BIOMARKER DISCOVERY THROUGH SECRETOME ANALYSIS OF PARKINSON'S DISEASE MODEL CELL LINES

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BIOMARKER DISCOVERY THROUGH SECRETOME ANALYSIS OF PARKINSON'S DISEASE MODEL CELL LINES

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Parkinson's disease (PD), a chronic degenerative brain disease, is characterized by a loss of dopiminergic neurons in the substantia nigra area of the brain and the abnormal presence of ubiquitinated cytoplasmic inclusions called Lewy bodies in affected cells. Parkinson's disease can be diagnosed precisely by post-mortem analysis of the affected areas of the brain whereas early clinical diagnosis of PD may be based on the patient's medical history and neurological examinations before a symptom calming treatment can be implemented. Thus, the interest in finding early biomarkers for this neurodegenerative diseases before clinical symptoms arise is great. Cerebrospinal fluid (CSF) is the most relevant biological fluid for biomarker study because CSF has direct contact with the extra cellular space in the brain. The CSF Proteome is, however, extremely complex and patient samples are often available only in small volume whereby direct analysis by specific PD biomarkers is a major analytical challenge. Alternatively, Conditioned media obtained from appropriate PD model cell lines enable identification of potential biomarkers for PD by investigation of expression profiles of secreted proteins and composition of micro vesicles.

We present here the methodology for purification and identification of secreted proteins and micro vesicle-associated proteins from PD cell lines that change the expression level as a consequence of overexpression of specific proteins (e.g. α-synuclein, Parkin or P25α) through a quantitative mass spectrometry based approach.

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