特 別 講 演 会

演　題：Functional Genomics: Phenotypic screening of large gene sets to identify genes that promote nerve regeneration

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場　所：　鹿児島大学医学部 第４講義室　　医学部講義棟２階

Research Abstract

Development and regeneration of the nervous system requires the regulated formation of axons and dendrites. A comprehensive understanding of neuronal process development on a molecular level is lacking. High Content Analysis (HCA) of primary neurons offers a powerful way to study how different genes influence neuronal differentiation. We have performed three different HCA screens to identify genes that enhance axon growth. One screen was to determine the effect of kinase and phosphatase expression on developing neurons in culture. Over 300 kinases and 124 esterases and phosphatases were studied by over expression in hippocampal neurons. We identified many novel neurite growth regulators that have little or no established role in neuronal function. Using novel cluster analyses, we explored families of related proteins with functionally similar effects. Additionally, pathway analysis revealed that members of pathways involved in cancer progression and axis formation can enhance neurite outgrowth. A second screen of over 1100 genes expressed in peripheral nervous system neurons but not cerebellar neurons uncovered transcription factors and other proteins that can enhance growth of CNS neurons. This screen involved the acquisition of more than one half a million images and the analysis of over 6 million neurons. The third screen of over 600 developmentally regulated genes in cortical neurons identified the KLF transcription factor family as a potent intrinsic regulator of axon growth. In the future, the comprehensive data from these screens will enable the mapping of small molecule HCA screens onto molecular pathways, thereby speeding the development of novel therapeutics.

主　催：　日本薬学会九州支部
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