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Identification of mitochondrial proteins related to nasopharyngeal carcinoma metastasis

Xianquan Zhan[1], Jianping Liu[1] and Zhuchu Chen[1]

[1]Central South University, China

To screen mitochondrial proteins for the elucidation of the molecular mechanisms of nasopharyngeal carcinoma metastasis and the discovery of metastasis-related biomarkers, mitochondria were isolated from nasopharyngeal carcinoma metastatic (5-8F) and nonmetastatic (6-10B) cell lines, respectively. After characterization of isolated mitochondria, mitochondrial proteins were extracted for two-dimensional difference in-gel electrophoresis (2D-DIGE) quantification. Sixteen differentially expressed proteins (DEPs) including PRDX3 and SOD2 were identified with mass spectrometry. Furthermore, siRNAs transient transfections were used to suppress expressions of some up-regulated DEPs in metastatic cells (5-8F), followed by Transwell Migration assay, and those 5-8F cells with suppression of PRDX3 showed an increased mobility potential. The functional enrichment analyses of DEPs discovered significant biological processes including cellular response to reactive oxygen species, hydrogen peroxide metabolic process, regulation of mitochondrial membrane potential, cell redox homestasis and oxidation reduction, and significant molecular functions including oxidoreductase activity, caspase inhibitor activity, peroxiredoxin activity, porin activity and antioxidant activity. A protein-protein interaction sub-network of DEPs was generated with literature data mining from HPRD and NCBI databases. Ten mitochondrial DEPs including PRDX3, PRDX6, SOD2, ECH1, SERPINB5, COX5A, PDIA5, EIF5A, IDH3B, and PSMC4 were rationalized in the tumor-stroma co-evolution model that mitochondrial oxidative stress directly contributes to tumor metastasis. These data would be helpful to understand the roles of mitochondria and oxidative stress in nasopharyngeal carcinoma metastatic process.

Biography

Xianquan Zhan received his undergraduate and graduate training at the West China University of Medical Sciences, Chengdu, China, where he spent 10 years, and obtained his B.M./M.D. degree in preventive medicine in 1994, M.S. degree in occupational epidemiology in 1996, and Ph.D. degrees in molecular toxicology in 1999. He received his post-doctoral training in oncology and cancer proteomics for two years at the Cancer Research Institute of Human Medical University, Changsha, China. In 2001, he went to the University of Tennessee Health Science Center (UTHSC), Memphis, Tennessee, USA, where he was a post-doctoral researcher (mass spectrometry, proteomics) supervised by Prof. Dominic M. Desiderio in the Charles B. Stout Neuroscience Mass Spectrometry Laboratory in the Department of Neurology. Then, he was appointed as an Assistant Professor of Neurology, UTHSC in 2005. He moved to the Cleveland Clinic (Cleveland, Ohio, USA) as a Project Scientist/Staff in 2006 where he focused on the studies of eye disease proteomics and biomarkers. In the end of 2007, he returned to UTHSC as an Assistant Professor of Neurology, engaging in proteomics and biomarker studies of lung diseases and brain tumors, and initiating the studies of predictive, preventive, and personalized medicine in cancer. In July 2010, he was promoted to Associate Professor of Neurology, UTHSC. Currently, he is a Distinguished Professor of disease proteomics and structural biology, Xiangya Hospital, Central South University, Changsha, China, the National Representative in China of European Association for Predictive, Preventive, and Personalized Medicine (EPMA), Associate Editor of BMC Genomic, and Associate Editor of BMC Medical Genomics. He has published 50+ peer-reviewed research articles including 30+ articles in the field of disease proteomics and transcriptomics, 4 book chapters, and 1 US patent. His current main research interest focuses on the studies of disease proteomics/biomarkers and structural biology, and the development and use of modern –omics techniques including proteomics for cancer predictive, preventive, and personalized medicine.

zhanx@ccf.org