Fiscal Year:	FY 2015	**Task Last Updated:**	FY 07/11/2014
PI Name:	Lorenzi, Hernan Ph.D.		
Project Title:	Study of the Impact of Long-term Space Travel on the Astronaut's Microbiome		
Division Name:	Human Research		
Program/Discipline:	HUMAN RESEARCH		
Program/Discipline--Element/Subdiscipline:			
Joint Agency Name:		**TechPort:**	No
Human Research Program Elements:	(1) **HHC**:Human Health Countermeasures		
Human Research Program Risks:	(1) **Medical Conditions**:Risk of Adverse Health Outcomes and Decrements in Performance Due to Medical Conditions that occur in Mission, as well as Long Term Health Outcomes Due to Mission Exposures (2) **Microhost**:Risk of Adverse Health Effects Due to Host-Microorganism Interactions		
Space Biology Element:	None		
Space Biology Cross-Element Discipline:	None		
Space Biology Special Category:	None		
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PI Organization Type:	NON-PROFIT	**Phone:**	301-480-0648
Organization Name:	National Institute of Health		
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City:	Bethesda	**State:**	MD
Zip Code:	20892	**Congressional District:**	8
Comments:			
Project Type:	FLIGHT	**Solicitation / Funding Source:**	2010 Crew Health NNJ10ZSA003N
Start Date:	10/01/2011	**End Date:**	09/30/2016
No. of Post Docs:	0	**No. of PhD Degrees:**	0
No. of PhD Candidates:	0	**No. of Master' Degrees:**	0
No. of Master's Candidates:	0	**No. of Bachelor's Degrees:**	0
No. of Bachelor's Candidates:	0	**Monitoring Center:**	NASA ARC
Contact Monitor:	Bhattacharya, Sharmila	**Contact Phone:**	
Contact Email:	Sharmila.Bhattacharya@nasa.gov		
Flight Program:	ISS		
Flight Assignment:	ISS NOTE: Extended to 9/30/2016 per A. Chu/ARC (Ed., 8/5/14) NOTE: Gap changes per IRP Rev E (Ed., 3/19/14)		
Key Personnel Changes/Previous PI:	August 2012: Scott Peterson (former co-PI of the project) and Shannon Williamson (key personnel) are not participating in this project any more. Drs. Mark Ott and Duane Pierson are collaborators on this project. July 2014: Manolito Torralba and Dr. Satish Mehta have been incorporated as key personnel.		
COI Name (Institution):	Pierson, Duane (Johnson Space Center) Ott, Charlie (Johnson Space Center)		
Grant/Contract No.:	NNX12AB02G		
Performance Goal No.:			
Performance Goal Text:			

Task Description:	Our goal is to determine how the composition of the human microbiome changes during long-term space exploration and to evaluate its potential impact on astronauts' health. Some microbial species from the human microbiome have a beneficial or protective effect on health; the loss of these species can lead to an altered metabolic function and, in conjunction with reduced immune response, may increase the chance of infection by opportunistic pathogens. In our proposal we will elaborate the notion of the microbiome as harbingers or sentinels to monitor a variety of aspects of the human host, including associations with health status, environmental stress, and exposure to space conditions. By sampling the microbiome of astronauts on Earth while in peak physical health and during subsequent times of stress, including long-term exposure to microgravity, g-forces, radiation, and changes in health status, we will be able to define signatures of human response to a variety of relevant aspects of space travel. We propose to characterize the bacterial and viral microbiome from various body sites of up to nine astronauts who travel to space at several time points before, during, and after a space mission. Also we will assess the astronauts' immune function before, during, and after the mission by analyzing their collected saliva samples for reactivated latent viruses and cortisol levels, two indicators commonly evaluated during spaceflight immune and stress studies and cytokines from blood samples. Finally, we will correlate the collected microbiome and immune function data with other measured metadata including astronaut health and hygiene as well as environmental factors such as temperature, humidity, and environmental microbial samples that will be collected, depending upon availability, from various surfaces on the International Space Station.
Rationale for HRP Directed Research:	
Research Impact/Earth Benefits:	The results of this study will provide insights into how the microbial population of the environment affects the composition and dynamics of the human microbiome. This is relevant to studies of respiratory diseases such as asthma and allergies. Investigating the impact of stress and status of the immune system on the human microbiome, and potentially on human health, during a space mission is also applicable to equivalent stressful situations on Earth. Some of the conclusions of this project will also be useful in situations where a group of individuals are confined in a relatively small and closed space for a long period of time, such as a submarine crew.
Task Progress:	1. Base Data Collection All nine subjects required for the study have been already recruited. Collection of pre-flight, in-flight, and post-flight samples started in February 2013. Three batches of swab and fecal samples have been delivered to JCVI and are currently being processed. Collected saliva and blood samples have been sent to JSC for measurement of cytokines and stress levels. 2. Comparative analysis of phylogenetic profiles The V1-V3 variable region of the bacterial 16S rRNA gene was amplified by PCR from total DNA extracted from 28 swab samples (7 forehead, 7 forearm, 7 nares, and 7 tongue) and 11 fecal samples derived from six different subjects and sequenced using Illumina technology. All samples correspond to baseline pre-flight time points (L-240, L-150, L-90, and L-60). To characterize spatial and temporal changes in the taxonomic composition of the samples, 16S rRNA sequences were run through the JCVI 16S pipeline to identify operational taxonomic units present in each of the pre-flight samples analyzed. The results show that microbial communities isolated from the same body-site presented similar taxonomic profiles that were consistent across subjects. As it has been previously described for the Human Microbiome Project, the baseline composition of microbial communities varied from site to site, with skin and nose microbiomes being more similar to each other than to those from feces or mouth. A more in-depth analysis of the most frequent genera present in each of the five body habitats sampled also demonstrated that taxonomic profiles were consistent with those from other 16S-based studies. To evaluate the stability of microbial communities assessed in our study we performed a spatial and temporal comparison of alpha and beta diversity. Our analysis did not reveal any significant change in alpha diversity (Shannon diversity index) between time points L-90 and L-60 for any of the five habitats tested (p-value > 0.05). Similarly, we did not find any significant shift in beta diversity (Sørensen similarity index) between time points L-90 and L-60 compared to the baseline community L-150. However, comparisons of intra- versus inter-site beta diversity confirmed that the human microbiota from the five sampled sites was significantly different (p-value < 0.01), with the exception of nares and forehead (p-value = 0.3). These results supported our previous observations that taxonomic profiles are similar among samples from the same body-site but not between different habitats. Finally, we did not find any significant difference between intra-vs-interpersonal variability of beta diversity. In conclusion, our results from baseline samples did not show any significant temporal change in alpha or beta diversity. Similarly, we did not observe any significant difference between beta diversity values within and between subjects, although it is known that interpersonal microbiome variability tends to be higher than samples isolated from the same individual. This apparent microbiome stability at the baseline is most likely to be the result of the small number of samples analyzed and it is expected that with the incorporation of additional samples we will be able to reach more conclusive results. Currently, we are processing two additional set of samples that include in-flight and post-flight samples as well as environmental samples from the ISS. The incorporation of these samples will provide the first indication of whether and to what extent space travel alters the human microbiome.
Bibliography Type:	Description: (Last Updated: 04/10/2021)
Abstracts for Journals and Proceedings	Ott CM, Mehta S, Torralba M, Gillis M, Pierson DL, Lorenzi HA. "Study of the impact of long-term space travel on the astronauts' microbiome." 2014 NASA Human Research Program Investigators' Workshop, Galveston, TX, February 12-13, 2014. 2014 NASA Human Research Program Investigators' Workshop, Galveston, TX, February 12-13, 2014. http://www.hou.usra.edu/meetings/hrp2014/pdf/3092.pdf , Feb-2014