Global Gene Expression Profiling in Lung Tissues of Rat Exposed to Lunar Dust Particles

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ABSTRACT

The Moon's surface is covered by a layer of fine, potential reactive dust. Lunar dust contain about 1-2% respirable very fine dust (< 3 μm). The habitable area of any lunar landing vehicle and outpost would inevitably be contaminated with lunar dust that could pose a health risk. The purpose of the study is to analyze the dynamics of global gene expression changes in lung tissues of rats exposed to lunar dust particles.

F344 rats were exposed for 4 weeks (6h/d; 5d/wk) in nose-only inhalation chambers to concentrations of 0 (control air), 2.1, 6.8, 21, and 61 mg/m^3 of lunar dust. Animals were euthanized at 1 day and 13 weeks after the last inhalation exposure. After being lavaged, lung tissue from each animal was collected and total RNA was isolated. Four samples of each dose group were analyzed using Agilent Rat GE v3 microarray to profile global gene expression of 44K transcripts. After background subtraction, normalization, and log transformation, t tests were used to compare the mean expression levels of each exposed group to the control group. Correction for multiple testing was made using the method of Benjamini, Krieger, and Yekuteli (1) to control the false discovery rate. Genes with significant changes of at least 1.75 fold were identified as genes of interest.

Both low and high doses of lunar dust caused dramatic, dose-dependent global gene expression changes in the lung tissues. However, the responses of lung tissue to low dose lunar dust are distinguished from those of high doses, especially those associated with 61mg/m^3 dust exposure. The data were further integrated into the Ingenuity system to analyze the gene ontology (GO), pathway distribution and putative upstream regulators and gene targets. Multiple pathways, functions, and upstream regulators have been identified in response to lunar dust induced damage in the lung tissue.