

Proteomic and transcriptomic analysis for molecular mechanism in capsaicin-induced apoptosis between human hepatocarcinoma and human neuroblastoma cells

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It was found that endogenous ROS levels were increased during hepatocarcinoma (HepG2) apoptosis, whereas they decreased during neuroblastoma (SK-N-SH) apoptosis in response to capsaicin treatments. To clarify this different phenomenon, we used 2-DE-based proteomics to analyze the altered protein levels in both cells, with special attention on oxidative stress proteins before and after capsaicin treatments. The 2-DE analysis demonstrated that 23 proteins were increased and 26 proteins were decreased in capsaicin-treated apoptotic HepG2 and SK-N-SH cells, respectively. Next, the global gene expression for oxidative stress and antioxidant defense genes was analyzed by the Human Oxidative Stress and Antioxidant Defense RT² ProfilerTM PCR Array. Surprisingly, the profiles of 84 gene expressions related to oxidative stress and antioxidant defense were not significantly different in HepG2 cells between control and capsaicin-treated cells. In contrast, a number of oxidative genes were down-regulated in SK-N-SH cells, supporting the evidence of low ROS environment in apoptotic SK-N-SH cells after capsaicin treatment.