The importance role of expression profile based RNA-seq in discovering the etiology of multiple sclerosis

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expression analyses provide a quite unbiased way to investigate complex traits and common disorders' pathogenesis. Therefore, whole-transcriptome analysis is increasingly acquiring a key role in the knowledge of mechanisms responsible for complex diseases. Interestingly Next-Generation Sequencing, particularly RNA-Seq, is taking first steps for studying neurodegenerative diseases (ND) as well as neuropsychiatric diseases. the emerging role of noncoding RNAs (ncRNAs) including miRNAs, long intergenic and long ncRNA (lincRNAs and lncRNA, respectively) in neurogenesis, strongly support the usage of RNA-Seq in brain transcriptome analysis.

Multiple sclerosis (MS) is an inflammatory demyelinating and neurodegenerative disease, chiefly affecting the central nervous system (CNS). Grey matter lesions are closely associated with disease progression and permanent disability in MS. Recently, Jun-ichi Satoh andet al have performed an expression profiles of RNA-Seq-based grey matter-specific genes(GMSG) versus white matter-specific genes(WMSG) in grey matter lesions of MS brains. They've shown that particularly 714 RNA-Seq-based GMSG closely related to neuronal functions and 378 WMSG with relevance to glial functions. Numerous WMSG, such as KLK6, GJB1 and MYRF, were downregulated in both grey matter and white matter lesions, whereas the expression of various GMSG, such as PVALB, NEUROD6 and LINGO1, was reduced exclusively in grey matter lesions. Furthermore the panel of RNA-Seq-based GMSG and WMSG serves as molecular markers for discrimination between grey matter and white matter lesions of MS. In addition since MS is a autoimmune disease then the assesment of expression profile based RNA-seq of T helper cells can be usefull for etiology and pathology of this disease and further studies should be performed to find the differebce transcriptom profile between control and patient samples. So RNA-Seq can significantly improve the way of looking at cell transcriptome in physiological and pathological conditions in MS.

Keywords: MS, RNA-seq, etiology, pathogenesis