

Fiscal Year:	FY 2015	Task Last Updated:	FY 04/16/2015
PI Name:	Lewis, Norman G Ph.D.		
Project Title:	An Integrated Omics Guided Approach to Lignification and Gravitational Responses: The Final Frontier		
Division Name:	Space Biology		
Program/Discipline:			
Program/Discipline--Element/Subdiscipline:	SPACE BIOLOGY--Developmental biology		
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:	(1) Reproductive Biology		
Space Biology Special Category:	(1) Bioregenerative Life Support		
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Comments:			
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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
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Flight Program:	ISS		
Flight Assignment:			
Key Personnel Changes/Previous PI:			
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Task Description:	<p>We propose a multi-omics study using the model plant Arabidopsis under both 1g and in microgravity conditions (spaceflight). Our approach spans comprehensive phenomics, metabolomics, transcriptomics, and proteomics strategies, and is incisively and uniquely melded via deployment of an integrated computational biology (ICB) approach we are pioneering. Our plant lines include wild type, various mutants we have generated with different lignin amounts through manipulation of the multigene family encoding arogenate dehydratases, and other lines enhanced in carbon assimilation capacity, and combinations thereof. We consider this places us in an unprecedented position to investigate how plants function in altered gravity environments.</p> <p>We are very well positioned for incisive spaceflight and definition stage (1g) studies to investigate gene/metabolic network relationships and adaptations resulting from varying lignin and carbon assimilation levels, e.g., on photosynthesis, C allocation; water use efficiency (WUE), vascular plant growth/development; vasculature performance; auxin transport, and gravitational adaptations. Our overarching hypothesis is that a comprehensive interrogation (an integrative omics study) of our Arabidopsis lines with varying lignin levels and/or modulated carbon concentrating mechanisms (CCMs) or combination thereof will identify gene/metabolic networks, mechanisms and/or pathways that are differentially modulated at 1g and on exposure to microgravity, i.e., various omics (phenomics, transcriptomics, genomics, proteomics, metabolomics, and ICB) will allow us to study these in a truly unprecedented way.</p> <p>Overall objectives:</p> <ol style="list-style-type: none">1. Establish multi ‘omics’ effects of modulating lignin and CCM levels i) at 1g and ii) in spaceflight.2. Compare/contrast data, using an ICB approach, to better define and understand gravity sensing and responses, and if threshold/induction parameters are modified or changed, when lignin and CCM levels are varied. <p>More specifically, we address distinct hypotheses for our various teams, and integrate, dissect, and incisively analyze them holistically in a manner hitherto not possible. These 5 hypotheses include that: modulating lignin and CCM levels differentially affect carbon assimilation/re-allocation, photosynthesis, and WUE (Team 1); modulating lignin and CCM levels differentially affect secondary and primary metabolite levels (metabolomics) (Team 2); system-wide modification in the transcriptome occurs through a common transcriptional regulatory mechanism, and transcriptome/proteome “discrepancies” result from over simplification of transcript analyses (Team 3); differential alterations in lignin and CCM levels can often be attributed to overall distinct changes in protein expression and phosphorylation patterns in a defined set of proteins (Team 4); an integrated omics analysis will provide urgently needed new insights into global effects on plant biological processes at both 1g and in microgravity (Teams 1-4). Each hypothesis draws upon the most advanced technologies available for study. We consider that our ICB approach will transform omics analysis through our advanced instrumentation and analytical tools. We will utilize (or design) computational tools/mathematical algorithms for integration and correlation of high resolution phenotype measurements (phenomics) with “low” resolution global subcellular system measurements (transcriptomics, etc.) through ‘nth’ dimensional analysis.</p> <p>Our study aligns with Research Emphasis 1 and 3, and decadal survey elements in Cell, Microbial, and Molecular Biology (CMM-3, CMM-5), Organismal and Comparative Biology (OCB 2-5), Developmental Biology (DEV-4), and Plant and Microbial Biology, chapter 4 (P2). Our data generation will also be seamlessly integrated with various web-based platforms to handle, disseminate, and inter-actively utilize through iPlant and OpenMSI, and thus are made available to NASA as well as being a community resource.</p>
	Rationale for HRP Directed Research:
	Research Impact/Earth Benefits:
	Task Progress: New project for FY2015.
	Bibliography Type: Description: (Last Updated: 04/30/2024)