

GeneLab: "Omics" Data System for Space Biology Research

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The GeneLab Team



ISS: Our Orbiting Laboratory





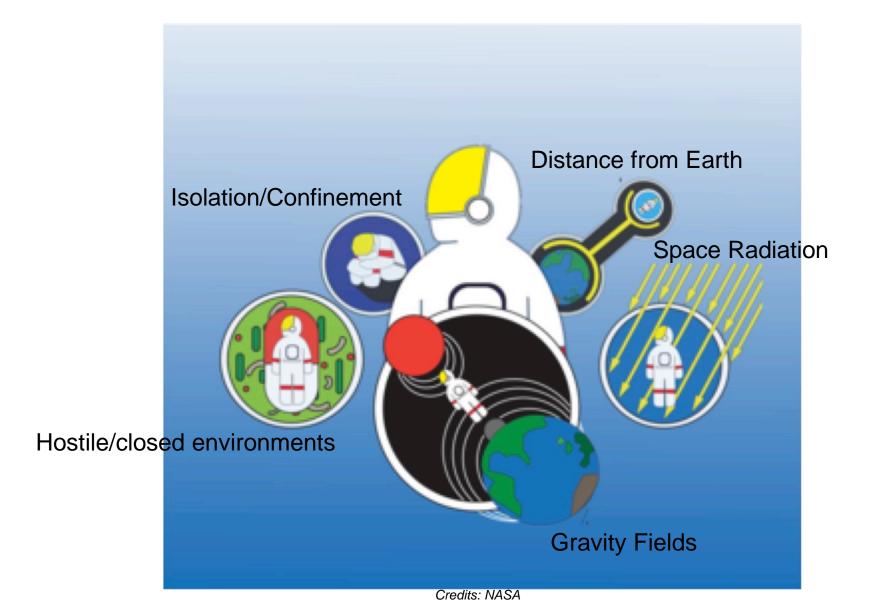
ISS enabling capability for research in cellular and molecular biology includes equipment for *in situ*, on-orbit analysis of biomolecules

Applications of this growing capability range from biomedicine and biotechnology to the growing field of Omics



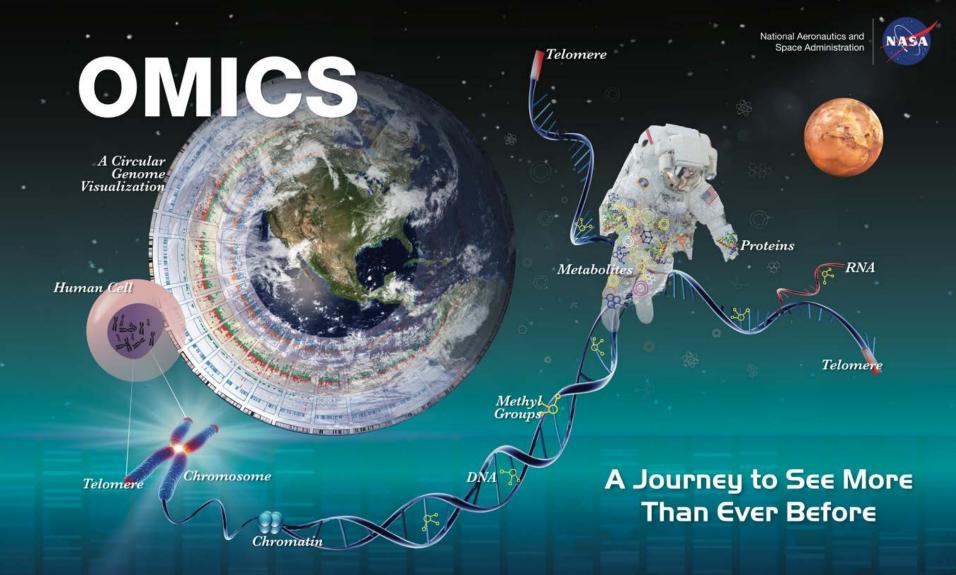
Challenges of Spaceflight





Opportunities of omics data

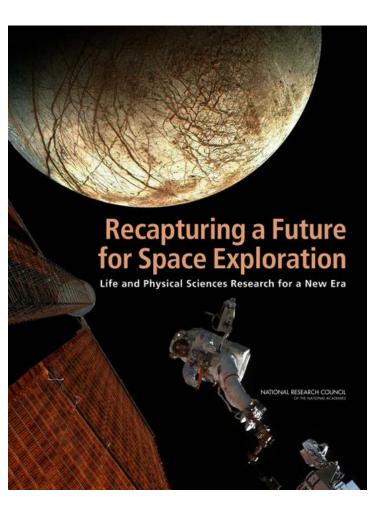






2011 NRC Decadal Survey





"...genomics, transcriptomics, proteomics, and metabolomics offer an immense opportunity to understand the effects of spaceflight on biological systems..."

"...Such techniques generate considerable amounts of data that can be mined and analyzed for information by multiple researchers..."



Omics Acquisition in Space is Now a Reality



This is truly an exciting time for cellular and molecular biology, omics and biomedicine research on ISS with these amazing additions to the suite of ISS Laboratory capabilities.



Sample Preparation Module



Oxford Nanopore MinION Gene Sequencer



Reaction tube containing lyophilized chemical assay bead (proprietary)



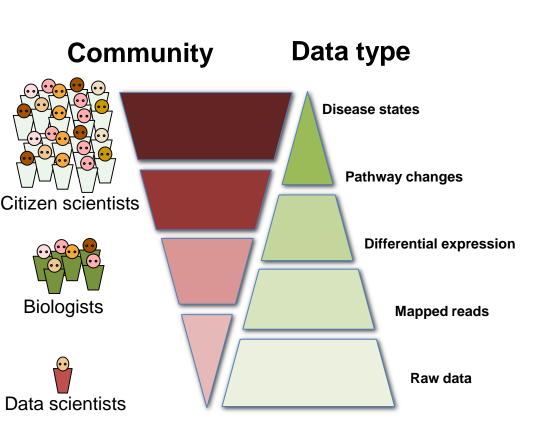
Mini-PCR

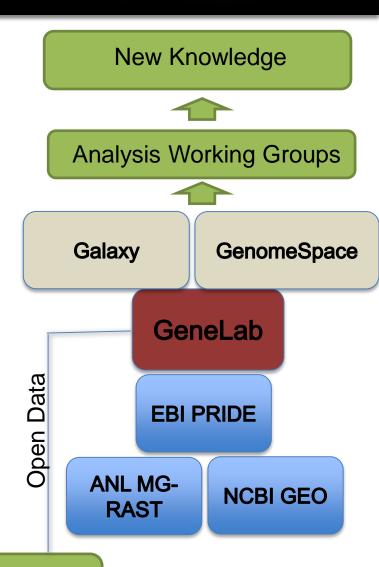
Cepheid Smart Cycler qRT-PCR



GeneLab







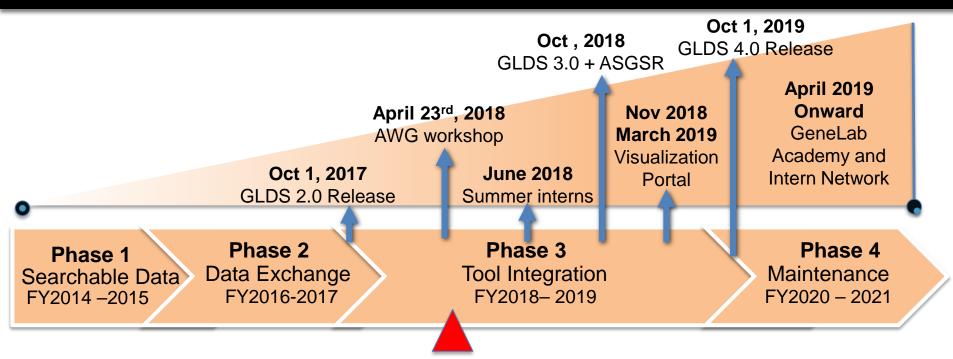
Missions/Experiments

GeneLab Sample Processing



Phased Implementation





Data System

- ✓ Public Website
- ✓ Searchable Data Repository
- ✓ Top Level Requirements
- ✓ New Data and Legacy Data

Data System

- ✓ Link to Public

 Databases via Data

 Federation
- ✓ Integrated Search (e.g., data mashup)

Data System

- Integrated Platform across model organisms
- Build Community via AWG
- Provide access to biocomputational tools for omics analysis
- Provide collaboration framework and tools

Open Source Maintenance

- User community becomes primary provider of new tools/knowledge
- Maintain integrity of data, and data system



GLDS Phase 2 (Release 2.0) Google-like Search, Federated Search



Data federation/integration with heterogeneous bioinformatics external databases (GEO, PRIDE, MG-RAST)

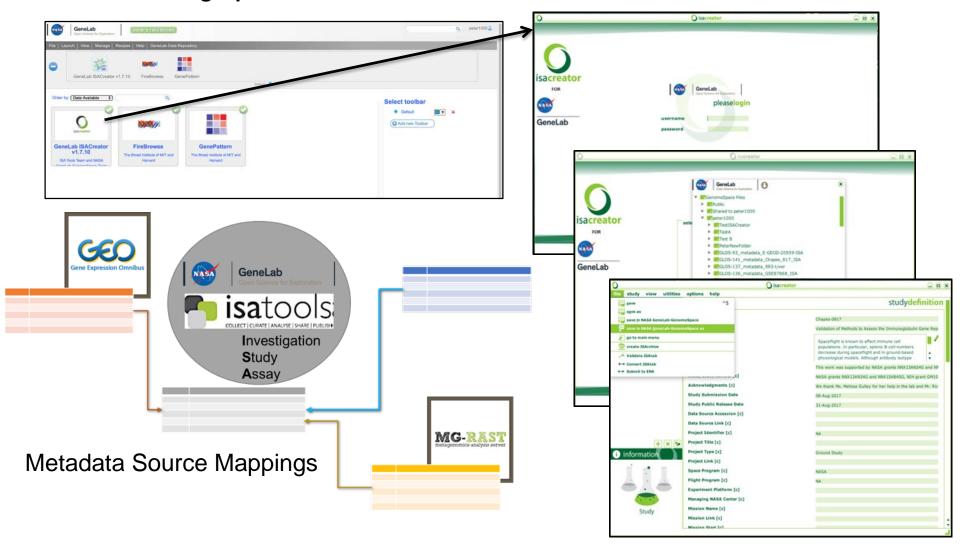
GeneLab Open Science for Exploration Fedel	rated Search					
Home Repository Data Data Mining Tools Submit Data Help Workspa mouse myostatin All Genelab NIH GEO EBI PRIDE ANL MG-RAST	GeneLab Open Science for Exploration Search Filters for	GeneLab				
Search results for: mouse myostatin using filter(s): Sort by Relevance 25 Myostatin inactivation effects on myogenesis in vitro and in vivo http://www.ncbi.nlm.nih.gov/geo/query/acc.cg/?acc=GSEZ8986 Key words: dystrophin, mdx mouse, Duchenne, fibrosis, dystrophy ABSTRACT Stim	Home Repository Data Data Mining Tools Submit Data Help Workspace					
(MDSC) into myogenic, as opposed to lipoflarogenic, lineages is a promising therapel counteracting myostatin, a negative regulator of muscle mass and a pro-lipoflarotic fibrogenic capacity of MDSC from wild Organism: Mus musculus Accession: GSE28988 PMContact: Robert Gelfand Re The transcriptomic signature of myostatin inhibitory influence on the differential	mouse x Q □ All ☑ GeneLab □ NIH GEO □ EBI PRIDE □ ANL MG-RAST					
Hitp://www.ncbi.mlm.ini.gov/geofuquery/acc.cg/?acc-g/SE59674 GDF8 (myostatin) is a unique cytokine strongly affecting the skeletal muscle phenoty molecular mechanism of myostatin influence on the differentiation of mouse C2C12 m technique. Treatment with exogenous GDF8 strongly affected the growth and developroliferation and differentiatio	Search Filters (GeneLab Only) Project Type					
Organism: Mus musculus Accession: GSE59874 PI/Contact: Zofia Wick Releas Development of gene expression signature for defining the cell potency of mu genotypes http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE39765	☐ Ground ☐ Age ☐ Mus musculus ☐ deletion pool profiling ☐ DNA methylation profiling ☐ environmental gene survey ☐ Sort by Relevance ☐ Atmospheric Pre ☐ Postose approximate ☐ genome sequencing ☐ Ground ☐ DNA methylation profiling ☐ environmental gene survey ☐ genome sequencing ☐ Ground ☐ Gr	Total Search Results Found: 3				
In order to determine the cell potency, by identification of genes responsible for plurif isolated from five week old male wild type(VTT), CSTBIsI, and another typetrophied microarray analysis and compared this gene expression to that of a standard mouse and Matn null mice using an esta Organism: Mus musculus Accession: GSE39765 PI/Contact: Bipasha Bose Rele	Age and Space Irra Bleomycin Treat Rattus norvegicus protein expression profiling cinogenesis Risk	(1)				
Rodent Research-3-CASIS: Mouse liver transcriptomic proteomic and epigend https://genelab-data.ndc.nasa.gov/genelab/accession/GLDS-137 The Rodent Research-3 (RR-3) mission was designed to study the effectiveness of occurs during spaceflight. Myostatin is a protein secreted by myoblasts that inhibits a block myostatin cause increases in muscle mass. The RR-3 experiment was sponso Advancement of Science in Space and ass Organism: Mus musculus: Factor: Microgravity Treatment	Age play CANONT:Part accumul cell culture decreas Organistr Clinical treatmen Staphylococcus aureus Age play CANONT:Part accumul cell culture decreas Staphylococcus prior profiling and profiling	is commonly attributed to a lifetime or many tumor sites it actually				



GLDS Phase 2 (Release 2.0) Metadata Curation via ISACreator Tool



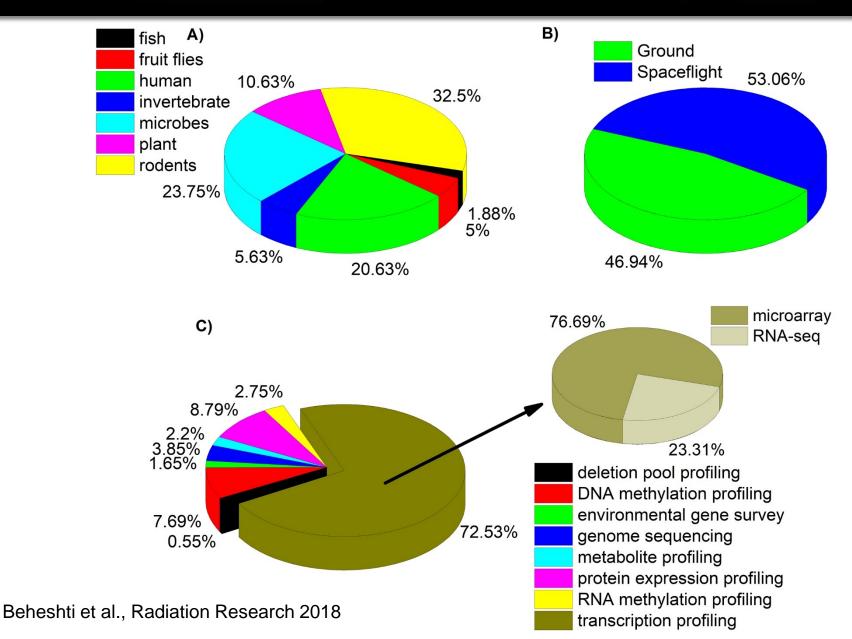
GeneLab-GenomeSpace Integration with ISACreator for Streamlining Data Processing Operations





GeneLab Database: >190 data sets

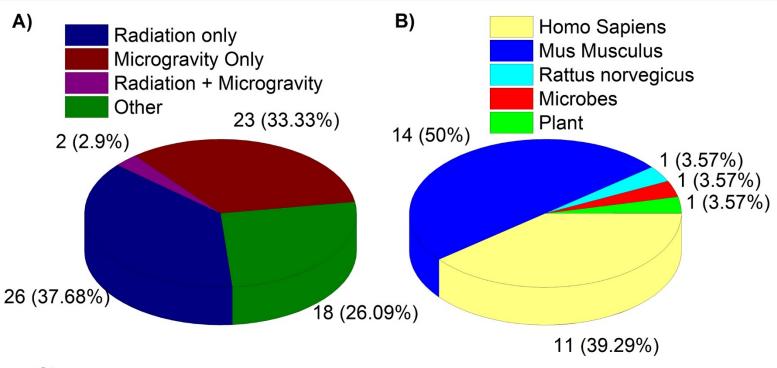


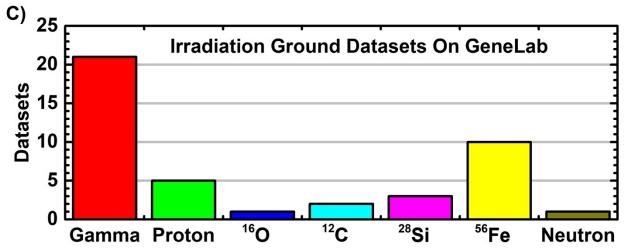




69 Ground Data Sets: Radiation and simulated microgravity





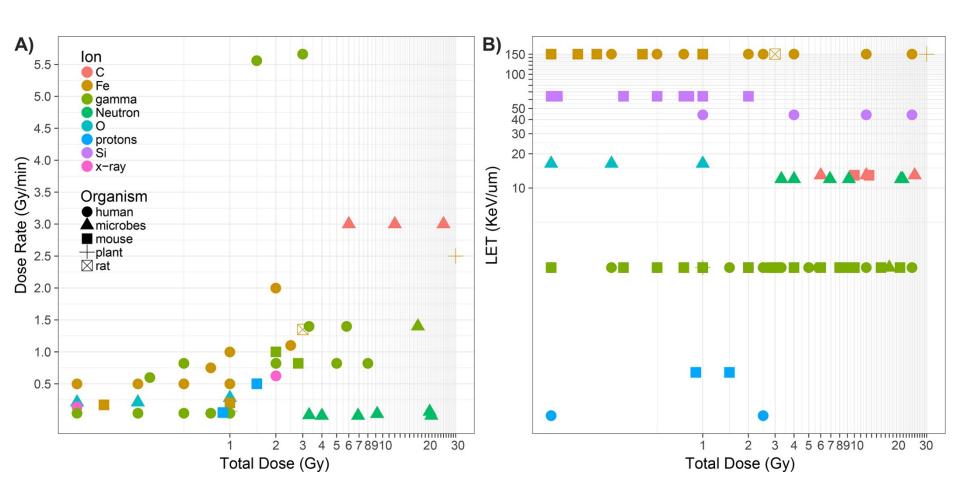


Beheshti et al., Radiation Research 2018



Radiation Ground Studies

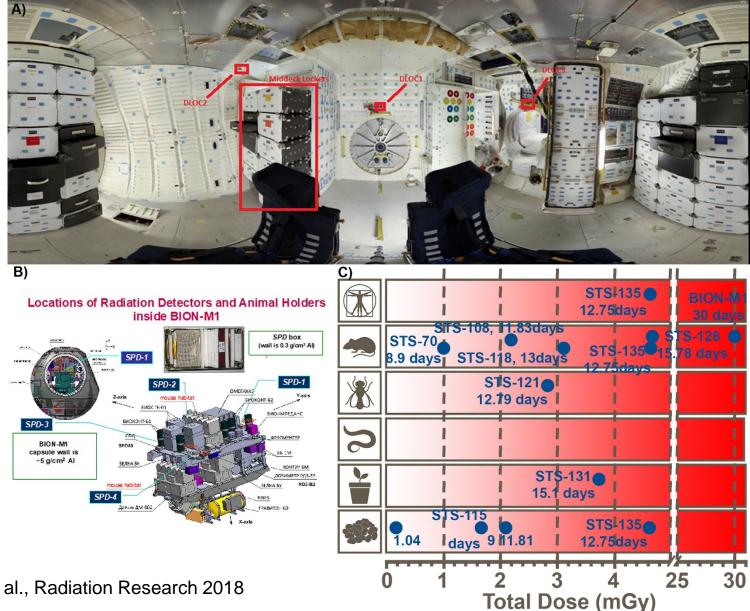






Radiation Dosimetry for STS samples (ISS to follow)



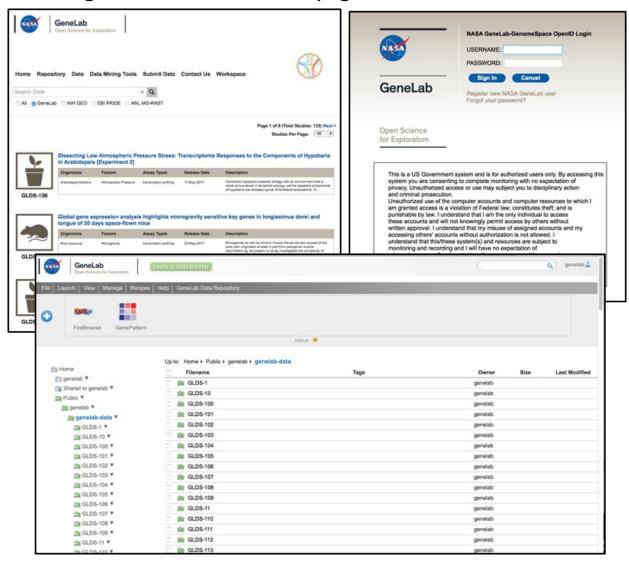




GLDS Phase 2 (Release 2.0) Customized NASA Collaborative Workspace



User Account Mgmt., Access Controls (e.g., Private, Shared, Public Folders)





Galaxy Platform



Barriers to reproducible analysis of omics data:

- Large files are difficult to move around and process
- 2. Workflows vary from user to user and details are sometimes poorly documented

Galaxy platform:

- Open source, extensible platform for cloud based analysis of omics data
- 2. Allows any command line tool or script to be run and chained together into workflows
- Workflows can published, shared and downloaded



Afgan et al. The Galaxy platform for accessible, reproducible and collaborative biomedical analyses: 2016 update. Nucleic Acids Research (2016)

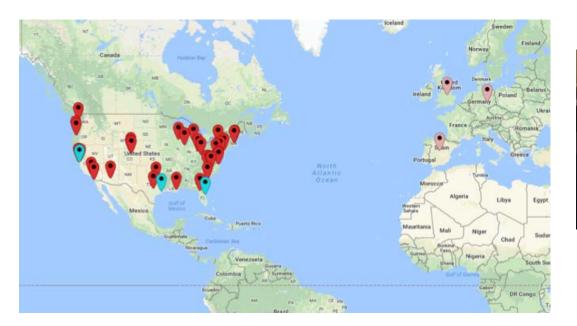


GeneLab Analysis Working Groups



- ~60 individuals
- 4 Groups: Plants, Microbes, Animals, Multi-omics
- **Monthly meetings**
- **Deliverables:**
 - Consensus pipelines for primary analysis of data (Microarray, RNASeq, Bisulfite sequencing, Proteomics, 16S metagenomics, Whole genome metagenomics)
 - Recommendations for visualization of data









GeneLab Analysis Working Groups



AWG (now)

Analysis Pipelines

Goal is to identify the best pipeline

Data to be added to GLDS or AWG scope

What additional data do you require to answer you scientific questions?

Metadata to be added to GLDS

What environmental or other metadata to you need to answer your questions?

Student interns (June - Aug)

Implementation (ideally in Galaxy)

Processed data for posting on GeneLab

Post processed data to GeneLab

Public portal for visualization of GeneLab data

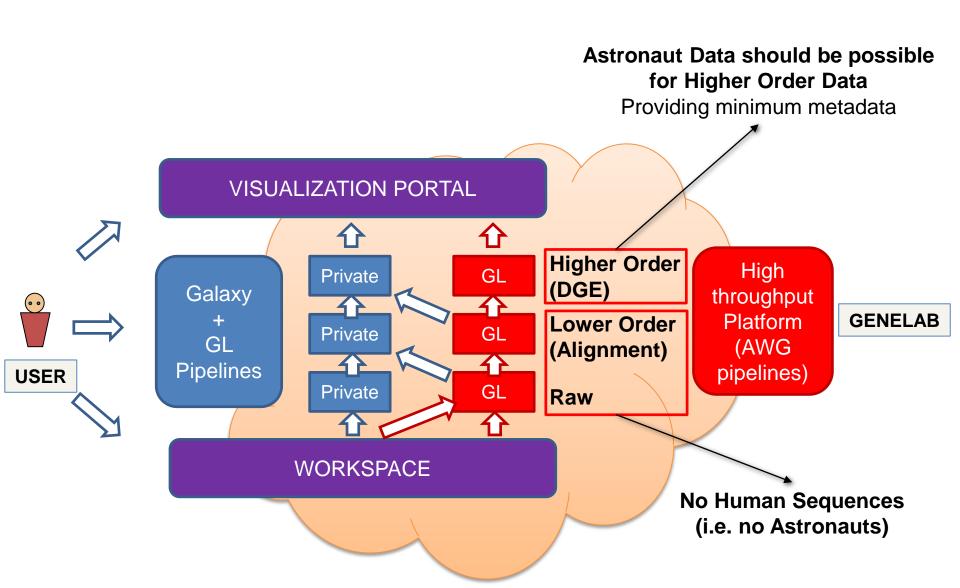
AWG (June - ?)

Visualization requirements and systems

Peer reviewed publication (s)

GLDS 4.0







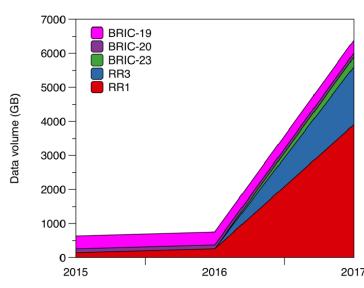
GeneLab Sample Processing Laboratory (SPL)



- Expertise:
 - DNA/RNA/protein extraction
 - Animal work
- Develop standards for sample processing (species dependent)
- Responsible for ~50% of GeneLab data by volume









Hypothesis and Science from GeneLab



- Cage Effects with rodent experiments: Carbon Dioxide as an Environmental Stressor in Spaceflight
- Systems Biology analysis reveals biological spaceflight master regulators
- AWG related work determines novel systemic biological factors causing damage due to spaceflight





Cage Effects with rodent experiments: Carbon Dioxide as an Environmental Stressor in Spaceflight

Beheshti A, Cekanaviciute E, Smith DJ, Costes SV. Global transcriptomic analysis suggests carbon dioxide as an environmental stressor in spaceflight: A systems biology GeneLab case study. Sci Rep. 2018;8(1):4191. doi: 10.1038/s41598-018-22613-1. PubMed PMID: 29520055; PMCID: PMC5843582.



Carbon Dioxide as an Environmental Stressor in Spaceflight



Atmospheric CO₂

1000

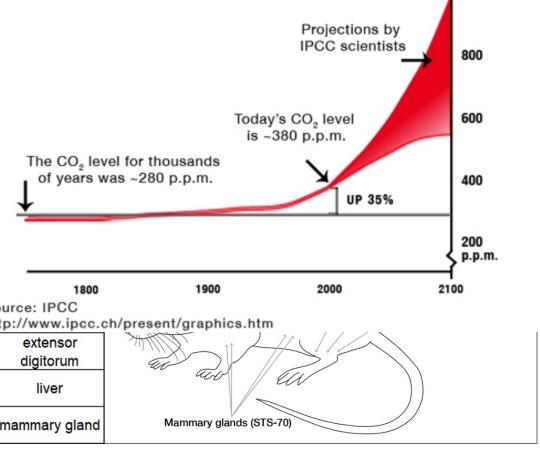
A) Cage Types



Animal Enclosure Module (AEM)

B)	oodio iliodo	(, ,,_,,,			<u>↓</u> .		UP 35	%
GeneLab Study	Mission	Species	CO ₂ (ppm)	Du (d				200 p.p.m.
GLDS-21	STS-108	mouse	~3000	1	1800	1900	2000	2100
GLDS-111	BF	mouse	~600		ource: IPCC ttp://www.ipcc.c	ch/present/graphics.htm	m	
GLDS-111	BF	mouse	~600	30	extensor digitorum			
GLDS-25	STS-135	mouse	~3000	13	liver	ais /	la	
GLDS-63	STS-70	rat	~3000 (est)	9	mammary gland	Mammary glands (ST	rs-70)	

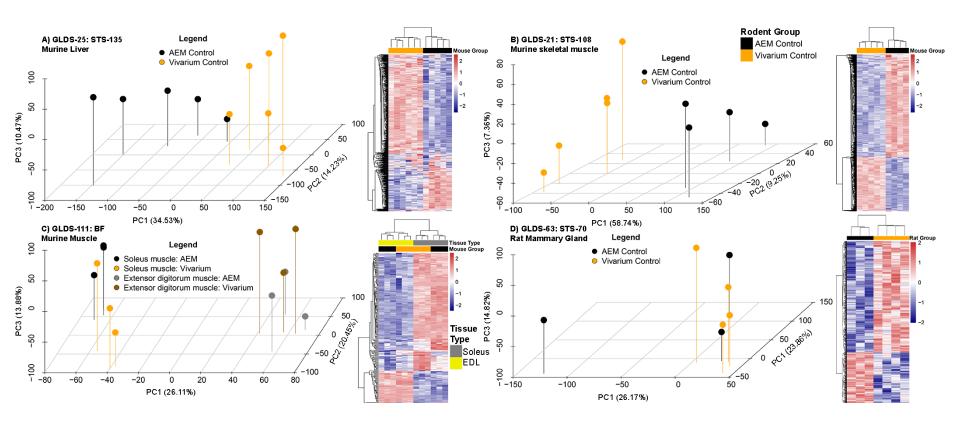
Historic and Projected CO2 **Atmospheric Concentrations**





Global Cage Differences





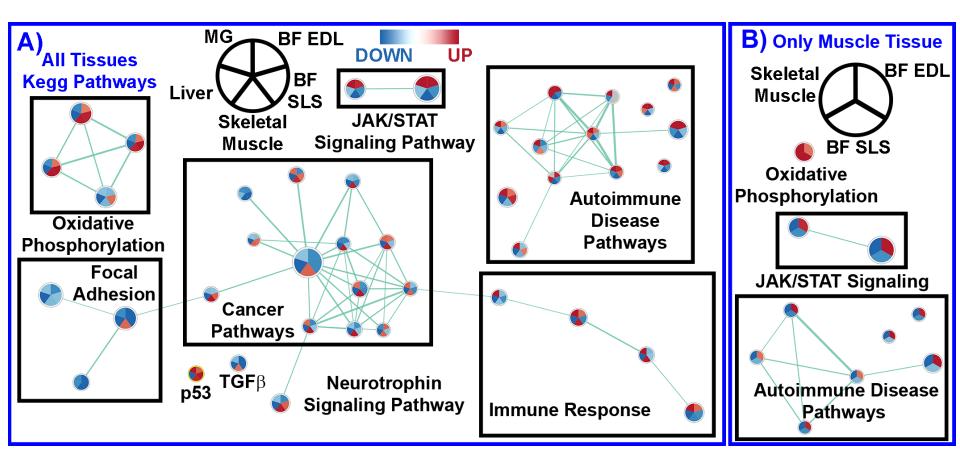
AEM = Animal Enclosure Modules (now referred to as Rodent Habitats) Vivarium = normal ground based rodent cages

Beheshti, et al., Scientific Reports, 2018



Major Pathways Regulated between Cages

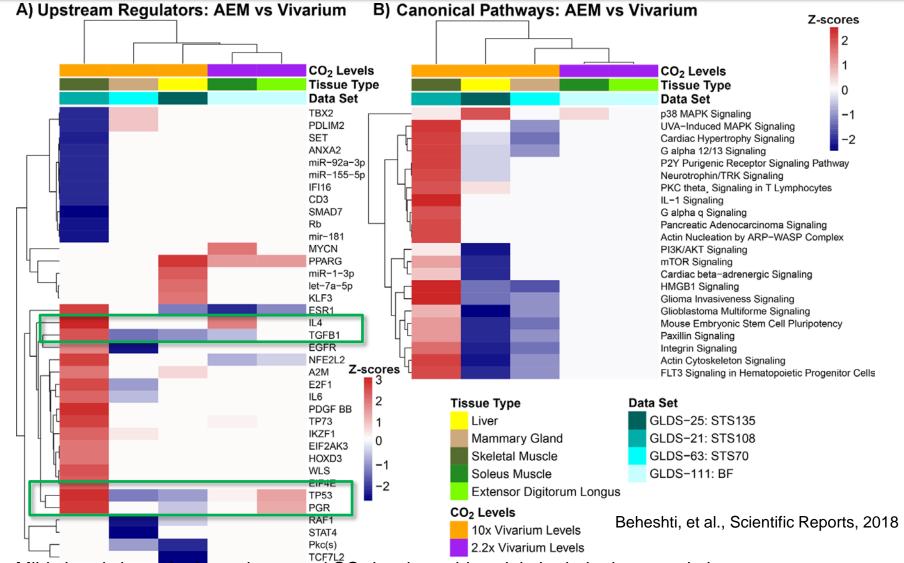




GSEA: Kegg Pathways (network displayed using EnrichmentMap plugin for Cytoscape)

Upstream regulators and canonical pathways show response is tissue specific and highest for high CO₂



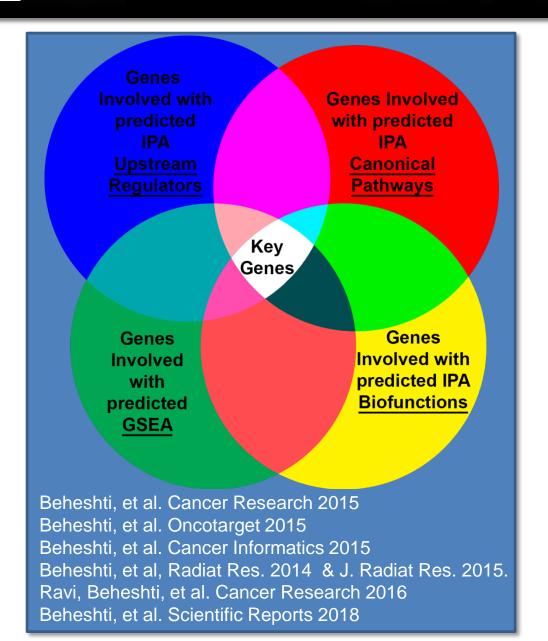


Mild chronic hypoxia due to increased CO₂ levels could explain both the increase in immune responses and a reduction in metabolism – Need to confirm with AEM experiments at ambient CO₂ levels.



Determination of Key Driving Genes

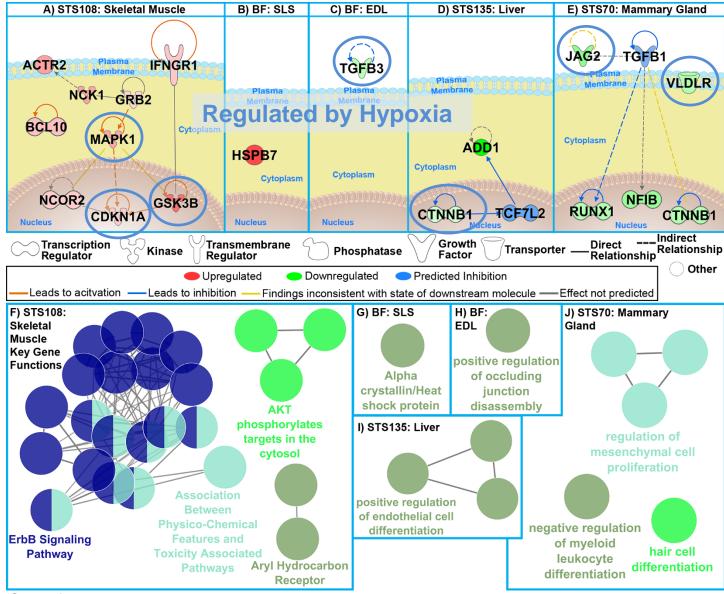






Identifying Key Cage-Dependent Drivers









Systems Biology analysis reveals biological spaceflight master regulators

Beheshti, et al., PLOS One, in press

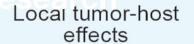


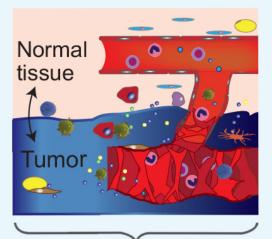
Systems Biology analysis reveals biological spaceflight master regulators

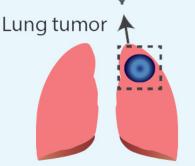


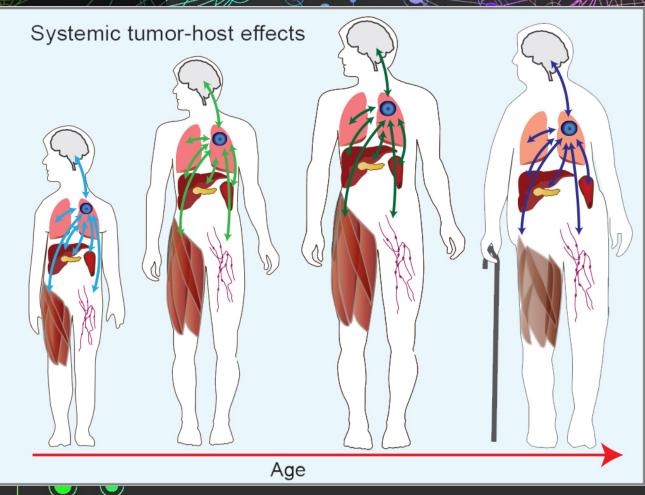
General Approach to Studying a Systematic Response in the Host

An example for cancer



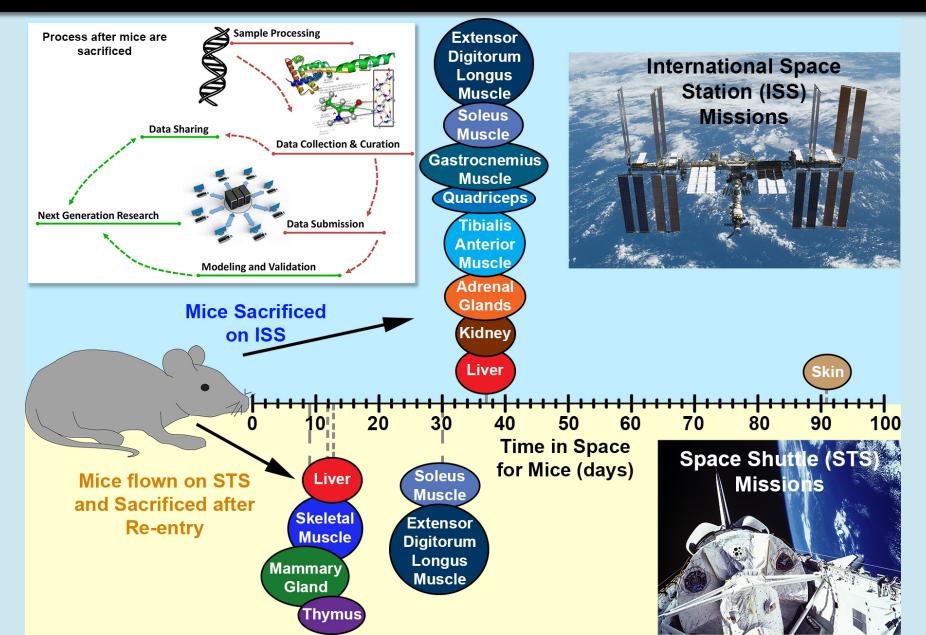






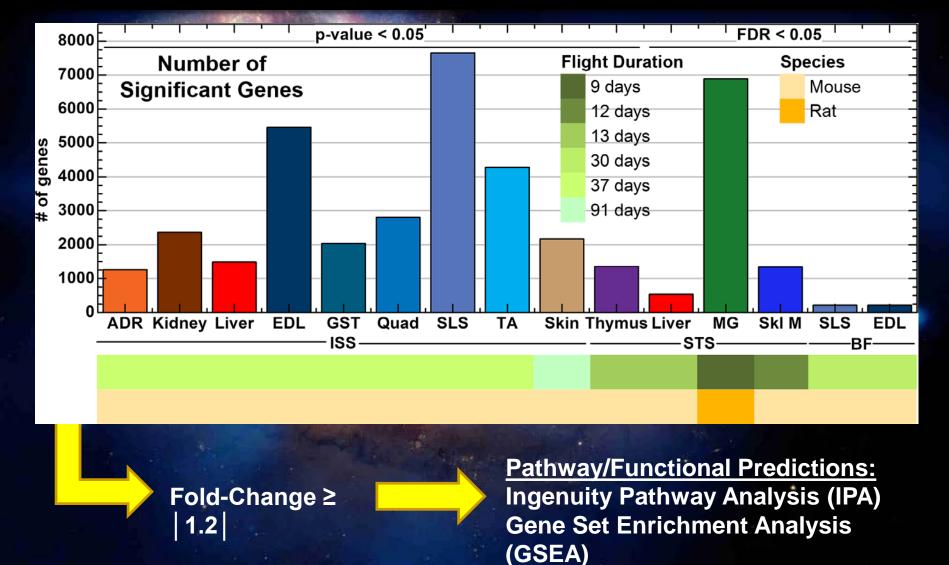
GeneLab Data Used to Generate Results





Number of Significant Genes from Each Dataset





Beheshti, et al., PLOS One, in press

15 (100%)

13 (86.7%)

11 (73.3%)

10 (66.7%)

12 (80%)

Extensor Digitorum Longus Flight Condition

STS

Tibialis Anterior

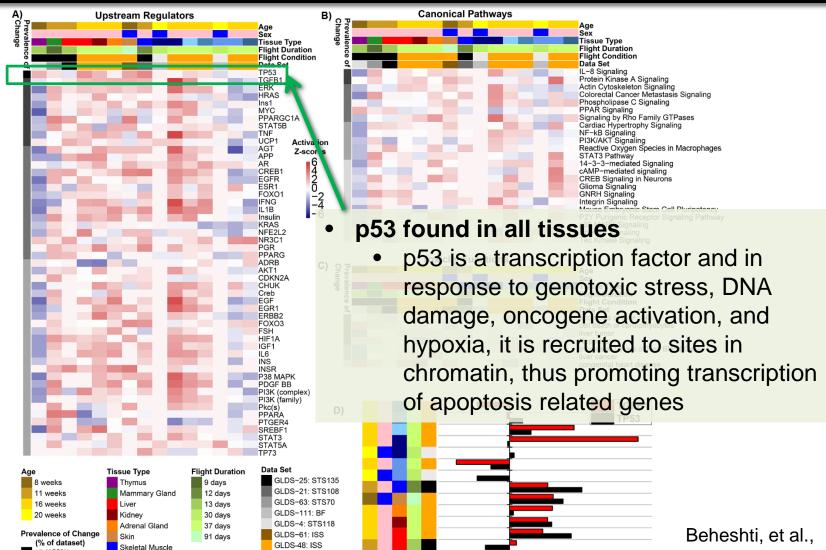
Soleus Muscle

Gastrocnemius

Quadricep

Predicted Master Regulators





PLOS One, in press

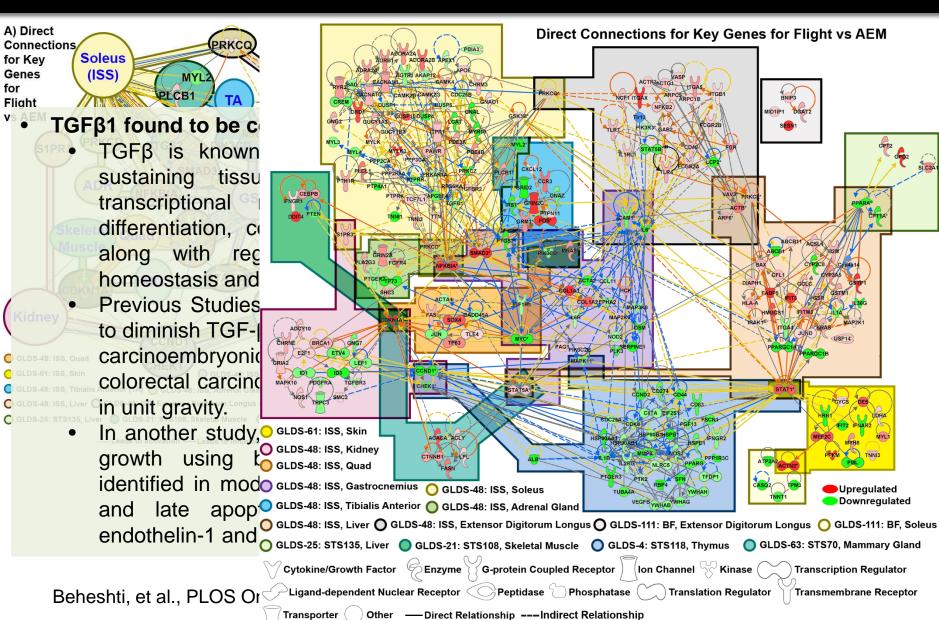
GeneLab

Open Science for Exploration

Key Genes and the Connections

leads to acityation — Leads to inhibition — Findings inconsistent with state of downstream molecule — Effect not predicted

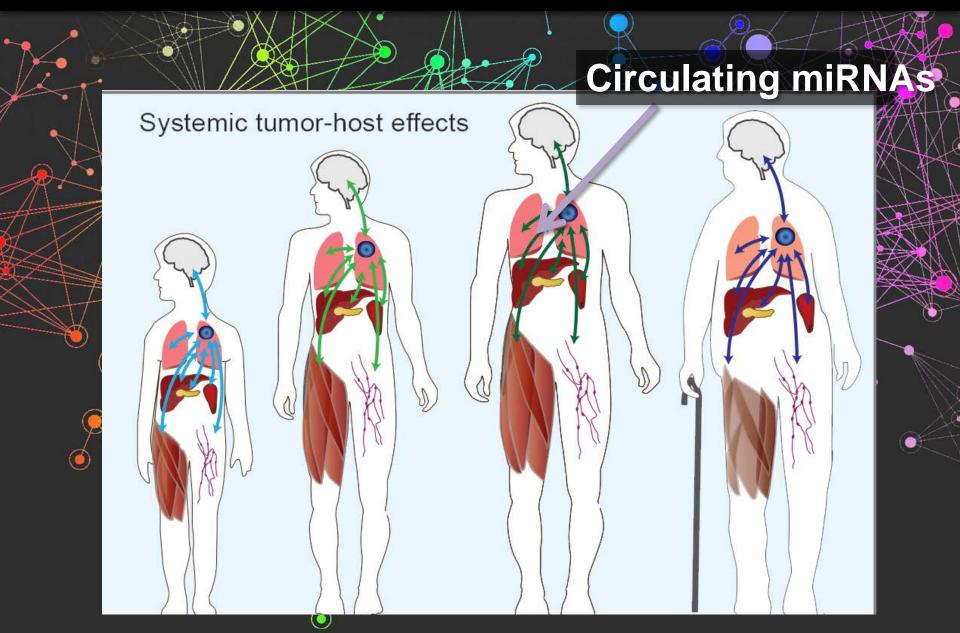






General Approach to Studying a Systematic Response in the Host

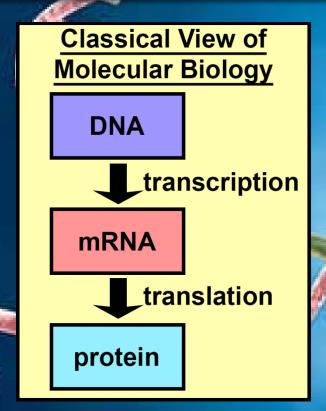


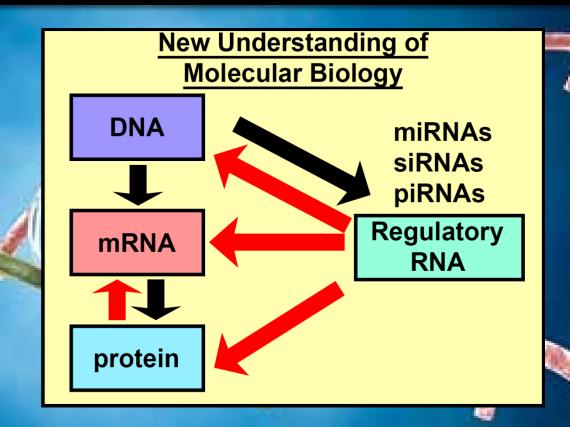




Revised View of Molecular Biology





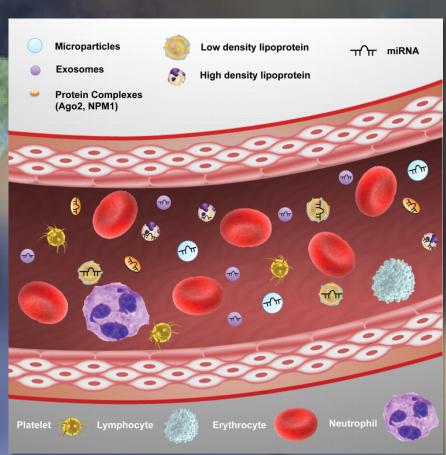


- A single miRNA has been estimated to regulate up to 500 mRNAs
- miRNAs are single-stranded RNA sequences, of about 22 nucleotides in length, processed from longer transcripts.
- miRNAs are important regulators that repress the translation of mRNA transcripts

Impact of Circulating microRNAs



- Circulating miRNAs can carry signals from organs to other various parts of the body through the blood stream.
- The miRNAs can be transported in Exosomes, microparticles, lipoproteins and outside any type of packaging.
- Our preliminary data shows that a miRNA signature is carried over from the spleen to the tumor with age.
 - Beheshti, et al. PLoS ONE 2017



Profiling of circulating microRNAs: from single biomarkers to re-wired networks Anna Zampetaki, Peter Willeit, Ignat Drozdov, Stefan Kiechl, Manuel Mayr. Cardiovascular Research, 2011.



Systems Biology View of miRNAs





Tumor Suppressor miRNAs



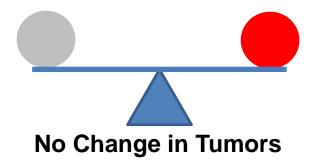
OncomiRNAs



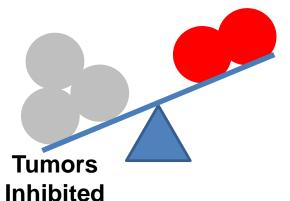


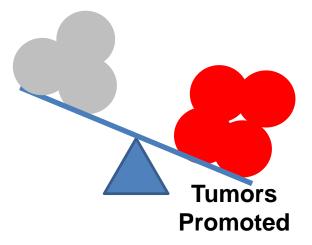
Inhibited

Only looking at a single miRNA



looking at a pair of miRNAs





Systems Biology
Approach: Looking at how the entire system impacts the most Important miRNAs

Beheshti, et al., PLOS One, in press

Predicted miRNAs Involved with Microgravity Effects

expressed in MMG-incubated PBLs compared with 1g incubated ones. Among these, miR-9-5p, miR-9-3p, miR-155-5p, miR-150-

3p, and miR-378-3p were the most dysregulated. To improve the detection of functional miRNA-mRNA pairs, we performed gene expression profiles on the same samples assayed for miRNA profiling and we integrated miRNA and mRNA expression

data. The functional classification of miRNA-correlated genes evidenced significant enrichment in the biological processes of

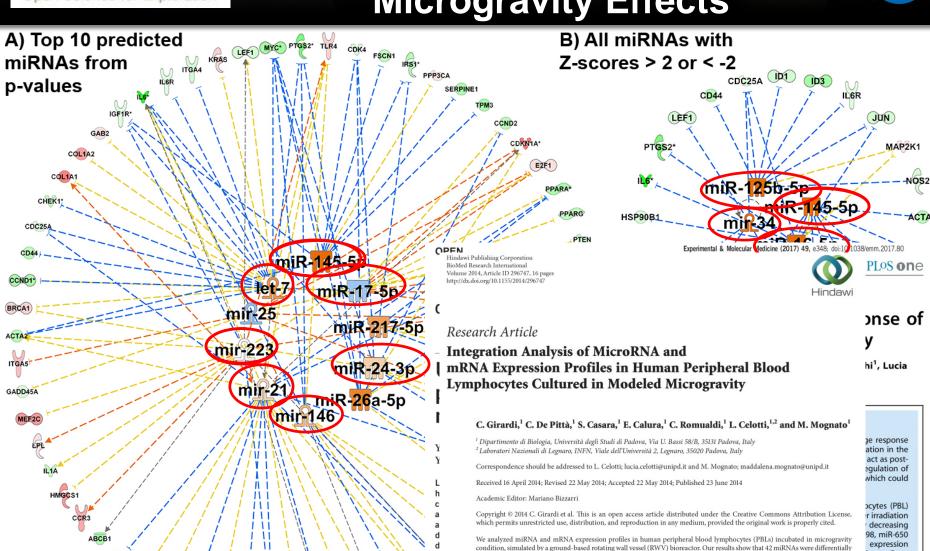
immune/inflammatory response, signal transduction, regulation of response to stress, regulation of programmed cell death, and regulation of cell proliferation. We identified the correlation of miR-9-3p, miR-155-5p, miR-150-3p, and miR-378-3p expression with that of genes involved in immune/inflammatory response (e.g., IFNG and ILI7F), apoptosis (e.g., PDCD4 and PTEN), and

cell proliferation (e.g., NKX3-1 and GADD45A). Experimental assays of cell viability and apoptosis induction validated the results

obtained by bioinformatics analyses demonstrating that in human PBLs the exposure to reduced gravitational force increases the

frequency of apoptosis and decreases cell proliferation.





ICAM1" FCGR2A CD274

ARF6

expression hway. Gene ncubated in etween 1 g ons derived

idence that



Predicted miRNAs Involved with Microgravity Effects

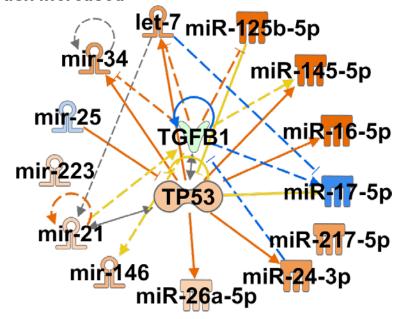


Health Risk Due to miRNAs



A recent report showed that inactivation of p53 altered TGF-β signaling, which ironically displayed both tumor-suppressive and pro-oncogenic functions. p53 functions to integrate crosstalk between Ras/MAPK and TGF-β signaling via binding to Smad3, dislocating the Smad3/Smad4 complex formation and differentially regulating subsets of TGF-β target genes

Biological Health Risk Increased







Analysis Working Group (AWG) Member related work determines novel systemic biological factors causing damage due to spaceflight

AWG Members Involved

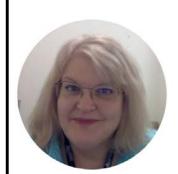








Brin Rosenthal



Deanne Taylor Hossein Fazelinia Komal Rathi







UNIVERSITY of CALIFORNIA, SAN DIEGO SCHOOL OF MEDICINE



Children's Hospital of Philadelphia





Helio Costa



Kathryn Grabek





J. Tyson McDonald





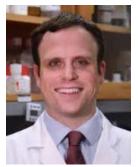


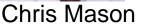
Gary Hardiman Willian da Silveira



AWG Members Involved











Cem Meydan Jonathan Foox



Flavia Rius



Yared Kidane





Cornell University.



Susana Zanello Scott Smith





Sara Zwart



Afshin Beheshti Sylvain Costes



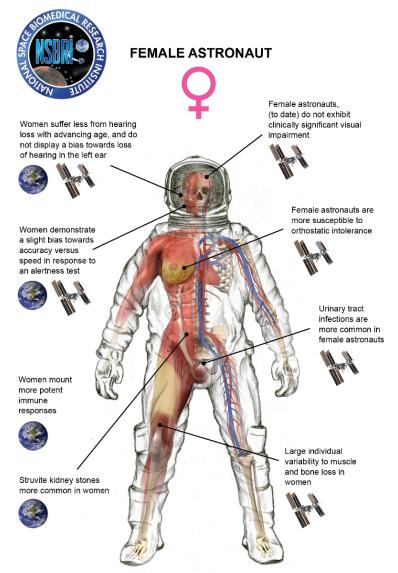




Manned Space Flight Education Foundation

Astronauts health problems



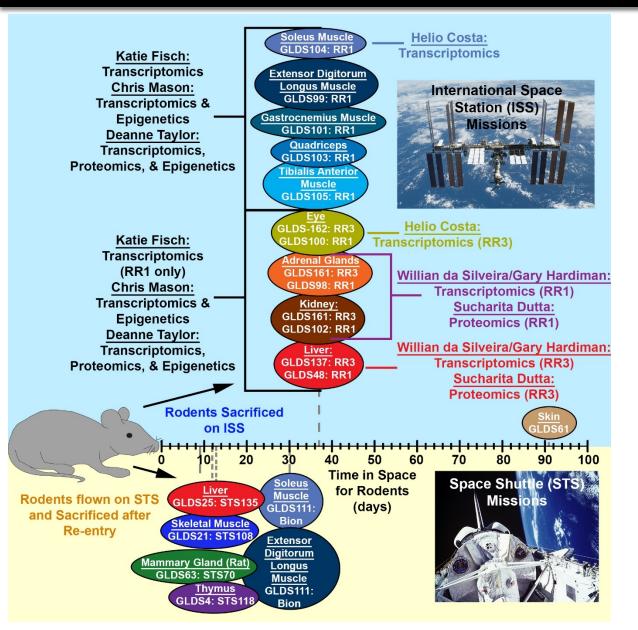


MALE ASTRONAUT Men suffer more from hearing Some male astronauts loss with advancing age, and exhibit clinically significant display a bias towards loss of visual impairment Male astronauts less susceptible to Men demonstrate a orthostatic intolerance slight bias towards speed versus accuracy in response to an alertness test Urinary tract infections less common in male astronauts Men mount less potent immune responses Large individual Calcium oxalate kidney variability to muscle stones more common and bone loss in men in men



Specific Datasets and Tissues AWG Members Analyzed





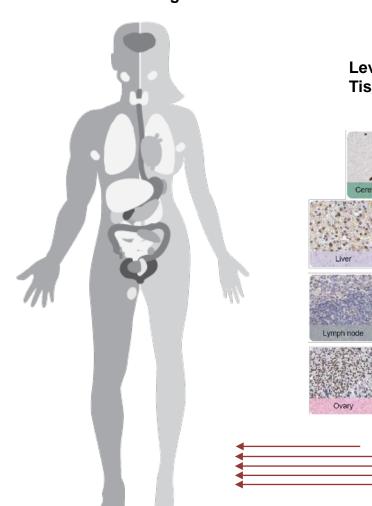
- Additional Datasets that are being analyzed:
 - Human datasets
 - GLDS-54, GLDS-174, GLDS-86, GLDS-118, GLDS-53, GLDS-54, GLDS-13. GLDS-52, or GLDS-114 (Tyson McDonald and Yared Kidane)



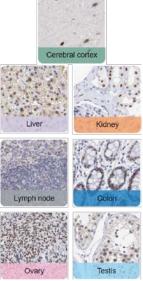
Structural Hierarchy of the Human Body



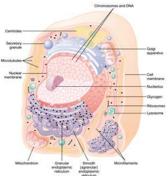
Level 7: The Body Level 6: Organs



Level 5: Tissues



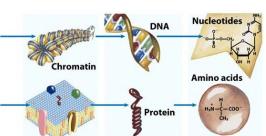
Level 4: The Cell and its Organelles



Level 3: Supra

Supra Level 2: molecular Macro Complexes molecules

Level 1: Monomeric Units



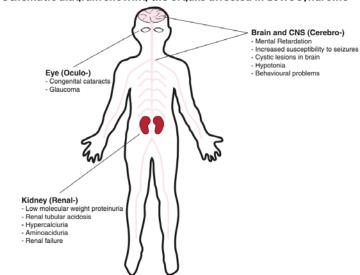


Hypothesis Developed and Being Worked On



- Spaceflight changes the physical properties of the cell components impacting from the molecular to the whole body level.
- The Mitochondria are the principal cellular component affect.
- The Liver is the principal organ affected in issues related to the metabolism.
- Possible disease that can be associated with liver damage and pathways is: <u>Oculocerebrorenal Syndrome of Lowe</u>
 - "Extensive research has demonstrated that OCRL-1 is involved in multiple intracellular processes involving endocytic trafficking and actin skeleton dynamics. This explains the multi-organ manifestations of the disease."
 - "The classic form of the oculocerebrorenal syndrome of Lowe (OMIM #309000), first described by Lowe et al. in 1952 [1], is characterized by the triad of congenital cataracts, severe intellectual impairment, and renal tubular dysfunction with slowly progressive renal failure"
 - Patients with this disease manifest Cataract, Glaucoma and Muscle hypotonia.

Schematic diagram showing the organs affected in Lowe syndrome

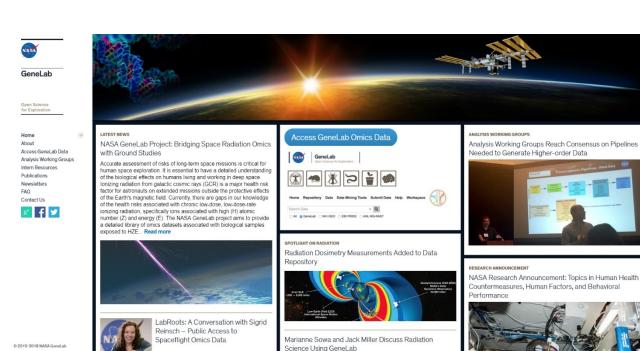


Mehta, Zenobia B et al. "The Cellular and Physiological Functions of the Lowe Syndrome Protein OCRL1." *Traffic* (2014).



Engaging with GeneLab





https://genelab.nasa.gov

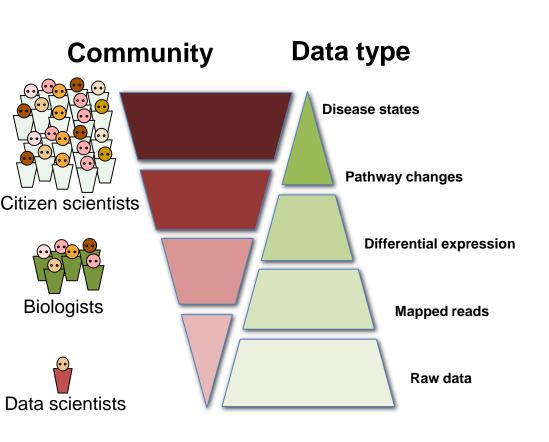
Participate in GeneLab Analysis Working Groups

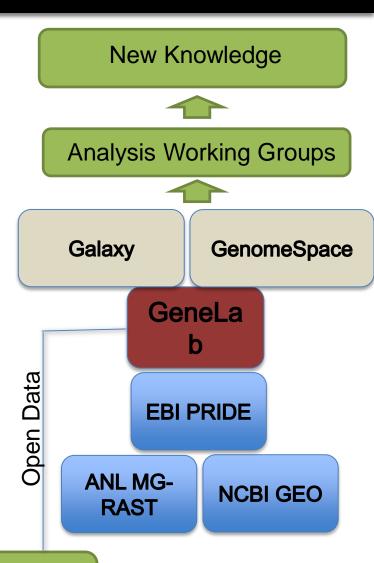
- Social media :
 - @NASAAmes Facebook
 - Twitter #GeneLab
 - ResearchGate: https://www.researchgate.net/project/Omics-for-Space-Biology-The-GeneLab-project



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Missions/Experiments

GeneLab Sample Processing

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Open Science for Exploration

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