Comparison of the Human Transcriptional Response to Three Hypoxic Environments

Data Collection

What data will you collect or create?

All data collected in the course of this work was completely de-identified. Blood samples were collected in PAXgene Blood RNA tubes from volunteer subjects at four timepoints in each of three hypoxia device session (altitude chamber, restricted oxygen breathing device, restricted oxygen breathing environment). RNA was then extracted from the blood samples and used to analyze gene expression profiles from each sample using Affymetrix HTA 2.0 microarrays. The data from these microarrays was collected as raw .CEL files. This data was then summarized in a variety of intermediate formats before being converted to gene expression intensity data in the form or .txt, .csv, and .xls files.

How will the data be collected or created?

RNA extracted from blood samples was used to analyze gene expression profiles from each sample using Affymetrix HTA 2.0 microarrays, read by an affymetrix 7G device scanner. The data from these microarrays was collected as raw .CEL files. This data was then summarized in a variety of intermediate formats before being converted to gene expression intensity data in the form or .txt, .csv, and .xls files.

Documentation and Metadata

What documentation and metadata will accompany the data?

Metadata concerning sample number, timepoint, experimental condition, data type, data collection method, research title, organism, experiment type, experimental summary, experimental design, contributing researchers, citation, submission date, contact name, contact email, performing organization, analytical platform, links to individual sample data, and bioproject number. The data was made available in NCBi Gene Expression Omnibus at GEO Accession viewer (nih.gov), record number GSE219264.

Ethics and Legal Compliance

How will you manage any ethical issues?

Consent for data collection and sharing was collected in the study IRB protocol. Data is protected by being completely de-identified, no identifying information was included as a part of the data collection or subsequent data processing, and no such information is available in the public data.

How will you manage copyright and Intellectual Property Rights (IP/IPR) issues?

Copyright is assigned to the Federal Aviation Administration as published by Office of Aerospace Medicine reports. No intellectual property claims have been made from this data.

Storage and Backup

How will the data be stored and backed up during the research?

The data was stored and backed up on multiple secured hard drives. Following publication, the data will be stored and backed up by the NCBI GEO repository.

How will you manage access and security?

While research was performed, data access was limited to directly-involved researchers; data was kept secured behind locked doors within a limited-access environment.

Selection and Preservation

Which data are of long-term value and should be retained, shared, and/or preserved?

The raw gene expression intensity files (.cel) files are of long-term value for other research purposes, and are preserved on the NCBI GEO repository.

What is the long-term preservation plan for the dataset?

The dataset will be kept on the NCBI GEO repository and will be avaliable from the NCBI for the foreseeable future.

Data Sharing

How will you share the data?

The data is publicly available in the NCBI GEO repository by searching for record number

GSE219264 (https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE219264).

Are any restrictions on data sharing required?

No.

Responsibilities and Resources

Who will be responsible for data management?

During the research, the FAA was responsible for data management. Following publication, the FAA will maintain the technical report in the Transportation Research Library, and the raw data will be maintained on the NCBI GEO repository.

What resources will you require to deliver your plan?

None.