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Analysis of bacterial profiles of AGBRESA participants – a study concerning terrestrial astronauts under simulated microgravity

Introduction:
Long-term space missions are accompanied by harmful environmental conditions like microgravity. Due to the reduced gravity, astronauts adapt to their environment resulting in tissue fluidic shifts. Since the knowledge about microbiome data in space is sparse and conduction of experiments at the ISS is complex, suitable analogs are needed. Therefore, the first cooperative bed-rest study called Artificial Gravity Bed-Rest study with ESA (AGBRESA), by NASA, ESA and DLR offered optimal features to investigate possible correlations between microbial shifts and physiological microgravity by using -6° head-down-tilt (HDT). The aim of this survey was to identify changes within the standardized conditions, such as diet and wrongly distributed tissue fluids to reveal causal connections among health state and microbial communities.

Methods:
Microbiological tests were performed in both, campaign I and II with each 12 participants. All test subjects experienced a 15-day Baseline Data Collection (BDC), a 60-day Head-Down-Tilt (HDT) and a Recovery (R) of 14 days. In campaign I, at regular intervals swab samples from forehead skin and ears were taken. Physiological skin parameters (pH, hydration level & sebum content) were measured using dermatological probes by Courage+Khazaka. For the analysis of changes in the gut microbiome, stool samples were taken from all test subjects during campaign II.
Microbial determination was performed by the isolation of genomic DNA (DNA powersoil Kit, Qiagen), amplification of V4 region of the 16S rRNA gene by PCR and sequencing of the products on Illumina platform.

Results:
During HDT the microbial analysis of the skin revealed a significant increase of lipophilic Cutibacteria and Corynebacteria with simultaneous accumulation of sebum and water on forehead skin whereas populations of *Acinetobacter sp*. decreased. As latter are usually found on dry skin, shifted skin parameters are confirmed, thus indicating an instable skin barrier. Concerning ear infections, *Pseudomonas sp*. was identified as the responsible pathogen while signatures of Staphylococci, Cutibacteria and Corynebacteria were only observed in the healthy ear. Hence, low abundances of these possibly beneficial genera could initiate the infection process of pseudomonads. After first antibiotic treatment, the pathogenic organism was highly reduced while healthy flora was almost restored to its origin state. Furthermore, the microbiome analysis showed individual compositions on participants' skin.

Conclusions:
The evaluation of the stool samples is still pending. To cover all fields of the systems biology, proteomics and metabolomics analyses will be here conducted.
In order to maintain astronauts' health and life-saving equipment for future space missions, these first data could help to develop appropriate countermeasures like probiotics or skincare.