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RNA-seq characterization of spinal cord injury transcriptome in acute/subacute phases: A resource for understanding the pathology at the systems level

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Spinal cord injury (SCI) is a devastating neurological disease without effective treatment. To generate a comprehensive view of the mechanisms involved in SCI pathology, we applied RNA-Sequencing technology to characterize the temporal changes in global gene expression after contusive SCI in mice. We sequenced tissue samples from acute and subacute phases SCI and systematically characterized the transcriptomes with the goal of identifying pathways and genes critical in SCI pathology. Based on the data generated, we developed a systems-based analysis framework in order to identify key determinants in the global gene networks of the acute and sub-acute phases. By applying our approach, we successfully identified candidate genes that have been shown to play important roles in SCI. There are also many genes whose functions in SCI have not been well studied and can be further investigated by future experiments. We then incorporated pharmacogenomic information into our analyses. Among the genes identified, the ones with existing drug information can be readily tested in SCI animal models. Therefore, in this study we have described an example of how global gene profiling can be translated to identifying genes of interest for functional tests in the future and generating new hypotheses. Additionally, the RNA-Seq enables splicing isoform identification and the estimation of expression levels, thus providing useful information for increasing the specificity of drug design and reducing potential side effect. In summary, these results provide a valuable reference data resource for a better understanding of the SCI process in the acute and sub-acute phases.

Biography

Kenian Chen obtained his Ph.D degree from Sun Yat-Sen University in China. After two years working as a lecturer in Guangzhou Medical University, he went on his postdoctoral studies in University of Texas, applying next generation sequencing technology in neuroscience research.

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