

<b>Fiscal Year:</b>	FY 2022	<b>Task Last Updated:</b> FY 05/13/2022	
<b>PI Name:</b>	Jaiswal, Pankaj Ph.D.		
<b>Project Title:</b>	Alternative Splicing and Transcriptome Modulation Under Space Flight Response in Plants		
<b>Division Name:</b>	Space Biology		
<b>Program/Discipline:</b>			
<b>Program/Discipline-- Element/Subdiscipline:</b>			
<b>Joint Agency Name:</b>		<b>TechPort:</b>	No
<b>Human Research Program Elements:</b>	None		
<b>Human Research Program Risks:</b>	None		
<b>Space Biology Element:</b>	(1) Plant Biology		
<b>Space Biology Cross-Element Discipline:</b>	None		
<b>Space Biology Special Category:</b>	None		
<b>PI Email:</b>	<a href="mailto:jaiswalp@oregonstate.edu">jaiswalp@oregonstate.edu</a>	<b>Fax:</b>	FY
<b>PI Organization Type:</b>	UNIVERSITY	<b>Phone:</b>	541-737-8471
<b>Organization Name:</b>	Oregon State University		
<b>PI Address 1:</b>	Department of Botany and Plant Pathology		
<b>PI Address 2:</b>	2082 Cordley Hall, 1500 SW Jefferson Street		
<b>PI Web Page:</b>			
<b>City:</b>	Corvallis	<b>State:</b>	OR
<b>Zip Code:</b>	97331	<b>Congressional District:</b>	4
<b>Comments:</b>			
<b>Project Type:</b>	GROUND	<b>Solicitation / Funding Source:</b>	2020 Space Biology NNH20ZDA001N-SB E.12. Flight/Ground Research
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<b>No. of PhD Candidates:</b>		<b>No. of Master' Degrees:</b>	
<b>No. of Master's Candidates:</b>		<b>No. of Bachelor's Degrees:</b>	
<b>No. of Bachelor's Candidates:</b>		<b>Monitoring Center:</b>	NASA KSC
<b>Contact Monitor:</b>	Aubrie, O'Rourke	<b>Contact Phone:</b>	
<b>Contact Email:</b>	<a href="mailto:aurourke@jcv.org">aurourke@jcv.org</a>		
<b>Flight Program:</b>			
<b>Flight Assignment:</b>			
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<b>Grant/Contract No.:</b>	80NSSC22K0855		
<b>Performance Goal No.:</b>			
<b>Performance Goal Text:</b>			

<b>Task Description:</b>	<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"> <li>1. Develop an alternative splicing atlas of Arabidopsis genes</li> <li>2. Identify novel genetic mutations gained in the transcribed regions of the genome during space flight (FLT)</li> <li>3. Validate alternative splicing events, subject to the availability of biological material sampled from the existing GeneLab studies.</li> </ol>
<b>Rationale for HRP Directed Research:</b>	
<b>Research Impact/Earth Benefits:</b>	
<b>Task Progress:</b>	New project for FY2022.
<b>Bibliography Type:</b>	Description: (Last Updated: )