

Plan Overview

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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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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Copyright information:

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Comparison of the Human Transcriptional Response to Three Hypoxic Environments

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.

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.

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 \(nih.gov\)](https://www.ncbi.nlm.nih.gov/geo/accessionviewer), record number GSE219264.

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.

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.

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.

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

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.

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

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>).

No.

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.

None.

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.

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 |