

## ABSTRACT

Immune dysregulation is a recognized phenomenon during spaceflight, including impaired macrophage differentiation and function. Activated macrophages exist in polarized phenotypes, such as M1 macrophages, which produce primarily pro-inflammatory mediators and M2 macrophages that are involved in anti-inflammatory processes and tissue repair. Effective macrophage polarization processes are vital for generating appropriate immune responses and facilitating recovery on Earth and in spaceflight. To gain deeper insight into macrophage polarization processes in spaceflight, we analyzed open-sourced, GeneLab lung tissue transcriptional datasets (OSD-248) from mice previously flown on the Rodent Research (RR)-6 mission. Mice were euthanized on-board the ISS after a 60-day mission. Preliminary analysis revealed an overall decrease in both M1/M2 biosignatures in spaceflight compared to ground controls. Interestingly, select M2 biosignatures were significantly reduced compared to M1, suggesting deficits in tolerogenic/anti-inflammatory activity and a shift towards pro-inflammatory states. In a ground-based study simulating spaceflight conditions, male and female C57BL/6J mice were exposed to simulated galactic cosmic ray radiation combined with hindlimb unloading and social isolation. To assess M1/M2 predominance in the lung and to test the fidelity of a single cell isolation protocol, total macrophages were isolated from frozen-stored lung tissue two weeks post-irradiation exposure. Cells were positively selected for using the F4/80 biomarker, and lung resident and infiltrating macrophage subtypes (M1 and M2) were characterized by flow cytometry, including F4/80, CD170, Arginase-1 (M2), and iNOS (M1). Future studies using tissues from space-flown RR-20 mice will further validate the definition of M1/M2 macrophages in the lung. In summary, characterizing polarized macrophage populations within the lung microenvironment is crucial for advancing our understanding of immune responses in spaceflight, particularly for lunar missions, where astronaut pulmonary physiology will be challenged by unique lunar environmental soil.

## INTRODUCTION

- Radiation exposure in the spaceflight environment can trigger immune-related responses, including oxidative stress and inflammation, which lead to immune suppression that is sexually dimorphic.
- (Alveolar macrophages) AM are lung tissue-resident cells that play a vital role in innate respiratory barrier immunity.
- AM functionality is compromised due to the heightened vulnerability of astronauts to infectious pathogens and the exacerbation of inflammatory responses from foreign molecules.
- M1 and M2 are polarized macrophage (AM and infiltrating) phenotypes, which can promote pro-inflammatory and tolerogenic/tissue repair processes, respectively.

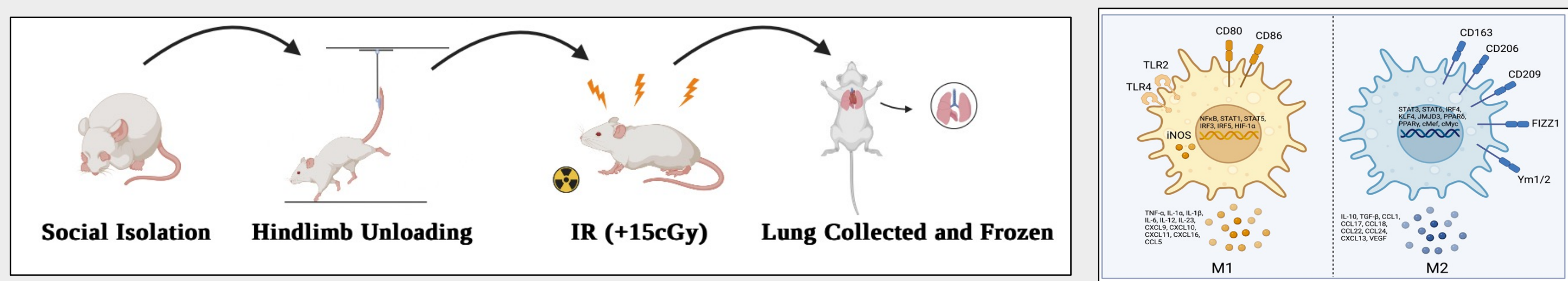
### Hypothesis

Males and females will produce elevated inflammation through elevated iNOS promoting M1 vs M2 populations in the lung, which may be enhanced in males.

### Objectives

- Characterize lung tissue profiles through NASA's Open Science Repository: ground v. spaceflight
- Develop an experimental protocol to isolate lung AM from ground and spaceflight studies, to prepare for upcoming Rodent Research (RR)-20 mission.

## EXPERIMENTAL DESIGN



- Raw transcriptome differential gene expression (DEG) datasets from the RR-6 mission characterizing M1 and M2-related genes from ISS and ground controls (GeneLab OSD-248).
- All mouse lung tissues were shared from the parent HRP funded grant (PI: Dr. April Ronca) for these studies. Male and female mice (24-weeks old) were socially isolated for 7-days prior to experiment start date. Mice experienced simSpace via hindlimb unloading for 14 days, followed by 5-ion simplified galactic cosmic ray (GCRsim) radiation at 15 cGy, followed by euthanization and lung tissue collection/frozen on day 28.
- Frozen lung samples were mechanically digested and positively selected using the EasySep™ Positive Selection Kit and magnetic separation (F4/80).
- Macrophages subjected to fluorophore staining (M1 = proinflammatory (F4/80+, CD170<sup>high</sup>, iNOS<sup>+</sup>); M2 = anti-inflammatory (F4/80+, CD170<sup>high</sup>, Arginase-1<sup>+</sup>) and acquired using a Sony SH800 flow cytometer with FlowJo post-processing analysis to identify population median fluorescence intensity (MFI) of M1 or M2 biomarkers per experimental cohort.

## RESULTS

M1 Biomarkers	Log FC	Negative Log p value	M2 Biomarkers	Log FC	Negative Log p value
Tnf	-1.066	2.526	Pparg	-1.701	5.481
Hif1a	-0.322	1.397	Cd163	-1.735	4.781
Cxcl10	-0.819	0.986	Arg1	-1.70712	2.22184875
Il1b	0.543	0.902	Ccl24	-1.732	2.197
Ccl8	-0.390	0.858	Cxcl13	-2.082	2.183
Ccl9	-1.104	0.842	Il10	-0.14655	1.29319737
Il1a	-0.284	0.575	Il10	-1.304	1.236
Stat1	-0.168	0.573	Mrc1/Cd206	-0.417	1.199
Nlrp1	0.123	0.461	Cd209a	-0.270	0.923
Tlr4	-0.225	0.451	Plehl1a	-0.433	0.725
Ccl5	0.234	0.395	Ccl68	-0.308	0.58670024
Irf5	-0.184	0.297	Ccl17	0.444	0.577
Cxcl16	0.101	0.245	Tgfb1	0.260	0.378
Il6	-0.250	0.231	Vegfa	0.135	0.302
Il12b	-0.120	0.216	Tlr8	-0.1160802	0.226056327
Ccl8	-0.129	0.168	Chil3	0.150	0.187
Il23a	-0.176	0.096	Ccl1	-0.526	0.139
Il12a	-0.078	0.095	Stat3	0.040	0.095
Irf3	0.042	0.092	Stat6	-0.039	0.070
Tlr2	0.023	0.078	Pparg	-0.045	0.048
Stat5b	-0.043	0.072	Il10ra	-0.03136	0.04261855
Nos2	-0.023	0.026	Ccl22	0.023	0.038
Cxcl11	0.020	0.007	Klf4	-0.008	0.015

Table 1. Table indicate depiction of the differential expression of M1 and M2 genes in AMs under ISS conditions compared to ground controls.

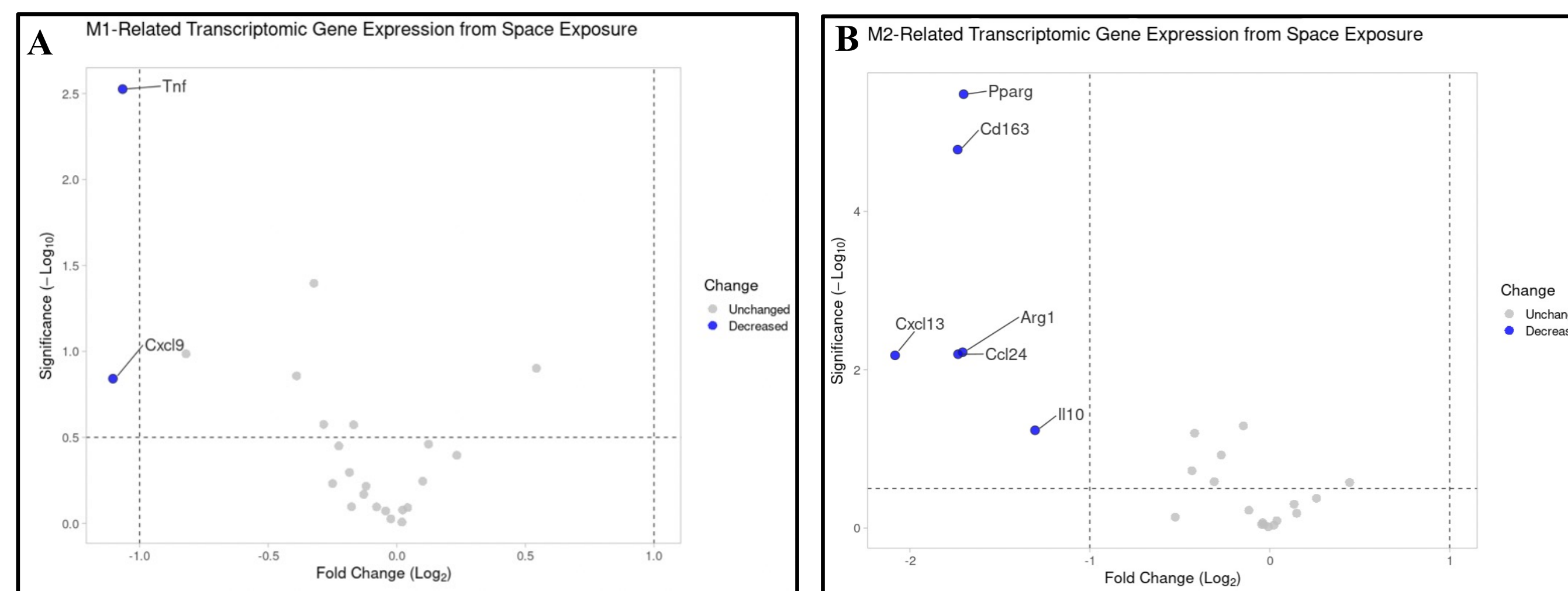


Figure 1. Volcano plot displays differential gene expression profile of M1 under ISS conditions compared to ground control (A) and profile of M2 macrophages in response to ISS conditions relative to ground control (B). Plots demonstrate distribution of log2 fold change (x-axis) against -log10 of the adjusted p-value (y-axis). Genes displaying a fold change greater than -1 and a significance level of 0.5 are highlighted. Notably Tnf and Cxcl9, identified as significantly downregulated genes in M1 (A) and significant downregulation of crucial genes including Pparg, Cd163, Cxcl13 (B).

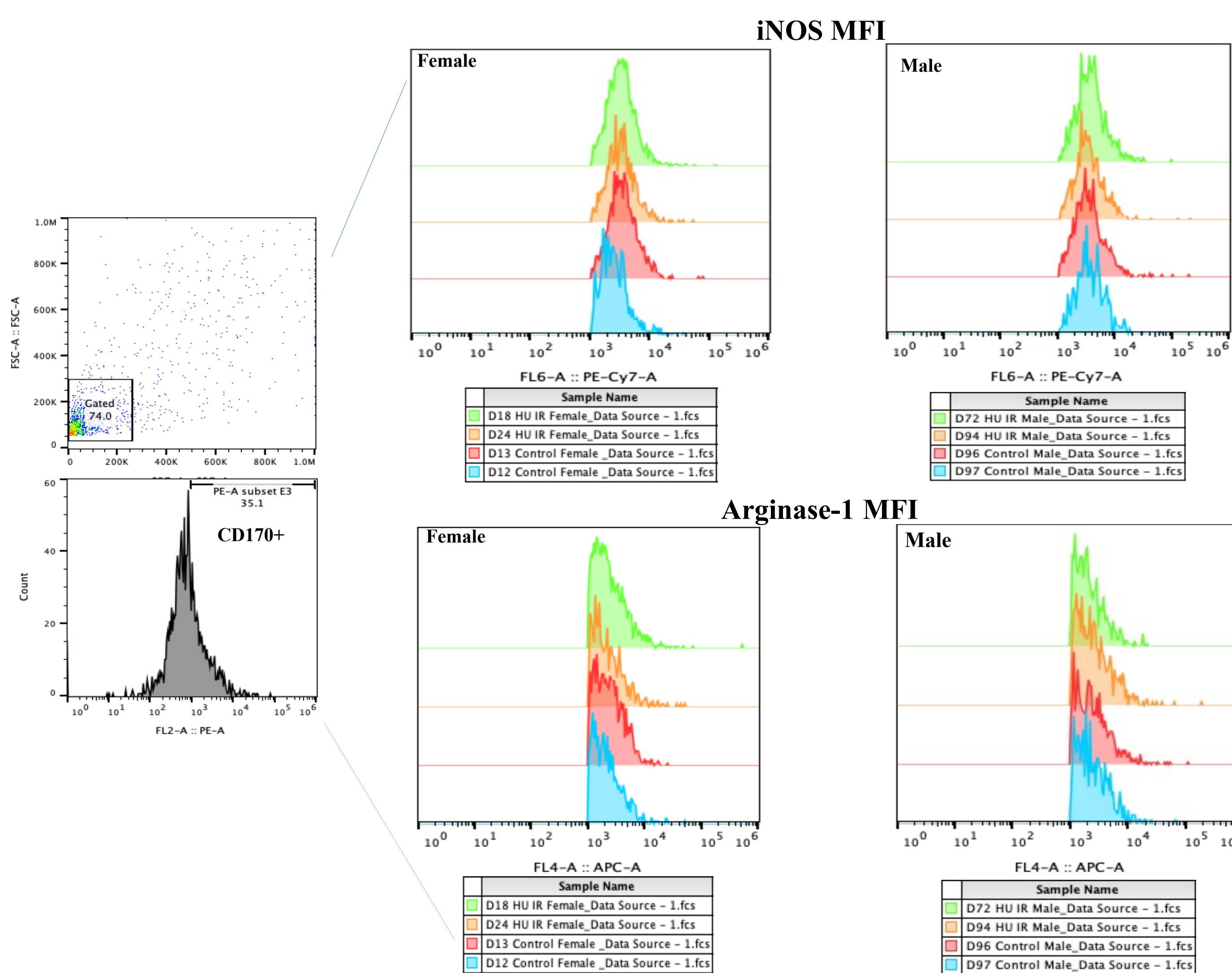


Figure 2. Flow cytometric analysis gating scheme of M1 and M2 Median Fluorescence Intensity (MFI) of iNOS (M1) and Arginase-1 (M2), within CD170+ AM. All flow acquisitions were performed on a Sony SH800 instrument and FlowJo (v10).

NASA GeneLab's Open Science Data (OSD)-248 RNA transcriptomic DEG profiling of female (32-week-old) C57BL/6NTac mice lung tissue collected on board the ISS day 30 of mission duration were preliminarily characterized.

- Overall decreased M1 and M2 biosignatures
- M2 biomarkers were significantly reduced more so than M1 biomarkers
- Suggest predominance of M1 macrophages phenotypes in spaceflight.

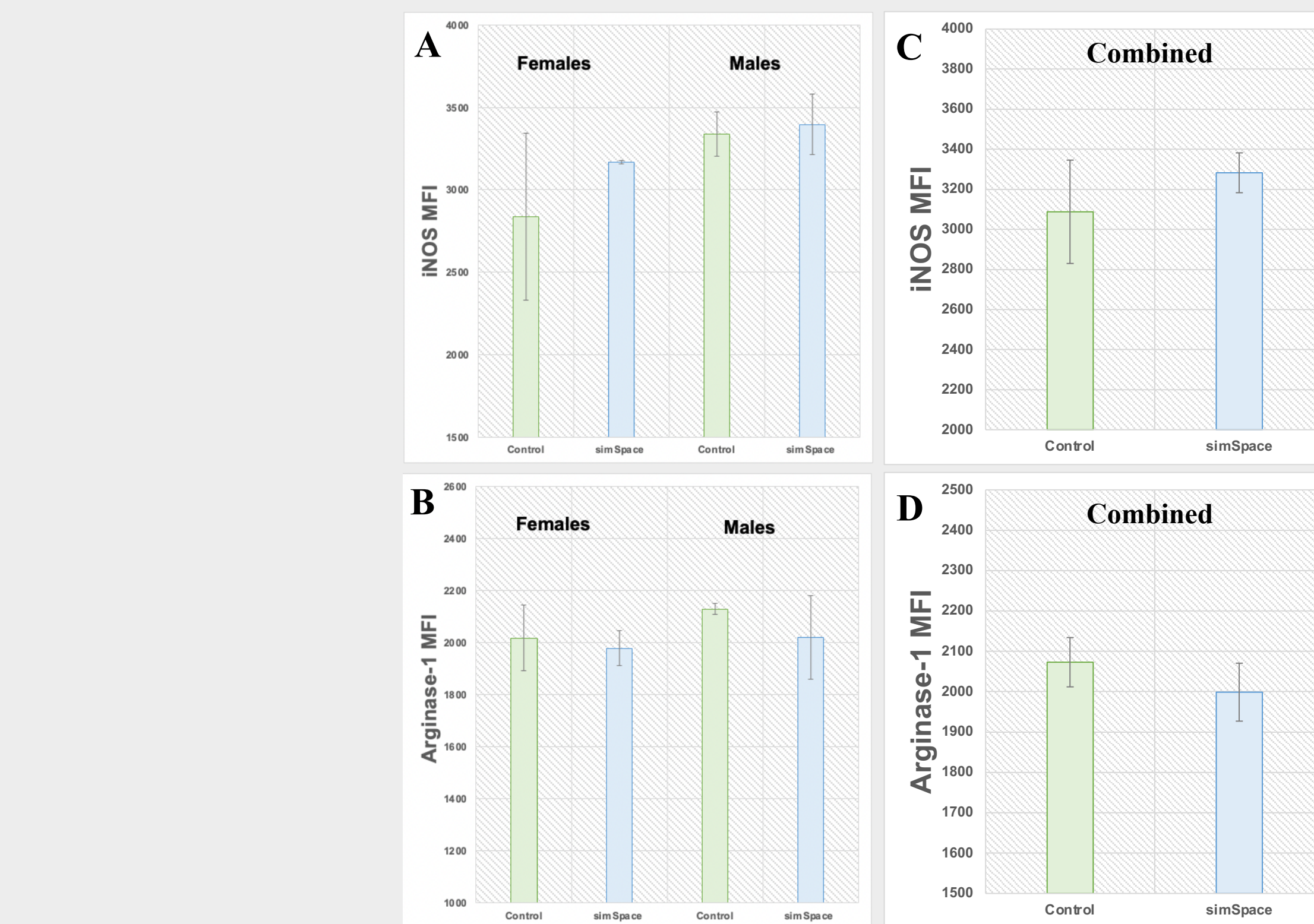


Figure 3. Bar chart represents dimorphic male and female expression levels of iNOS (M1) and Arginase-1 (M2) (A and B) and combined male and females are displayed (C and D). MFI results for M1 (iNOS) and M2 (Arginase-1) phenotypes within CD170+ AM.

- Absence of statistically significant differences, due to low sample size (n=3M/3F per group) and variance.
- Observable decrease in the mean fluorescence intensity (MFI) of Arginase-1 was detected in the simSpace group when compared to the controls.
- Reduced trends in Arginase-1 MFI suggests potential predominance of M1 phenotypes within the simSpace environment, implying a shift towards a pro-inflammatory state within the lung in response to simSpace conditions.

## CONCLUSION

- Analysis from the OSD-248 revealed downregulation in the expression of both Arginase-1 and iNOS between the control and simSpace conditions, suggesting impaired differentiation/polarization processes, with a predominance of M1 macrophages are noted.
- Ground simSpace studies displayed observable differences in M1 and M2 population shifting in simSpace, favoring M1 predominance.
- Observed dimorphism, with males displaying higher M1 mean fluorescence intensity (MFI) compared to females, suggests potential sex-specific responses post simSpace recovery.

## LIMITATIONS OF STUDY

- Availability of a limited number of frozen lung samples constrained the depth of the analysis and restricted the ability to draw robust conclusions. Frozen cells have reduced cell viability, integrity, and staining variability potentially influencing the obtained results.
- Accessibility to fresh lung samples from spaceflown mice will be instrumental in advancing research in this area, allowing for the implementation of the newly developed protocol.

## FUTURE STUDIES

- Future research aims to elucidate the precise molecular mechanisms underlying the observed phenotypic changes in lung macrophages in response to simulated microgravity.
- Ongoing investigation with space-flown RR-20 mice aims to further validate the definition of M1/M2 macrophages in the lung, emphasizing the role of characterizing polarized lung macrophage populations in comprehending immune responses during spaceflight and the challenges posed to astronaut pulmonary physiology by unique environmental conditions.

## ACKNOWLEDGMENTS

This research was funded in part by the Gerald A. Soffen Memorial Fund, NASA Human Research Program (HRP) Human Factors Behavioral Performance Element Grant 18-18FLAG-2-0028, and Embry-Riddle Aeronautical University startup funding.