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

Ye Zhang \(^1\), Chiu-Wing Lam \(^1\), Selina M. Zalesak \(^3\), Yared H. Kidane \(^3\), Alan H. Feiveson \(^1\), Robert Ploutz-Snyder \(^3\), Robert R. Scully \(^1\), Kyle Williams \(^4\), Honglu Wu \(^1\), John T. James \(^1\)

\(^1\) NASA Johnson Space Center, Houston, TX; \(^2\) Wyle, Science, Technology & Engineering Group, Houston, TX; \(^3\) Universities Space Research Association, Houston, TX; \(^4\) Texas Southern University, Houston, TX

ABSTRACT

The Moon’s surface is covered by a layer of fine, reactive dust. Lunar dust contain about 1-2% of very fine dust (< 3 \(\mu\)m), that is respirable. 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 from 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. Five rats per group were euthanized 1 day, and 3 months after the last inhalation exposure. The total RNAs were isolated from lung tissues after being lavaged. The Agilent Rat GE v3 microarray was used to profile global gene expression (44K). The genes with significant expression changes are identified and the gene expression data were further analyzed using various statistical tools.