Fiscal Year:	FY 2020	**Task Last Updated:**	FY 03/06/2020
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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:			
Project Type:	FLIGHT	**Solicitation / Funding Source:**	2014 Space Biology Flight (ILSRA) NNH14ZTT002N
Start Date:	05/01/2015	**End Date:**	04/30/2021
No. of Post Docs:	1	**No. of PhD Degrees:**	1
No. of PhD Candidates:	1	**No. of Master' Degrees:**	
No. of Master's Candidates:		**No. of Bachelor's Degrees:**	
No. of Bachelor's Candidates:	1	**Monitoring Center:**	NASA KSC
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Flight Program:	ISS		
Flight Assignment:	ISS NOTE: End date change to 4/30/2021 per NSSC information (Ed., 3/10/2020) NOTE: End date changed to 4/30/2020 per PI (Ed., 3/4/19) NOTE: End date changed to 4/30/2019 per NSSC information (Ed., 8/16/18)		
Key Personnel Changes/Previous PI:			
COI Name (Institution):	Davin, Laurence Ph.D. (Washington State University) Hanson, David Ph.D. (University of New Mexico) Lipton, Mary Ph.D. (Battelle Memorial Institute) Sayre, Richard Ph.D. (New Mexico Consortium) Starkenburg, Shawn Ph.D. (Los Alamos National Security)		
Grant/Contract No.:	NNX15AG56G		
Performance Goal No.:			
Performance Goal Text:			

Task Description:

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.
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.

Overall objectives:

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.

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.

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.

Rationale for HRP Directed Research:

Research Impact/Earth Benefits:

1). This research will provide NASA and science in general with the first “big 'omics' data” analysis, integration, and assessment – at the gene, protein, and metabolic outcome levels – as to how microgravity alters the basic responses of plants when the influence of gravity is removed/minimized. This will serve as the foundation “omics” analyses in subsequent spaceflight and colonization experiments in space, as well as shedding new insights into the manifold effects of gravity during plant growth and development.
2). We have partnered with Ms. Kathy Lucchesi (K-7/8 teacher), at McCaffrey Middle School in Galt, California, and their largely Hispanic students. Supplemental funding was provided to the school by NASA and the California Space Grant Consortium so that these middle school students can safely follow and utilize many of the plant growth and development protocols developed for the International Space Station (ISS) experiments. One purpose here is that the students grow plants under similar conditions and obtain information and insights on how the research impacts or benefits life on Earth and beyond (in the future).

Written materials on, and seeds for, the experiments at hand are also routinely provided. The additional aim here is in helping teach and inspire these young students about the joys and fun of the scientific method in experimental plant biology. Periodically, the middle school students present results to Dr. Lewis over where such work is routinely evaluated.

3). The Lewis lab hosted Pullman Lego Robotics Team to discuss their project and help them prepare for their competition (January 2019).

4). David Hanson was the lead organizer for a NASA supported In-flight Education Downlink with Astronaut Christina Koch on the International Space Station (https://). This event had an audience of over 700 people, including over 500 K-12 students that traveled to University of New Mexico (UNM) to participate in person as well as others watching via an internet live stream (live.unm.edu). The event had many hands-on activity booths from local STEM (Science, Technology, Engineering, and Mathematics) education programs and guest presentations by NASA scientists and student interns. It was also co-hosted by The Children’s Hour radio program and part of a subsequent hour-long show that was broadcast nationwide. Research from APH-01 was highlighted in the live event (found online at live.unm.edu as well as directly through the NASA past downlinks site- https://) and on the radio show (https://).

5). David Hanson gave two lectures, one for the Science on Tap series and the other for the Interesting Conversations Series (see Bibs Patents Awards).

6). Miss Bianca Serda, a Hispanic student with Dr. Hanson gave three oral and three poster presentations. She was the recipient of a NASA Space Life Science Training Program (SLSTP) fellowship at Ames Research Center (from June 10, 2019 to August 16, 2019), results of which she presented at the American Society for Gravitational & Space Research (ASGSR) meeting in Denver.

Oral Presentations:

• Serda, B., Turpin, M., Hudson, P., and Hanson, D. “Plants in Space: Interactions between Morphology, Lignification, and Carbon Isotopic Composition.” UNM Center for Stable Isotopes Seminar, Albuquerque, NM, October 2019

• Serda, B., Turpin, M., Lewis, N., and Hanson, D. “Plants in Space: Do Lignification Levels and Microgravity Interact to Impact Photosynthesis? University of New Mexico Department of Biology 28th Annual Research Day, Albuquerque, NM, March 2019

Poster Presentations:

• Serda, B., McKaig, J., Waters, S., Venkateswaran, K.J., Smith, D.J. Methylation pattern detection of the genome of Bacillus pumilus strain SAFR-032. 35th Annual Meeting American Society for Gravitational and Space Research, Denver, CO, November 20 - 23, 2019

• Serda, B., Turpin, M., Hudson, P., and Hanson, D. “Plants in Space: Interactions between Morphology, Lignification, and Carbon Isotopic Composition.” SACNAS Conference, Honolulu, HI, November 2019

• Serda, B., Turpin, M., Hudson, P., and Hanson, D. “Plants in Space: Interactions between Morphology, Lignification, and Carbon Isotopic Composition.” New Mexico AMP Conference, New Mexico State University, Albuquerque, NM, October 2019.

7). This project has been showcased on the Space Biology Facebook page at: https://

8). Dr. Lewis and Dr. Davin were judges for the High School Student Poster competition at the annual ASGSR meeting in Denver, CO, November 20 – 23 2019.

Our ongoing investigation consisted of two Arabidopsis grow-outs on International Space Station (ISS), with plants grown and monitored in the Advanced Plant Habitat (APH), with frozen specimens returned to Earth for multi-omics analyses. The corresponding ground control growth experiments were carried out at Kennedy Space Center (KSC) by KSC-affiliated collaborators in a second APH unit. The overall study had six Arabidopsis lines, one wild type (WT) line for the four lines of lignin-reduced arogenate dehydratase (adt) mutants, with these encompassing a single mutant (adt5), a double mutant (adt4/5), a quadruple mutant (adt3/4/5/6), as well as a second WT line used to generate a carbon capture mechanism CCM mutant, and an adt3/4/5/6/CCM quintuple mutant. The adt mutants differed in their levels of lignin reduction, relative to WT, with the largest reduction in lignin content being with the quadruple mutant (adt3/4/5/6).
1. ISS and KSC grow-outs:

• The first grow-out in the APH (APH-01) was initiated by NASA astronaut Ricky Arnold on ISS on June 8, 2018 (Day 0). On June 22, 2018 (Day 14), manual FluorPen photosynthesis measurements were carried out, followed by thinning of the Arabidopsis seedlings to give one viable plant per growth site in the APH. The “thinnings,” to remove “excess” numbers of seedlings, were placed in foil, immediately frozen, and stored in the GLACIER freezer at –160°C on ISS.

• Spaceflight environment effects were observed with the remaining plant lines growing in APH-01. Following the thinning operation, several plants unexpectedly died, and others grew somewhat smaller in size. The impact on our experiment was that only one harvest at 45 days was possible in order to ensure sufficient plant material availability for our multi-omics analysis. FluorPen photosynthesis measurements were, however, again conducted after 31 days (4 weeks and 3 days) of growth (July 9, 2018). All remaining plants were finally harvested on ISS on July 23, 2018, and immediately frozen and stored in the GLACIER freezer at –160°C (as for the thinnings). The frozen ISS-grown plant specimens were returned to Earth on January 13, 2019, and transported/delivered frozen to the Institute of Biological Chemistry (IBC), Washington State University (WSU), on January 15, 2019.

• The corresponding ground control APH-01 study, at Kennedy Space Center (KSC), was initiated a week later (June 15, 2018; Day 0), with FluorPen photosynthesis measurements/thinnings done on June 29, 2018 (Day 14). FluorPen photosynthesis measurements were again carried out on July 13, 2018 (Day 28), with the final harvest on July 27, 2018 (Day 42). Ground control plants were transported/ delivered to IBC/WSU on January 25, 2019.

• The second ISS grow-out was initiated by astronaut Serena Auñón-Chancellor on September 18, 2018. Following FluorPen photosynthesis measurements, the subsequent thinning operation on ISS (October 2, 2018) removed the “excess” plants that were immediately frozen and stored in the GLACIER freezer at –160°C. The thinning procedure may have adversely affected growth/development of some Arabidopsis plants in APH-01 with several again dying after the thinnings had been harvested. FluorPen measurements were carried out on ISS on October 19, 2018 (Day 31). Slightly slower Arabidopsis growth was observed in the ISS APH facility, relative to our ground control expectations, with only a single harvest at ~6 weeks (November 2, 2018; Day 45) being possible, in order to obtain the required plant material for our multi-omics analysis. The 6 week old harvested plants were immediately frozen and stored in the GLACIER freezer at –160°C. All frozen specimens were returned to Earth on January 7, 2020, and transported/delivered frozen to IBC/WSU on January 09, 2020.

• The corresponding ground control was initiated at KSC a week later (September 25, 2018; Day 0), with FluorPen photosynthesis measurements/thinning occurring on October 9, 2018 (Day 14), FluorPen photosynthesis measurements were again conducted on October 26, 2018 (Day 31), with the final harvest being on November 9, 2018 (Day 45). The ground control plants were transported/delivered to IBC/WSU on January 25, 2019.

• This Progress Report largely focuses on analyses of Arabidopsis plants on ISS and KSC (ground controls) from Grow-out #1, with Grow-out #2 data as available.

2. Consortium Member (David Hanson Lab, University of New Mexico, UNM) Activities for Arabidopsis Grow-out #1 and Grow-out #2 on APH-01 (ISS and KSC)

2.1. Estimated growth behavior of Arabidopsis wild type (WT) and arogenate dehydratase (adt), carbon capture mechanism (CCM), and adt/CCM mutant plants on ISS and KSC (ground controls)

Photographic images of all six Arabidopsis lines (described above), during growth and development, were downloaded to Earth twice a day, with the images being processed to estimate relative growth of rosette tissue size for each

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plant/plant line. In both grow-outs, growth/development lagged on ISS relative to KSC ground contols. The same trends were observed in both grow-outs. In addition, estimates of flowering stem growth and their abilities to have an upright (vertical) orientation were made for both ISS and ground control (KSC) plant lines. In all ISS-grown plants, an off-vertical growth displacement of the stems was observed regardless of the plant line being analyzed. This was in contrast to the KSC grown lines that generally had vertically growing flowering stems.

2.2. Photosynthesis measurements

Fluorpen-based estimations of photosynthetic function (chlorophyll fluorescence) showed much greater variability and overall higher values on ISS relative to ground contols. These data consisted of light-adapted measurements of pulse amplitude modulated (PAM) chlorophyll fluorescence at lower (150 µmol photons m–2 s–1) and higher (800 µmol photons m–2 s–1) light levels, these being collected at least 20 minutes after opening the APH to allow for effects from the high ISS cabin CO2 (4000 ppm versus 400 ppm in the APH) to equilibrate. Two light intensities were used to determine the electron transport rate (ETR) of photosynthesis in growth conditions and the ability to be stimulated by higher light that was near saturation in pre-grow-out experiment trials on Earth.

3. Consortium Members (Laurence Davin and Norman Lewis, WSU/IBC) - Arabidopsis Multi-omics Sample Preparation

ISS and KSC (ground control) rosette leaf and stem tissues samples were processed individually at WSU/IBC as described below in order to obtain: • RNAs for transcriptomics, • Proteins for proteomics, • Metabolites for metabolomics, • Intact stem tissues for microscopy analysis, • Ground stem tissue for lignin and stable isotope analyses.

Samples from both ISS and ground controls (KSC), stored individually in double-pocketed foil bags (one pocket containing rosette leaves, and the other pocket containing stems with flowers, siliques, and cauline leaves), were each removed from the –80ºC freezer and placed in dry ice. Each sample was first weighed in its foil bag, and then placed into liquid nitrogen. Following sample removal for processing, each foil bag was re-weighed in order to obtain the fresh (frozen) weight of each sample.

4. Arabidopsis multi-omics analyses

These have been initiated on specimens from ISS Grow-out #1 tissues, and the corresponding KSC (ground control) samples. Following sample preparation as indicated above, these were sent to Los Alamos National Lab (LANL), Pacific Northwest National Lab (PNNL), and UNM consortium members. The data will be re-processed in future work in order to compare and integrate all multi-omics analysis results per individual plant.

4.1. Consortium member (Shawn Starkenburg, LANL) - Transcriptomics

All samples provided by WSU/IBC, and meeting Quality Control expectations, from Arabidopsis Grow-out #1 were provided to LANL for analysis. These were sequenced using the LANL Illumina sequencer at an approximate depth of 100 fold coverage. Total number of reads for each sample ranged from 10,000 to 50,000. Each tissue, leaves and stems, were sequenced independently. Raw reads were trimmed for quality using FaQCs and mapped to the Arabidopsis thaliana genome using HiSat2. Reads were counted using FeatureCounts and analyzed for differential expression using edgeR, implemented in R.

Differential gene expression analysis was preliminarily performed in two ways: examination of i) global gene expression differences and ii) specific pathways differentially regulated, based on previous work with adt lignin deficient mutants. Multidimensional clustering of samples demonstrated that samples clustered primarily by tissue type, then by ISS/KSC origin.

For global gene expression analysis, ISS Arabidopsis genotypes were compared to respective tissue WT (KSC) ground control samples. A total of 1,403 genes were differentially expressed, as compared to the WT KSC ground control data. In this preliminary analysis, most genes were differentially expressed in leaves, as compared to stems. Additionally, ISS samples, as compared to the KSC (ground control) counterparts, displayed most differentially expressed genes. A preliminarily examination of the potential function of genes that were significantly differentially regulated in ISS leaf samples was carried out.

Specific analyses were performed to examine effects upon phenylpropanoid pathways in lignin-reduced mutants. Significant upregulation of phenylpropanoid pathway genes amongst mutant genotypes was observed relative to WT, but also for WT samples grown in ISS, provisionally suggesting that pathways examined were biologically relevant.

4.2. Consortium members (Laurence Davin and Norman Lewis, WSU/IBC) – Arabidopsis lignin analyses and metabolomics

ISS and KSC (ground control) samples from Arabidopsis Grow-out #1, processed as described at the beginning of Section 3, were subjected to lignin content/composition and metabolomics analyses, for each stem and leaf tissue type.

4.2.1. Arabidopsis estimated lignin analyses

The overall average lignin levels were estimated (in micromoles of thioacidolysis products per gram cell wall residue (CWR)) for the Arabidopsis stems from the six different Arabidopsis lines grown on ISS and at KSC, respectively, in their corresponding APH units. With the exception of the adt5 mutant, most lines (average of 3-4 plants/line) gave similar lignin levels (contents/compositions) for both ISS and KSC (ground control) APH-grown plants, whether the line was reduced in lignin amount via ADT mutations or not.

This data was further scrutinized, whereby each individual plant lignin level for all six lines was determined. This clearly established that most plant lines had fairly similar lignin levels (or similar variability) for ISS and KSC plant lines grown in the 2 APH units, with the exception of three of the four ISS grown adt5 mutants; this anomaly presumably resulted from 3 of their 4 growth sites in the APH on ISS not receiving adequate watering. Taken together, the data would suggest that constitutive lignification levels in all six Arabidopsis lines were not greatly affected when grown on ISS, relative to the ground controls at KSC; similar observations were made by us on growing dwarf wheat on the Space Shuttle.

4.2.2. Arabidopsis metabolomics

Metabolomics analyses were conducted on each Arabidopsis plant stem and leaf sample from the six Arabidopsis lines

	that were ISS and KSC (ground control) grown in their respective APH units, as follows: Each sample analysis involved UPLC-qTOF-MS for metabolomics. LC-MS analysis and identification of metabolites in each sample were performed as previously described. Representative chromatograms of the main Arabidopsis metabolite classes present in leaf and stem tissues of the WT line, grown in APH units on ISS and KSC, respectively, were obtained. Under these chromatographic conditions, the metabolites analyzed were mainly annotated as apocarotenoids (A), flavonoids (F), glucosinolates (G), galactolipids (GL); phenolic glucosides (PG), and phenylpropanoids (P), respectively. It was of considerable interest to additionally determine whether there were significant changes in the plant metabolic profiles grown on ISS, relative to the ground controls at KSC. An example shown is that of the comparison of the metabolic profiles of Arabidopsis WT and adt3/4/5/6 lines, grown on ISS and at KSC (ground control) in their respective APH units. This involved pair-wise comparisons of the metabolites obtained for ISS and KSC (ground control) samples, after normalization of data to the internal standard naringenin in XCMS. The respective sPLS-DA (Sparse Partial Least Squares Discriminant Analysis) plots for the Arabidopsis leaf and stem samples (4 biological and 2 technical replicates each) for WT ground control (KSC), WT ISS, adt3/4/5/6 ground control (KSC) and adt3/4/5/6 ISS) samples were generated by performing statistical analyses of identified secondary metabolites using MetaboAnalyst version 4.0. Processing the metabolomics data in this way resulted in clear segregation of ISS and KSC (ground control) WT Arabidopsis leaf metabolite clusters, and also those of the adt3/4/5/6 lines from the ISS and KSC samples. While there was some very minimum overlap for each of these clusters, all sample sets were readily distinguished as to both genotype and whether they were ISS or ground control (KSC) grown. An analogous situation holds for the stem samples. 4.3. Consortium members (Kim Hixson and Mary Lipton, PNNL) – Proteomics, phosphoproteomics, and lipidomics 4.3.1. Proteomics WSU/IBC provided samples of all stem and leaf tissues for individual Arabidopsis plants prepared for global proteomics and phospho-proteomics analyses at PNNL. Samples received were of precipitated proteins. Precipitated proteins were individually solubilized in a denaturing solution and digested into peptides using trypsin. The isobaric tagging protocol (iTRAQ) method was used to quantitatively determine the abundances of peptides in each sample, with each peptide identified and quantified by searching the fragmentation pattern against the Arabidopsis genome. For the global proteomics in Arabidopsis Grow-out #1, 16,499 proteins could be identified by matching against the Arabidopsis genome, this corresponding to almost 60% of the protein coding regions. A PLS-DA showed separations of leaf and stem samples from the KSC (ground control) and ISS in Arabidopsis Grow-out #1. This PLS-DA plot, along with coefficient of variation analysis between ISS grown plants and KSC ground control plants, also showed that ISS-grown Arabidopsis leaf and stem samples were more variable than the KSC (ground control) plants. The proteomics data provisionally suggest that plants grown on ISS had much stronger responses in their proteomes, as compared to plants grown at KSC (ground control). Several more proteins increased in abundance as ADT and lignin levels were reduced. These results indicate that as lignin is reduced, and plants are grown on ISS, they perhaps perceive more stress in the form of radiation and microbial perception/susceptibility, the result of which triggers higher numbers of cell signaling, transport, and exosome related proteins. Additional work is underway to complete the proteomic analyses of each leaf and stem sample from all six Arabidopsis lines in Grow-out #1. 4.3.2. Phosphoproteomics and lipidomics Analyses on pertinent mass spectrometer platforms and pipelines have all been completed for WT, adt mutant and CCM-engineered Arabidopsis from Grow-out #1. The data is currently being assessed and interpreted. 5. Consortium member (David Hanson Lab, UNM) 13C analyses The 13C analyses were carried out on plant leaf samples (ISS and KSC grown) that were ground to a powder and provided by the WSU/IBC in May 2019. The 13C data obtained to date, however, from the six Arabidopsis Grow-out #1 samples showed few differences between genotypes grown on ISS vs KSC ground controls, although ISS plant tissues gave much higher variability in these measurements.
Bibliography Type:	Description: (Last Updated: 04/30/2024)
Abstracts for Journals and Proceedings	Turpin MM, Serda BM, Hanson DT, Monje O, Richards JT, Carver J, Dimapilis D, Levine HG, Dufour N, Onate B, Davin LB, Lewis NG. "Effects of the ISS spaceflight environment and lignin reductions on plant anatomy and gas diffusion in leaves." 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. Abstracts. 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. , Nov-2019
Abstracts for Journals and Proceedings	Hanson, DT, Turpin, MM, Serda, BM, Monje, O, Richards, JT, Carver, J, Dimapilis, D, Levine, HG, Dufour, N, Onate, B, Davin, LB, Lewis, NG. "Measurements of photosynthesis via pulse-amplitude modulated chlorophyll fluorescence on the ISS." 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. Abstracts. 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. , Nov-2019
Abstracts for Journals and Proceedings	Monje O, Richards JT, Hanson DT, Turpin MM, Moinuddin SGA, Costa MA, Davin LB, Lewis NG, Carver J, Dimapilis D, Levine HG, Dufour N, Onate B. "New perspectives for watering substrate-based root modules in microgravity in the Advanced Plant Habitat (APH)." 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. Abstracts. 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. , Nov-2019

Abstracts for Journals and Proceedings	Hixson KK, Costa MA, Moinuddin SGA, Engbrecht KM, Weitz KK, Hanschen ER, Starkenburg SR, Sayre RT, Lipton MS, Hanson DT, Monje O, Richards JT, Davin LB, Lewis NG. "Investigation of spaceflight environment effects on differentially expressing lignin and carbon capture pathways in Arabidopsis using integrated omics methods." 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. Abstracts. 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. , Nov-2019
Abstracts for Journals and Proceedings	Hanschen ER, Hixson KK, Costa MA, Moinuddin SGA, Engbrecht KM, Weitz KK, Starkenburg SR, Sayre RT, Lipton MS, Hanson DT, Monje O, Richards JT, Davin LB, Lewis NG. "Patterns of gene expression in Arabidopsis thaliana in response to microgravitational environment." 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. Abstracts. 35th Annual Meeting of the American Society for Gravitational and Space Research, Denver, CO, November 20-23, 2019. , Nov-2019
Significant Media Coverage	Washington Grown, Season 6, Episode 13. " 'Herbs.' This episode is out of this world! Not only will we be talking about herbs, including visiting Steel Wheel Farm and Mesa de Vida, but we'll also head to Washington State University to learn about the Final Frontier Plant Habitat - where we talk about growing plants in space! Video with principal investigators." Washington Grown, Season 6, Episode 13. April 27, 2019. See http://www.wagrown.com/episodes-and-clips/-kfn2eSdUUU/ , Apr-2019
Significant Media Coverage	NASA Space Biology Facebook post. " 'Success! From splashdown of SpaceX16's Dragon capsule to Dr. Norman Lewis' lab. Our #PlantHabitat01 samples arrived safely at Washington State University. Ground controls arrived from Kennedy Space Center; analysis will soon begin!' " NASA Space Biology Facebook post, January 31, 2019. See post at: https://www.facebook.com/spacebiology/posts/1116954005145182 , Jan-2019
Significant Media Coverage	Hanson DT. " 'Extraterrestrial botany: Fundamental research and inspirational education.' A general public interactive lecture at the Science on Tap series, with CoInvestigator David Hanson. May 2, 2019, O'Neil's, Albuquerque, NM. Hosted by Explora and the National Museum of Nuclear Science and History." General public interactive lecture at the Science on Tap series, May 2, 2019, O'Neil's, Albuquerque, NM., May-2019
Significant Media Coverage	Hanson DT. " 'Plants in Space!' A general public interactive lecture for the Interesting Conversations Series, with CoInvestigator David Hanson." Lecture. May 10, 2019, Pentola Restaurant, Albuquerque, NM. Hosted by Sheryl Brown. May 2019., May-2019