Title *

Comparing the Basal-level Inflammatory Gene and Protein Expressions of Three Normal and Three Cancer-Derived Lung Cell Lines

Abstract *

Using cell culture-based models to measure the hazards of particle systems has become routine and derivative over the past few years. The research presented in this study analyzes the differences among cells retrieved from varying depths of the pulmonary system and in varying diseased states. There is a need to advance cell line use and suggest guidelines on which cells to use for specific experiments. The gene and protein expressions of normal cell lines derived from the airway, bronchiole, and pleural spaces of the lung are compared against cancer-derived cell lines from similar anatomical areas. With this enhanced understanding of *in vitro* methods, next generation particle toxicology data sets have the potential to be more translatable to other areas of science and policy. For example, the nanotoxicology literature is populated with differential use of cell lines and endpoints often producing inconsistencies in observed effects. The basal expressions of six cell lines were collected using microarrays, ELISA, and western blotting in order to assemble the full spectrum of cytokine, gene, and protein expressions of each cell-type. Microscopy techniques were used to document the morphology of the different cell-types over time. Results showed that while the cancer-derived cell lines exhibited similar basal gene/protein expressions, the normal cell lines exhibited a differential response. Specifically, cells cultured from the pleural space contained less antioxidant protecting enzymes and cells cultured from the upper airway were more protected. This research has the potential to influence *in vitro* nanotoxicology studies and may influence policy and guidance documents.

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Affiliations and Authors *

Author Information
Henry Lujan (Presenting)

Affiliations
Baylor University, Waco, USA

Author Information
Christie M. Sayes

Affiliations
Baylor University, Waco, USA