Fiscal Year:	FY 2024	**Task Last Updated:**	FY 11/07/2023
PI Name:	Mason, Christopher Ph.D.		
Project Title:	Spatiotemporal Mapping of the Impact of Spaceflight on the Heart and Brain		
Division Name:	Space Biology		
Program/Discipline:			
Program/Discipline--Element/Subdiscipline:			
Joint Agency Name:		**TechPort:**	No
Human Research Program Elements:	None		
Human Research Program Risks:	None		
Space Biology Element:	(1) Cell & Molecular Biology (2) Animal Biology: Vertebrate		
Space Biology Cross-Element Discipline:	None		
Space Biology Special Category:	None		
PI Email:	chm2042@med.cornell.edu	**Fax:**	FY
PI Organization Type:	UNIVERSITY	**Phone:**	203-668-1448
Organization Name:	Weill Medical College of Cornell University		
PI Address 1:	1305 York Ave, Room Y13-04, Box 140		
PI Address 2:			
PI Web Page:			
City:	New York	**State:**	NY
Zip Code:	10021-5663	**Congressional District:**	12
Comments:			
Project Type:	Ground	**Solicitation / Funding Source:**	2020 Space Biology NNH20ZDA001N-SB E.12. Flight/Ground Research
Start Date:	12/01/2021	**End Date:**	11/30/2024
No. of Post Docs:	1	**No. of PhD Degrees:**	1
No. of PhD Candidates:	2	**No. of Master' Degrees:**	1
No. of Master's Candidates:	0	**No. of Bachelor's Degrees:**	1
No. of Bachelor's Candidates:	0	**Monitoring Center:**	NASA ARC
Contact Monitor:	Griko, Yuri	**Contact Phone:**	650-604-0519
Contact Email:	Yuri.V.Griko@nasa.gov		
Flight Program:			
Flight Assignment:			
Key Personnel Changes/Previous PI:	NA		
COI Name (Institution):	Costes, Sylvain Ph.D. (NASA Ames Research Center) Galazka, Jonathan Ph.D. (NASA Ames Research Center) Giacomello, Stefania Ph.D. (Kungliga Tekniska Hogskolan)		
Grant/Contract No.:	80NSSC22K0254		
Performance Goal No.:			
Performance Goal Text:			

Task Description:	To prepare for future human exploration missions far from Earth, NASA's Space Biology Program is seeking to build a better understanding of the effects of spaceflight and zero gravity on the biology of microorganisms, plants, and animals in spacecraft, the International Space Station (ISS), and also in ground-based analog experiments. The National Research Council recommended that NASA undergo studies to elucidate the effects of short and long duration spaceflight on the biology of all three categories of organisms. Technological advances in next-generation sequencing (NGS), spatial transcriptomics, and proteomics (spatial omics), several of which we describe below, create an unprecedented opportunity for in-depth molecular studies applicable to the purposes of NASA's Space Biology Program. This provides scientists, engineers, and clinicians a more comprehensive view of the functional dynamics of organisms as they evolve and respond to unique or highly selective environments including the ISS. Spaceflight causes changes in cell signaling pathways that are better understood only by increasing the analysis resolution level. In this project, we will deploy new technologies, i.e. spatial transcriptomics, single-nucleus RNA-sequencing, multi-omic spatial mapping (human and microbial), and systems biology algorithms to discover new insights relevant to the impact of spaceflight on human health. These data and methods will shed light on the complex biosystem dynamics that spaceflight causes in humans. We will be able to clearly dissect the gene expression changes occurring at the single-cell level, analyze how these changes affect the cell-cell genetic and physical interactions, and begin the first-ever in vivo human-microbial interaction maps from spaceflight. To do so we will conduct rigorous and cutting-edge omics analysis using two complementary platforms (10x Genomics Visium and Nanostring's GeoMx) with six main rodent organs collected throughout several past spaceflight missions and their corresponding ground controls. Our integrated biology approach will allow us to understand physiological, anatomic, and molecular mechanisms of adaptation and response in animals to spaceflight. For our organism-wide study we will leverage the extensive amount of samples collected throughout several Rodent Research (RR) missions which are accessible through the Life Sciences Data Repository (LSDA). Several of these specimens have already been allocated for Dr. Mason through LSDA. Our study will represent the first-of-its-kind in space biology and will provide foundational discoveries that will allow us to understand not only how astronaut conditions can be improved during spaceflight, but also how the changes induced by spaceflight can be translated into modern medicine to improve human health on Earth. Moreover, we will apply several statistical and machine learning techniques in order to predict changes induced by spaceflight at the organism level for future long-term missions.
Rationale for HRP Directed Research:	
Research Impact/Earth Benefits:	We will be able to clearly dissect the gene expression changes occurring at the single-cell level, analyze how these changes affect the cell-cell genetic and physical interactions, and begin the first-ever in vivo human-microbial interaction maps from spaceflight. To do so we will conduct rigorous and cutting-edge omics analysis using two complementary platforms (10x Genomics Visium and Nanostring's GeoMx) with six main rodent organs collected throughout several past spaceflight missions and their corresponding ground controls. Our integrated biology approach will allow us to understand physiological, anatomic, and molecular mechanisms of adaptation and response in animals to spaceflight.
Task Progress:	In the past year, we have focused efforts on curating and testing banked tissues for processing with spatial and single-cell methods. Specifically, we have focused on the retinal tissues (acquired and tested), liver, brain, femur, heart, and duodenum. We have dissected test samples from donor mice in our laboratory, analyzed the data from Visium and GeoMx, and also we have run four samples through single-nucleus RNA-seq (snRNA-seq) using the 10xGenomics Chromium controller and assay. So far, we have: 1) Generated the first GeoMx profiles of the mouse retina tissues, and now generating additional replicates. 2) Continued sample selection and quality control (QC), including the RNA Integrity Number (RIN) and cell count matrices for tissues. 3) Tested snRNA-seq on retina tissues, and have updated our Seurat annotations and database for the analysis.
Bibliography Type:	Description: (Last Updated: 11/05/2024)
Articles in Peer-reviewed Journals	Cope H, Willis CR, MacKay MJ, Rutter LA, Toh LS, Williams PM, Herranz R, Borg J, Bezdan D, Giacomello S, Muratani M. "Routine omics collection is a golden opportunity for European human research in space and analog environments." Patterns. 2022 Oct 14;3(10):100550. https://doi.org/10.1016/j.patter.2022.100550 , Oct-2022
Articles in Peer-reviewed Journals	Overbey EG, Das S, Cope H, Madrigal P, Andrusivova Z, Frapard S, Klotz R, Bezdan D, Gupta A, Scott RT, Park J. "Challenges and considerations for single-cell and spatially resolved transcriptomics sample collection during spaceflight. " Cell Rep Methods. 2022 Nov 21;2(11):100325. https://doi.org/10.1016/j.crmeth.2022.100325 , Nov-2022
Articles in Peer-reviewed Journals	Park J, Kim J, Lewy T, Rice CM, Elemento O, Rendeiro AF, Mason CE. "Spatial omics technologies at multimodal and single cell/subcellular level." Genome Biol. 2022 Dec 13;23(1):256. https://doi.org/10.1186/s13059-022-02824-6 , Dec-2022
Articles in Peer-reviewed Journals	Simpson AC, Eedara VVR, Singh NK, Damle N, Parker CW, Karouia F, Mason CE, Venkateswaran K. "Comparative genomic analysis of Cohnella hashimotonis sp. nov. isolated from the International Space Station." Front Microbiol. 2023 Jun 15;14:1166013. https://doi.org/10.3389/fmicb.2023.1166013 ; PMID: 37396358; PMCID: PMC10308117 , Jun-2023