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Proteomics study of polyethylenimine interaction with cell surface proteins in human colon adenocarcinoma cell line

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Background and Aims: Polyethylenimine (PEI), an organic branched or linear polyamine polymer, has been successfully used in the past for DNA complexation and transfection in vitro and in vivo into several cell lines and tissues. It is also cytotoxic, but the molecular basis of mechanism of its cytotoxicity is poorly understood. During this process PEI can interfere with the cell function by means of channel formation in the outer mitochondrial membrane. Subsequently, activation of the "mitochondrial mediated apoptotic pathway" will lead to cell death. Using proteomics technique to identify the involved proteins is very helpful in this regard. The aim of this research is the separation and recognition of the proteins that connect to PEI and identification of the toxicity mechanism. The effect of PEI on proteome and cell transcriptom has also been studied.
Methods: Initially the stable phase of PEI and homogenized human colon adenocarcinoma cell was prepared. The PEI stable complex phase was added to the prepared sample. The stable phase of PEI protein complex was purified and collected. The proteins were separated by two-dimensional polyacrylamide gel electrophoresis and the protein bands were cut and sent to Hong Kong for identification using MALDI/TOF/TOF, the results of which are under evaluation.
Conclusions: The reported observations have important implications for the design and execution of gene therapy protocols as well for controlling intracellular distribution of drugs with cationic-based polymer-delivery systems.

Keywords: Binding pattern; Transcriptomics; Proteomics; Polyethylenimine; Target deconvolution