

## Plan Overview

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*A Data Management Plan created using DMPTool*

**DMP ID:** <https://doi.org/10.48321/D1XP7W>

**Title:** Comparison of the Human Transcriptional Response to Three Hypoxic Environments

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**Funder:** United States Department of Transportation (DOT) (transportation.gov)

**Template:** Digital Curation Centre

### **Project abstract:**

Hypoxia training is a standard facet of military aviator training, performed to familiarize airmen with the symptoms of hypoxia. The three most common devices used for this training are the hypobaric altitude chamber (AC) or the normobaric restricted oxygen breathing device (ROBD) and restricted oxygen breathing environment (ROBE). The AC creates hypoxic conditions by means of reduced atmospheric pressure. The ROBD and ROBE create normobaric hypoxic conditions by supplying a controlled reduced-oxygen gas mixture to trainees who don an aviation-style breathing mask or occupy a sealed chamber, respectively. In order to determine if differences in the transcriptional response to each of these training devices exist, blood RNA from ten volunteer subjects was analyzed by microarray, and resulting gene expression measures were screened for significant changes across timepoints within and across device runs. Few genes were significant in these comparisons, most significant differences between timepoints were in small nucleolar RNAs and non-coding RNAs, as well as one microRNA and transfer RNA. As unique genes were changed by each device, the transcriptional response to each device does differ slightly. However, the role of these transcriptional changes is unclear, as little information exists as to their function or role in the hypoxic response. As all of the examined devices induce hypoxic symptoms, and very little difference was observed in gene expression within devices, this limited study did not detect the presence of substantial differences between hypoxia training devices. Future studies utilizing more sensitive sequencing-based gene expression analysis techniques may improve detection of transcriptional differences induced by each device.

**Start date:** 12-12-2022

**End date:** 04-10-2023

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# Comparison of the Human Transcriptional Response to Three Hypoxic Environments

## Data Collection

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### 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 of .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 of .txt, .csv, and .xls files.

## Documentation and Metadata

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### 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

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### 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

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### 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

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### 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 available from the NCBI for the foreseeable future.

## Data Sharing

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### 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

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**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.

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## Planned Research Outputs

### Dataset - "Comparison of the Human Transcriptional Response to Three Hypoxic Environments"

Collection of .CEL files maintained on NCBI GEO repository, record number GSE219264

### Data paper - "Comparison of the Human Transcriptional Response to Three Hypoxic Environments research paper"

Research Manuscript, Office of Aerospace Medicine Technical Report.

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### Planned research output details

Title	Type	Anticipated release date	Initial access level	Intended repository(ies)	Anticipated file size	License	Metadata standard(s)	May contain sensitive data?	May contain PII?
Comparison of the Human Transcriptional Response t ...	Dataset	2022-12-04	Open	None specified	50 MB	None specified	None specified	No	No
Comparison of the Human Transcriptional Response t ...	Data paper	2023-01-30	Open	None specified	20 MB	None specified	None specified	No	No