Analyzing alternative splicing data of splice junction arrays from Parkinson patients' leukocytes before and after deep brain stimulation as compared with control donors

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Abstract:

Few studies so far examined alternative splicing alterations in blood cells of neurodegenerative disease patients, particularly Parkinson's disease (PD). Prototype junction microarrays interrogate known human genome junctions and enable characterization of alternative splicing events; however, the analysis is not straightforward and different methods can be used to estimate junction-specific alternative splicing events (some of which can also be applied for analyzing RNA sequencing junction-level data). In this study, we characterized alternative splicing changes in blood leukocyte samples from Parkinson's patients prior to, and following deep brain stimulation (DBS) treatment; both on stimulation and following 1 h off electrical stimulation. Here, we describe in detail analysis approaches for junction microarrays and provide suggestions for further analyses to delineate transcript level effects of the observed alterations as well as detection of microRNA binding sites and protein domains in the alternatively spliced target regions spanning across both untranslated and the coding regions of the targets. The raw expression data files are publically available in the Gene Expression Omnibus (GEO) database (accession number: GSE37591) and in Synapse, and can be re-analyzed. The results may be useful for designing of future experiments and cross correlations with other datasets from PD or patients having other neurodegenerative diseases.

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