Proteomic analysis on the effect of water-soluble fraction of cigarette smoke on bovine aortic endothelial cells

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In this study, we utilized two-dimensional electrophoresis(2-DE) and mass spectrometry(MS) technologies to explore protein changes in bovine aortic endothelial cells in response to cigarette smoke extracts (CSE). Among 161 individual protein resolved using 2-DE, the expression level of 101 proteins significantly increased as measured by spot intensity and 60 had dreased. All of 161 spots with sufficient amount of protein were exicised for identification by performing matrix-assisted laser desorption/ionization (MALDI)-TOF MS analysis. Using a peptide mass fingerprinting(PMF) to search the rNCBI database, we identified all these 161 proteins, which were either increased or decreased after CSE treatment. All these proteins have known functions, however, none have been reported to be altered after CSE treatment. The findings from our study suggest that utilizing a systemic investigative tool may play an important role in discovering novel molecular mechanisms for cigarette smoking-induced pathological changes.