Fiscal Year:	FY 2023	Task Last Updated:	FY 11/07/2022
PI Name:	Hada, Megumi Ph.D.		
Project Title:	Combined Effects of Simulated Microgravi	ty and Space Radiation on Hun	nan Cells
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:	<ol> <li>(1) Cell &amp; Molecular Biology</li> <li>(2) Animal Biology: Vertebrate</li> </ol>		
Space Biology Cross-Element Discipline:	None		
Space Biology Special Category:	<ul><li>(1) Cell Culture</li><li>(2) Translational (Countermeasure) Potentia</li></ul>	al	
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PI Organization Type:	UNIVERSITY	Phone:	936-261-3155
Organization Name:	Prairie View A&M University		
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Zip Code:	77446	<b>Congressional District:</b>	10
Comments:			
Project Type:	GROUND	Solicitation / Funding Source:	2016-17 Space Biology (ROSBio) NNH16ZTT001N-FG. App G: Flight and Ground Space Biology Research
Start Date:	10/26/2018	End Date:	10/27/2022
No. of Post Docs:	0	No. of PhD Degrees:	0
No. of PhD Candidates:	2	No. of Master' Degrees:	0
No. of Master's Candidates:	0	No. of Bachelor's Degrees:	0
No. of Bachelor's Candidates:	0	Monitoring Center:	NASA KSC
Contact Monitor:	Zhang, Ye	<b>Contact Phone:</b>	321-861-3253
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Flight Program:			
Flight Assignment:	NOTE: End date changed to 10/27/2022 pe	r NSSC information (Ed., 9/15/	21)
Key Personnel Changes/Previous PI:			
COI Name (Institution):	Wang, Jing Ph.D. (University of Texas M Takahashi, Akihisa Ph.D. (Gunma Univer Fujiwara, Keigi Ph.D. (University of Texa	sity Heavy Ion Medical Center,	
Grant/Contract No.:	80NSSC19K0133		
Performance Goal No.:			
Performance Goal Text:			

Rationale for HRP Directed Research:         Research Impact/Earth Benefits:       Completion of this proposal will allow us to determine how the combination of microgravity and radiation will affect the transcriptomic, metabolomic, and proteomic states of cells as well as heritable changes in DNA. These findings will allow us to help develop the countermeasure for the future space missions.         Post-translational modification of proteins To identify post-translational modification (PTM), as well as changes in protein expression levels, we used a high throughput method called reverse-phase protein array (RPPA), which is available at the University of Texas MD Anderson Cancer Center. This method uses an array of close to 500 well-characterized antibodies, to which proteins in cell lysates will bind, and the amount of bound proteins. Before exposing cells to both radiation and µG, we first analyzed how cells respond to altered gravitational environments. In this year, we have completed the manuscript of the changes in expression and modification of protein after gravity changes with actin dynamics.         Gene expressions On the basis of our RNA sequencing (RNA-seq) results, we are proceeding data analysis focusing on human aging reverseleted with information from the RT2 Profiler PCR Array panel (QIAGEN polymerase chain reaction/PCR array panel), including several functions (e.g., genomic instability, inflammatory response, cellular sensecance, cytoskeleton regulator, oxidative stress, transcriptional regulation, and epigenetics alterations). After combined treatled genes Systekleton regulator, and gingencies alterations). After combined resultament with C-ion irradiation and simulated µG, the expressions of collager, type I, µahpa I (COLLAI) and collager, type I, µahpa I (COL	Task Description:	Space radiation and microgravity are two major environmental stressors for human in space travel. One of the findamental questions in space biology research is whether the combined effects of microgravity and exposure to cosmic radiation are synergistic. While studies addressing this question have been carried out for half a century in space or using simulated microgravity on the ground, the reported results are conflicting. Although the reason for the variation in results is not known, it is possible that it may be due to the diversity of biological systems used but more importantly to the experimental designs and hardware used in these studies. For the assessment and management of human health risks in future Moon and Mars Missions, it is necessary to obtain more basic data on the molecular and cellular responses to combined effects of radiation and microgravity. To establish a firm baseline database, we propose to undertake a systematic study on cultured mammalian cells' responses to the simultaneous insult of radiation and microgravity (both immediate and long term) to elucidate the molecular biological bases for the assessment and management of human health risks in space.
Research Impact/Earth Benefits:       transcriptionic, metabolomic, and proteomic states of cells as well as heritable changes in DNA. These findings will allow us to help develop the countermeasure for the future space missions.         Post-translational modification of proteins To identify post-translational modification (PTM), as well as changes in protein expression levels, we used a high throughput method called reverse-phase protein array (RPPA), which is available at the University of Texas MD Anderson Cancer Center. This method uses an array of close to 500 well-characterized antibodies, to which proteins in cell lysates will bind, and the amount of bound proteins to each antibody is quantified. Needless to say, many of the antibodies are against post-translationally modified proteins. Before exposing cells to both radiation and µG, we first analyzed how cells respond to altered gravitational environments. In this year, we have completed the manuscript of the changes in expression and modification of protein after gravity changes with actin dynamics.         Gene expressions On the basis of our RNA sequencing (RNA-seq) results, we are proceeding data analysis focusing on human aging-related genes. Specifically, 84 genes encoding key molecules involved in human aging were selected with information from the RT2 Profiler PCR Array panel (QIAGEN polymerase chain reaction/PCR array panel), including several functions (e.g., genomic instability, inflammatory response, cellular sensecence, cytoskeleton regulator, oxidative strass, runscriptional regulation, and egipentics alterations). After combined treatment with C-ion irradiation and will allow the expressions of collagen, type I, alpha 1 (COLIAI) and collagen, type II, alpha 1 (COLIAI) and collagen, type II, alpha 1 (COLIAI), known as cytoskeleton regulators, were decreased (3 h, 24 h); and transcriptional regulation.         Task Progress	Rationale for HRP Directed Researc	h:
<ul> <li>Task Progress:</li> <li>Task Progress:</li> <li>Task Progress:</li> <li>Task Progress:</li> <li>Task Progress:</li> </ul>	Research Impact/Earth Benefits:	transcriptomic, metabolomic, and proteomic states of cells as well as heritable changes in DNA. These findings will
Bibliography Type:         Description: (Last Updated: 02/07/2024)	Task Progress:	protein expression levels, we used a high throughput method called reverse-phase protein array (RPPA), which is available at the University of Texas MD Anderson Cancer Center. This method uses an array of close to 500 well-characterized antibodies, to which proteins in cell lysates will bind, and the amount of bound proteins to each antibody is quantified. Needless to say, many of the antibodies are against post-translationally modified proteins. Before exposing cells to both radiation and μG, we first analyzed how cells respond to altered gravitational environments. In this year, we have completed the manuscript of the changes in expression and modification of protein after gravity changes with actin dynamics. Gene expressions On the basis of our RNA sequencing (RNA-seq) results, we are proceeding data analysis focusing on human aging-related genes. Specifically, 84 genes encoding key molecules involved in human aging were selected with information from the RT2 Profiler PCR Array panel (QIAGEN polymerase chain reaction/PCR array panel), including several functions (e.g., genomic instability, inflammatory response, cellular senescence, cytoskeleton regulator, oxidative stress, transcriptional regulation, and epigenetics alterations). After combined treatment with C-ion irradiation and simulated μG, the expressions of collagen, type I, alpha 1 (COL1A1) and collagen, type III, alpha 1 (COL3A1), known as cytoskeleton regulators, were decreased (3 h, 24 h); and transcriptional regulation related genes (PHF3 and SMAD2) and DNA binding/RNA binding related gene ZFR (Zinc Finger RNA Binding Protein) were increased. A manuscript is under preparation.
	Bibliography Type:	Description: (Last Updated: 02/07/2024)

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