Discovery Through Biospecimen Sharing: NASA Biological Institutional Scientific Collection (NBISC)

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OVERVIEW:

- The NASA Biological Institutional Scientific Collection (NBISC) hosts over 90,000 flight and ground analog biospecimens.
- Biospecimens are searchable and available for request through the NASA Life Sciences Portal (NLSP) public website.

Goals:

- maximize the scientific return of unique biospecimens from spaceflight investigations.
- encourage broader participation of space biology-related research within the scientific research community.

WHICH TYPES OF BIOSPECIMENS AND DATA?

- Biospecimens from organisms flown on Shuttle, ISS and ground spaceflight-model experiments.
- Tissue types: musculoskeletal, neurosensory, reproductive, respiratory, circulatory, and digestive systems primarily from rodents.
- Samples are fixative dependent and are stored at -80° C, -20° C +4° C or ambient.
- Detailed metadata are available for all samples.
- Tissues have been used for a wide range of analyses, including histology, genomics, and transcriptomics.
- Recent acquisitions from HRP Space Radiation–funded experiments include ~50,000 rodent tissues exposed to HZE particles and high-LET radiation.
- Future expansion will include a broad range of microbial isolates from spaceflight studies.

REQUESTING BIOSPECIMENS:

- Biospecimens are requested at the NASA Life Sciences Portal (NLSP) via an online biospecimen request.

- Availability of requested biospecimens are confirmed by NBISC and instructions relayed to the requestor for a short proposal submission.
- Proposals are assessed by merit, scientific significance, and innovation of proposed research.

KNOWLEDGE AND INSIGHTS GAINED THROUGH BIOSPECIMEN SHARING

UC San Francisco

- Regenerative medicine
- Organ transplantation
- Vascular biology
- Cardiac biology
- Immunology
- Stem cell immunobiology
- Tissue preservation analysis

November 17th, 2016

Tissue-Quality-Results from vessels RR1 (2nd thaw) and RR3 dissections

Transplant and Stem Cell Immunobiology Lab (TSI)
University of California San Francisco (UCSF)
Department of Surgery

Sonja Schrepfer, MD, PhD

Rodent Research 1 (RR1; 2nd thaw)
RNA Quality (thoracic aorta)

Ground sample — RIN: 6.5, Total RNA: 2547 ng
Flight sample — RIN: 4.1, Total RNA: 3118 ng

Details:
- RNA Isolation using the mirVana-Kit
- Qiagen Tissue Lyser (30Hz, 2min)
- Microarrays using the FFPE method

Payload	Biospecimen	Fixative	Session Type	Storage	Strain	Gender
RR-1	Thoracic aorta	RNAlater	Baseline, FIt, GC, Viv	-80C	C57BL/6J	Female
RR-1	Abdominal aorta	RNAlater	Baseline, FIt, GC, Viv	-80C or 4C	C57BL/6J	Female
RR-3	Thoracic aorta	RNAlater	CB, CF, CGC	-80C	C57BL/6J	Female
RR-3	Abdominal aorta	LN2 or 4% PFA	CB, CF, CGC	-80C or 70% EtOH/Paraffin	C57BL/6J	Female
RR-3	Carotid arteries (right)	RNAlater	CB, CF, CGC	-80C	BALB/c	Female
RR-3	Carotid arteries (left)	4% PFA	CB, CF, CGC	70% EtOH/Paraffin	BALB/c	Female
RR-3	A. Iliaca (right)	RNAlater	CB, CF, CGC	-80C	BALB/c	Female
RR-3	A. Iliaca (left)	4% PFA	CB, CF, CGC	70% EtOH/Paraffin	BALB/c	Female
RR-3	A. Jugular	RNAlater	CB, CF, CGC	-80C	BALB/c	Female

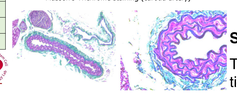
Rodent Research 3 (RR3)
RNA Quality (carotid artery)

Ground sample — RIN: 7.4, RNA Concentration: 5,472 pg/µl
Flight sample — RIN: 6.6, RNA Concentration: 1,620 pg/µl

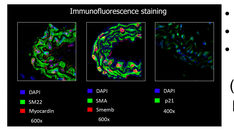
Details:
- RNA Isolation using trizol
- Qiagen Tissue lyser (30Hz, 2min)
- RNA Sequencing: Nugen RNAseq Kit (strand-specific); Hiseq 4000

NBISC Biospecimens:
- Rodent Research 1 (female): 80
- Rodent Research 3 (female): 120

Masson's Trichrome staining (carotid artery)



Immunofluorescence staining



Summary:

The quality of frozen tissue is suitable for:
- RNA Sequencing
- Microarray analysis
- Histopathology
- Immunofluorescence staining

(when using prescribed preservation methods)

Brock University

- Muscle remodeling
- Calmodulin regulation
- Regulation of the sarco(endo)plasmic reticulum Ca^{2+}-ATPase (SERCA) pump
- Muscular dystrophy
- Spaceflight
- Aging, obesity, and diabetes

Characterizing SERCA Function in Murine Skeletal Muscles after 35–37 Days of Spaceflight

by Jessica L. Braun [1,2,3], Mia S. Geromella [1,2,3], Sophie I. Hamstra [1,2,3], Holt N. Messner [1,2,3] and Val A. Fajardo [1,2,3,*]

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Conclusions:
- Observed reductions in Ca2+ uptake and increases in reactive oxygen/nitrogen species (RONS) in the soleus.
- Found significant enhancements in Ca2+ uptake, a fast fiber type shift with increase MHC IIb and SERCA 1a, and no changes in RONS in the tibialis anterior.
- Determined future studies should further examine the role of biological sex on SERCA function and whether protecting SERCA function can resist the atrophy and weakness observed in the soleus muscles with spaceflight.

Payload	Biospecimen	Fixative	Session Type	Storage	Strain	Gender
RR-9	Soleus	LN2	Basal, CC1/FViv CC2, FIt, Viv, GC	-80C	C57BL/6J	Male
RR-9	Femur	LN2 or RNAlater	Basal, CC1/FViv CC2, FIt, Viv, GC	-80C or 4C	C57BL/6J	Male
RR-9	Tibialis anterior	LN2	Basal, CC1/FViv CC2, FIt, Viv, GC	-80C	C57BL/6J	Male
RR-9	Tibia	LN2 or RNAlater	Basal, CC1/FViv CC2, FIt, Viv, GC	-80C or 4C	C57BL/6J	Male

Fajardo Research Team — MPHS Lab

NBISC Biospecimens:
- Rodent Research 9 (male): 187

Other (PI-exchange) samples:
- Rodent Research 1 (female): 12

Georgia State, Florida State and Loma Linda Universities

- Genomics
- Microcirculation
- Cardiovascular biology/physiology
- Vasodilation
- Mitochondrial apoptosis
- Characterizing effects of spaceflight on eyes and brain

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Research Article

RESEARCH ARTICLE

Spaceflight decelerates the epigenetic clock orchestrated with a global alteration in DNA methylome and transcriptome in the mouse retina

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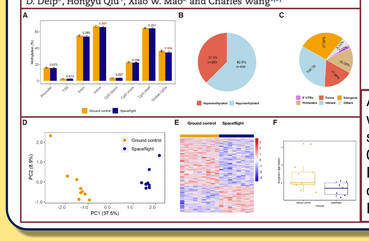

Payload	Biospecimen	Fixative	Session Type	Storage	Strain	Gender
RR-1	Eye	RNAlater	Baseline, FIt, GC, Viv	-80C	C57BL/6J	Female

Conclusions:
- Results indicate that spaceflight decelerated the retinal epigenetic clock.
- The study demonstrated that spaceflight impacts the retina at the epigenomic and transcriptomic levels.
- Hypothesized the above changes could be involved in the etiology of eye-related disorders among astronauts.

NBISC Biospecimens:
- Rodent Research 1 (female): 47

A – F: Spaceflight caused global epigenomic changes in mouse retina. (A) Genome-wide CpG methylation status at various genome regions. (B) and (C) Characteristics of significant differentially methylated CpGs (DMCs, methylation change > 10% and P ≤ 0.05). (D) Principal component analysis (PCA) based on the spaceflight induced DMCs. The beta values of all differentially methylated CpGs were used for PCA computation and no filtering was applied. (E) HCA plots based on DMCs. (F) Epigenetic ages calculated using Stubb's age estimator based on retinal methylomes.

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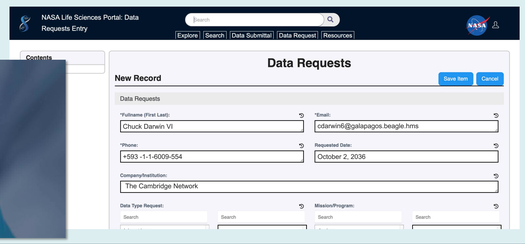
NASA LIFE SCIENCES PORTAL

Data Request
User's Guide for Requesting NASA Life Sciences Data and Biospecimens
Request Data

The Next Generation of the Life Sciences Data Archive for Human, Animal and Plant Research

NASA's Human Research Program (HRP) conducts research and develops technologies that allow humans to travel safely and productively in space. The Program uses evidence from data collected on astronauts, as well as other supporting studies. These data are stored in the research data repository, Life Sciences Data Archive (LSDA).



PLANNING, COORDINATION AND DATA COLLECTION:

- Preparations by the NASA Space Biology Biospecimen Sharing Program (BSP) begin approximately one year before an experiment start date or scheduled mission launch.

- Tissue list and internal sharing is established among PI's, PI Self-Forming BSP Team, International Partners, GeneLab, and BSP.
- Preservation options and dissection flow are carefully planned and executed to preserve tissue integrity and collection efficiency.
- Approximately 50 metadata details are recorded and assigned for each tissue collected.
- Metadata fields are standardized to accommodate data across multiple projects.

MORE ABOUT NBISC:

- NBISC is part of the Open Science initiative at NASA. This includes NASA GeneLab and the Ames Life Sciences Data Archive.
- This NASA Open Science initiative enables scientists to find, access, and reuse spaceflight data and samples to further understand how fundamental building blocks of life adapt to spaceflight.

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