of cytosolic Ca^{2+} mobilization in activated platelets. In the present study, the effect of NQ301 on arachidonic acid cascade in activated platelets was examined. NQ301 concentration-dependently inhibited washed rabbit platelet aggregation induced by collagen (10 μg/ml), arachidonic acid (100 μM) and U46619 (1 μM), a thromboxane A_2 receptor agonist, with IC_{50} values of 0.60±0.02, 0.79±0.04 and 0.58±0.04 μM, respectively. NQ301 also produced a shift to the right of the concentration-effect curve of U46619, suggesting a competitive type of antagonism. NQ301 slightly but concentration-dependently inhibited collagen-induced arachidonic acid liberation. In addition, NQ301 potently suppressed thromboxane (TX) B_2 formation by platelets that were exposed to arachidonic acid in a concentration-dependent manner, but had no effect on the production of prostaglandin (PG) D_2, indicating an inhibitory effect on TXA_2 synthase. This was supported by a TXA_2 synthase activity assay that NQ301 concentration-dependently inhibited TXB_2 formation conversed from PGH_2. Moreover, NQ301 also concentration-dependently inhibited 12-hydroxy-5,8,10,14-eicosatetraenoic (12-HETE) acid formation by platelets that were exposed to arachidonic acid. Taken together, these results suggest that NQ301 has a potential to inhibit TXA_2 synthase activity with TXA_2/PGH_2 receptor blockade, and modulate arachidonic acid liberation and 12-HETE formation in platelets. This may also be one convincing mechanism for the antithrombotic actions of NQ301.

[PA3-24] [2003-10-11 09:00 - 12:30 / Grand Ballroom Pre-function]

Proteomic Analysis of Cytokine-Like Proteins Secreted from Human Bronchial Epithelial Cells in Response to Pathogenic Bacterial Infection

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Bacterial infection is a very complex process in which both pathogens and host cells play crucial roles, and the host cells undergo drastic changes in their physiology, releasing various proteins in response to the pathogenic infection. Human airway epithelial surface serves as a first line of defense against microorganisms and the external environment. It is well known that bronchial epithelial cells secrete various chemokines and cytokines such as IL-6 and IL-8 to cope with various respiratory pathogens. Although many kinds of these cytokine proteins are identified and characterized for their biological roles, such cytokine-like proteins as a functionally unknown protein could be found through high-throughput identification of the proteins in the extracellular space. In this study, the proteomics approach was employed to compare the proteins from pathogenic bacteria-infected human bronchial epithelial cells with uninfected cells and to identify the proteins that specifically secreted to the culture medium. We used a strategy that combined a high-resolution two-dimensional electrophoresis (2-DE) and matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF). At least twenty different proteins stained by Coomassie G, were identified by mass spectrometry analyses after in-gel tryptic digestion. Some of them were associated with inflammation, transcription and the other proteins were revealed as novel proteins to be functionally studied.

[PA4-1] [2003-10-10 09:00 - 13:00 / Grand Ballroom Pre-function]

Quantative Analysis of dextromethorphan, Carisoprodol and their metabolites in hair by GC/MS

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Dextromethophan and carisoprodol have been abused to obtain a hallucination for longer than 10 years in Korea. Due to their seriousness of abuse liablility, recently government decided to control them as a psychotropic agents. As these are controlled, it is necessary for us to establish the analysis of these medicine and their metabolites in hair to prove the abuse of these drugs. This study is described for the determination of dextrometorphan and carisoprodol in hair. The method is applied to simultaneous quantify those drugs and