Study of the impact of long-term space travel on the astronauts' microbiome.

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The human microbiome (HM) is defined as the collection of all microorganisms that inhabit the human body. Many studies have shown that the HM plays an important role in human health contributing to the processing and absorption of nutrients and/or playing a protective role by stimulating the immune system or competing for resources with pathogenic organisms. Therefore, changes in the dynamic or composition of the HM may alter the human metabolism or increase the likelihood of infections. It is known that factors such as stress, diet and deregulated immune system can trigger changes in the HM, increasing the risk of contracting a disease. During a space mission, astronauts are continuously exposed to a series of stressors (microgravity, anxiety, various g-forces, increased radiations, diet changes, etc.) that can potentially alter the composition and dynamic of the astronauts' microbiome. In agreement with this hypothesis, studies done on culturable bacteria from the astronauts' gastrointestinal tract revealed that space travel not only affects the composition of the intestinal flora but also may increase the virulence of pathogenic bacteria. In this context, our working hypothesis is that long-term exposure to stressors specifically associated with spaceflight alter the dynamics and composition of the HM posing a risk to the health of astronauts. To test this hypothesis, we are carrying out a longitudinal study to characterize the changes in the prokaryotic and viral microbiome from the skin, nares, mouth and gastrointestinal tract of up to nine astronauts that will travel and remain in the International Space Station for at least 6 months. We will measure cortisol levels and reactivated latent viruses from saliva samples, two indicators commonly used to evaluate stress levels and immune function. The immune response will also be assessed by measuring cytokine levels from blood samples. Finally, we will investigate if changes in the HM correlate with other measured metadata including astronaut health and hygiene as well as environmental factors such as temperature, humidity and environmental metagenomic data that will be collected from various surfaces of the International Space Station. Currently we have recruited 6 subjects to the study and collection of samples has started on February 2013. Initial processing of the first batch of swab samples showed that it is possible to extract enough DNA per sample to amplify the v1-v3 variable region of the 16S ribosomal gene from the isolated DNA. Here we will present an update of the current status of the project.