related to neurodegeneration.