

Fiscal Year:	FY 2023	Task Last Updated:	FY 04/19/2023
PI Name:	Wyatt, Sarah E Ph.D.		
Project Title:	Step 2: Comparative Analysis of Multi-Gravity Studies on Earth and ISS		
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) Plant Biology		
Space Biology Cross-Element Discipline:	None		
Space Biology Special Category:	None		
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Comments:			
Project Type:	GROUND	Solicitation / Funding Source:	2020 Space Biology NNH20ZDA001N-SB E.12. Flight/Ground Research
Start Date:	12/15/2021	End Date:	02/14/2022
No. of Post Docs:		No. of PhD Degrees:	
No. of PhD Candidates:		No. of Master' Degrees:	
No. of Master's Candidates:		No. of Bachelor's Degrees:	
No. of Bachelor's Candidates:		Monitoring Center:	NASA KSC
Contact Monitor:	O'Rourke, Aubrie	Contact Phone:	
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Flight Program:			
Flight Assignment:	NOTE: End date changed to 12/31/2023 per NSSC information (Ed, 4/18/23)		
Key Personnel Changes/Previous PI:	The postdoctoral scholar originally associated with this grant moved to a NASA postdoc. Thus, although the study is on course with the personnel we have, an extended timeframe is needed to complete the analysis.		
COI Name (Institution):	Meyers, Alexander Ph.D. (Ohio University)		
Grant/Contract No.:	80NSSC22K0366		
Performance Goal No.:			
Performance Goal Text:			

Task Description:	<p>In response to the ROSES2020 Space Biology solicitation for NASA GeneLab Analytical Investigations, we propose a comparative meta-analysis of available fractional-g datasets in Arabidopsis to address Focus Area B: combined effects of space-relevant stressors and altered gravity. Over the past 20 years, the space biology community has made great advances in understanding plant transcriptional networks under Earth's 1g and the microgravity environment of spaceflight. However, beyond-Earth exploration will require plant growth at Lunar (0.16g) and Martian (0.38g) gravities. Molecular data at these fractional g levels is sparse and offers little information on the interactions between partial gravity signaling networks and other stressors. We propose to use an integrative meta-analysis approach combining comparative differential expression, contrast analyses, analyses of the plant responses across the gravitational continuum, and weighted gene co-expression network analyses (WGCNA) of the five available partial-g, transcriptomic datasets, to: (Aim 1) identify core trends in molecular/physiological responses to partial g, (Aim 2) leverage the diversity of the experimental factors in those experiments to delineate the influences of those influences, and (Aim 3) use the series of 1g flight and ground controls across the datasets to identify specific artifacts of simulated micro and partial g. Three of the datasets (Seedling Growth 1, 2, and 3) were flown using European Modular Cultivation System (EMCS) experiments that used variation of 4 genotypes, and 5 different g levels under unidirectional blue or red light aboard the International Space Station (ISS). The second dataset comes from the EMCS-Plant Gravity Perception (PGP) spaceflight experiment, which resulted in tissue-specific transcriptomes at 12g levels between 0.003 and 1g. And the third derives from a series of experiments using simulated partial gravity on ground analogs to treat seedlings at simulated 0g, 0.38g, 1g, and 2g. By leveraging all of these datasets, we can determine molecular and physiological changes that result from gravitational intensity and other environmental stressors. The project directly addresses several questions relating to plant growth and development and the functional use of existing datasets to answer novel questions; i.e., PB-1 ("How does gravity affect plant growth, development & metabolism?") and PB-5 ("How do plants sense and react to gravity and what are the molecular mechanisms involved?"), GL-2 ("Can raw datasets, including unprocessed molecular data that can be subjected to subsequent analyses lead to increased use of ISS data to facilitate new science products?") GL-3 ("What are the key cellular and molecular systems necessary for biological organisms to thrive in the space environment that can be discovered from 21st century bioinformatics tools?")</p>
Rationale for HRP Directed Research:	
Research Impact/Earth Benefits:	
Task Progress:	<p>The first two quarters of this grant were spent retrieving the data that was not yet published on GeneLab. Data was then tested to optimize trimming and alignment parameters and running the differential expression for the two largest datasets. The current period has seen the completion of the differential expression and the contrast analyses for all five datasets.</p>
Bibliography Type:	Description: (Last Updated: 05/03/2023)
Abstracts for Journals and Proceedings	<p>Wyatt SE. "At the intersection: Meta-analysis of transcriptomic datasets." NASA GeneLab Analytics Working Group Symposium 2022, Virtual, June 30, 2022. Abstracts. NASA GeneLab Analytics Working Group Symposium 2022, Virtual, June 30, 2022. , Jun-2022</p>
Articles in Peer-reviewed Journals	<p>Barker R, Kruse CPS, Johnson C, Saravia-Butler A, Fogle H, Chang HS, Trane RM, Kinscherf N, Villacampa A, Manzano A, Herranz R, Davin LB, Lewis NG, Perera I, Wolverson C, Gupta P, Jaiswal P, Reinsch SS, Wyatt S, Gilroy S. "Meta-analysis of the space flight and microgravity response of the Arabidopsis plant transcriptome." npj Microgravity. 2023 Mar 20;9(1):21. https://doi.org/10.1038/s41526-023-00247-6 ; PMID: 36941263; PMCID: PMC10027818 , Mar-2023</p>