Single cell analysis and RNA amplification in neurodegenerative disorders

Ginsberg SD
Nathan Kline Institute and New York University School of Medicine, New York, USA

Technical and experimental advances in microaspiration techniques, RNA amplification, quantitative real-time PCR (qPCR), and cDNA microarray analysis have led to an increase in the number of studies of single cell gene expression. In particular, the central nervous system (CNS) is an ideal structure to apply single cell gene expression paradigms. Unlike an organ that is comprised of one principal cell type, the brain contains a constellation of neuronal and noneuronal populations of cells. A goal is to sample gene expression from similar cell types within a defined region without potential contamination by expression profiles of adjacent neuronal subpopulations and noneuronal cells. The unprecedented resolution afforded by single cell RNA analysis in combination with RNA amplification methods and cDNA microarrays allows for relative gene expression level comparisons across cell types under different experimental conditions and disease states. The ability to analyze single cells is an important distinction from global and regional assessments of mRNA expression, and can be applied to optimally prepared tissues from animal models as well as postmortem human brain tissues. This presentation illustrates the potential power of single cell gene expression studies within the CNS in relation to neurodegenerative disorders such as Alzheimer's disease.

Stephen D Ginsberg, Center for Dementia Research, Nathan Kline Institute, Departments of Psychiatry and Physiology & Neuroscience, New York University School of Medicine, 140 Old Orangeburg Road, Orangeburg, NY 10962, USA, t 1-845 398 2170, e-mail ginsberg@nki.rfmh.org

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