3 newly discovered ERK pathway proteins related to CagA induced disease

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Cytotoxin-associated gene A protein (CagA) from type I H.pylori has been proved by epidemiological and experimental studies to be closely associated with the H.pylori induced gastric diseases, especially gastric cancer. However, the precise role of CagA in cell function after H. pylori infection remains unclear and no study on exploring the global protein expression pattern which can reflect host cells response to CagA has been reported.

A research article to be published on January 28, 2008 in the World Journal of Gastroenterology addresses this question. The research team led by Prof. Zheng from Cancer Institute of Zhejiang University used ProteinChip platform, which is based on surface enhanced laser desorption / ionization time-of-flight mass spectrometry (SELDI-TOF-MS) technology, to study the global protein expression changes in AGS cells transfected with CagA gene.

As various researches indicated a relationship among CagA, ERK/MAPK pathway activation and gastric cancer, the article further investigate the relationship of these protein expression differences and activation of ERK pathway by adding specific mitogen-activated protein kinase kinase (MEK) inhibitor during transfection.

When 16 proteins showed expression differences after CagA transfection, three proteins with molecular weights of 4 229, 8 162 and 9 084 Dalton were found have no expression differences under the treatment of MEK inhibitor, indicating they are downstream molecules of ERK1/2 in ERK/MAPK signaling pathway. Matching information from Swiss-Prot/TrEMBL database indicates these three proteins may be related with cell apoptosis, cell antimicrobial defense, chemotactic function, cell proliferation, differentiation and carcinogenesis, and therefore have great potential to be identified as cancer-associated proteins in further research.

Due to the high sensitivity and resolution in low molecular weight range of SELDI-ProteinChip technology, biomarkers discovered in this study are mainly low mass range and/or low abundance disease related proteins, which are difficult to detect by traditional methods. These results demonstrate a new view of molecules involved in the CagA related signaling pathways, and thus may provide new targets for further understanding of the biological function of CagA and new therapeutic targets.

Source: World Journal of Gastroenterology