

Fiscal Year:	FY 2023	Task Last Updated:	FY 02/12/2023
PI Name:	Jaiswal, Pankaj Ph.D.		
Project Title:	Alternative Splicing and Transcriptome Modulation Under Space Flight Response in Plants		
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) Plant Biology		
Space Biology Cross-Element Discipline:	None		
Space Biology Special Category:	None		
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Project Type:	GROUND	Solicitation / Funding Source:	2020 Space Biology NNH20ZDA001N-SB E.12. Flight/Ground Research
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No. of Post Docs:	2	No. of PhD Degrees:	2
No. of PhD Candidates:	0	No. of Master' Degrees:	1
No. of Master's Candidates:	0	No. of Bachelor's Degrees:	2
No. of Bachelor's Candidates:	1	Monitoring Center:	NASA KSC
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Flight Program:			
Flight Assignment:	NOTE: End date changed to 03/31/2024 per NSSC information (Ed., 2/23/23)		
Key Personnel Changes/Previous PI:	None		
COI Name (Institution):			
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Task Description:	<p>The space flight transcriptome studies collected by the NASA GeneLab and analyzed by its Plant Analysis Working Group (PlantAWG) have facilitated analysis and tool development around profiling the differentially expressed genes (DEG), enrichment of pathways, and Gene Ontology-based (GO-based) functional annotation. To explore additional novel molecular events from the same GeneLab studies, we will (1) analyze the alternatively spliced (AS) forms of transcripts (RNA molecules) identified from the ground control (GC) and the space flight (FLT) samples; (2) identify mutations (if any) gained due to cosmic radiation in the transcribed regions of the genome; and (3) diagnose the AS and somatic mutation consequences on the structure and function of the genes.</p> <p>Our data analysis and collaborative work will extend the current functionality of the NASA GeneLab data by adding alternative splicing, novel transcribed regions and genes, and any functional significance, thus providing researchers insights into the modulated transcriptome's structural and functional consequences in response to space flight. The project workflows will help improve the reference genome annotation of Arabidopsis and set up a platform for analyzing current and future data from non-plant eukaryotes like humans, mice, yeast, and other models.</p> <p>In order to develop a deeper understanding of the causal effects of alternative splicing (AS) in the model plant <i>Arabidopsis thaliana</i> and other space travel-bound plant species, we propose to build an AS Atlas for plants in response to microgravity. The AS atlas will analyze the core set of NASA GeneLab plant studies and put forth a plan to build and extend resources for current and future studies on plants and other eukaryotes, including humans and mouse models. Our data analysis and collaborative work will extend the differential gene expression tools and functional enrichment analysis tools currently provided by the GeneLab data. The identification of novel AS sites and genes is anticipated to provide candidate genes to target for developing smart crops and synthetic biology-based approaches to improve adaptation to microgravity. The project-specific aims include:</p> <ol style="list-style-type: none"> 1. Develop an alternative splicing atlas of Arabidopsis genes 2. Identify novel genetic mutations gained in the transcribed regions of the genome during space flight (FLT) 3. Validate alternative splicing events, subject to the availability of biological material sampled from the existing GeneLab studies.
Rationale for HRP Directed Research:	<p>This project explores the identification of novel alternative spliced isoforms of <i>Arabidopsis thaliana</i> genes, mutations acquired, and downstream effects on the structure and function of the genes transcribed in response to space flight and microgravity. By analyzing the data from the GeneLab data portal, the project will extend the functionality limited by the existing differential gene expression and Gene Ontology enrichment analysis. The analyzed data will provide researchers additional insights into the modulated transcriptome's structural and functional consequences in response to space flight, hardware and growth conditions. The identification of novel AS sites and genes is anticipated to provide candidate genes to target for developing smart crops and synthetic biology-based approaches to improve adaptation to microgravity. The proposed development of methodologies and data analytics workflows may also help analyze the current and future data from plant and non-plant eukaryotes like humans, mice, yeast, and other models.</p>
Task Progress:	<p>We targeted the following five NASA GeneLab studies for analyzing data in our project. - GLDS-37 - GLDS-38 - GLDS-120 - GLDS-208 - GLDS-210 - GLDS-218</p> <p>Alternative splicing and Single Nucleotide Polymorphism (SNP) scoring methods were standardized.</p> <p>Alternative splicing data analysis completed on the Ground Control (GC) and Flight (FLT) transcriptomes from GLDS-37 and 38. A four way comparison of columbia-0 genotype data across two studies and 2 treatments revealed that they share ~8000 genes in common from both studies and treatments. Anywhere between 550-1800 genes show unique splicing patterns from the two studies. Early analysis of the genes encoding for auxin transporters, cell wall biosynthesis, and oxidative stress response show alternate splicing events between the two treatments.</p> <p>SNP identification from the columbia-0 genotype from the GC and FLT transcriptomes completed from GLDS-37 and 38. Detailed analysis is underway.</p> <p>The project continues to make progress on analyzing the rest of the above mentioned GLDS studies.</p> <p>All the project data and publicly available GeneLab data for the above mentioned studies is being mapped to the <i>A. thaliana</i> genome and development of a Genome Browser instance development is underway.</p>
Bibliography Type:	<p>Description: (Last Updated:)</p>