

# International Congress on **Neuroimmunology and Therapeutics**

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## **Biomarker discovery for neuroendocrine cervical cancer**

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**N**euroendocrine cervical cancer is an aggressive but rare form of cervical cancer. The majority of neuroendocrine cervical cancer patients present with advanced-stage diseases. However, the limited numbers of neuroendocrine tumor markers are insufficient for clinical purposes. Thus, we used a proteomic approach combining lysine labeling 2-dimensional difference gel electrophoresis (2D-DIGE) and matrix-assisted laser desorption-ionization time-of-flight mass spectrometry (MALDI-TOF MS) to investigate the biomarkers for neuroendocrine cervical cancer. By analyzing the global proteome alteration between the neuroendocrine cervical cancer line, HM-1, and non-neuroendocrine cervical cancer lines, CaSki cells, ME-180 cells and HeLa cells, we identified 82 proteins exhibiting marked changes between HM-1 and CaSki cells, and between ME-180 and HeLa cells. Several proteins involved in protein folding, cytoskeleton, transcription control, signal transduction, glycolysis and redox regulation exhibited significant changes in abundance. Proteomic and immunoblot analyses indicated respective 49.88-fold and 25-fold increased levels of transgelin in HM-1 cells compared with that in other non-neuroendocrine cervical cancer cell lines, implying that transgelin is a biomarker for neuroendocrine cervical cancer. In summary, we used a comprehensive neuroendocrine / non-neuroendocrine-cervical-cancer-model-based proteomic approach for identifying neuroendocrine cervical cancer markers, which might contribute to the prognosis and diagnosis of neuroendocrine cervical cancer.

### **Biography**

Hong-Lin Chan is Head of the National Tsing-Hua University (Taiwan) for Quantitative Proteomics Group and has more than 10 years of experience in proteomic method development and application. He received his PhD degree from University College, University of London in 2005. After 2 year Post-doctoral training in the Wolfson Institute for Biomedical Sciences, he took the current Professorship from National Tsing-Hua University in Taiwan. He was one of the first users of 2D-DIGE technology which is routinely used for protein expression profiling and the group has also established platforms which perform quantitative phosphoproteomics and redox-proteomics analysis.

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