

Letter

Revamping Space-omics in Europe

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Space science is having a new awakening with the recent launch of the SpaceX Crew Dragon capsule on May 30 to the International Space Station (ISS), the NASA Perseverance Rover Mission to Mars in July, the launch in 2022 of ExoMars to search biosignatures of past Martian life, and other future human exploration missions. Many of these initiatives involve molecular biology experiments, some related to extra-terrestrial astrobiology but most to understand how radiation and microgravity affect terrestrial known forms of life in space when compared with a ground control. Among these projects are the introduction of nanopore sequencing on board of the ISS (Castro-Wallace et al., 2017) and the planned creation of a new ISS stem cell laboratory to better understand some forms of hematological malignancies or neurodegenerative diseases using brain organoid technology by UC San Diego and Space Tango. This research might accelerate our understanding of many (patho)physiological processes such as cellular development, cancer, and aging. Furthermore, these experiments are necessary to ensure that the health of astronauts during long-term spaceflight is not at risk because of a depressed immune response or an increased risk of opportunistic bacterial infection (Sonnenfeld and Shearer, 2002; Taylor, 2015), the recently uncovered mitochondrial impairment (da Silveira et al., 2020), bone and muscle

loss (Collet et al., 1997), and possibly cardiovascular disease, cognitive decline, or tumor development (Löbrich and Jeggo, 2019).

Many of these molecular biology experiments will generate big omics datasets by next-generation sequencing. Currently, big data is not a major feature of space biology research. However, the recent NASA twins study (Garrett-Bakelman et al., 2019) highlights part of the potential increase in omics data that we can capture in people and biological organisms in space. This study included epigenomics, transcriptomics, metabolomics, and proteomics, among others. In order to consider how we use big data in space to predict and prevent health related issues in astronauts, and to advance on medical and biological research on Earth, several questions arise: what data to capture, and how to store, process, use, and understand this data?

To facilitate the storage, analysis, and visualization of omics data from spaceflight and corresponding analog experiments in Earth, NASA created GeneLab, an open access resource for space biology experiments (Ray et al., 2019). Its core mission is to enable scientific discovery and space exploration through multi-omics data-driven research. The GeneLab Data System (GLDS) includes experiments with various levels of gravity, high radiation, extreme temperatures, and suboptimal composition of the atmo-

sphere and culture media (e.g., nutrients, pH, humidity). GLDS includes an interface to search datasets on key repositories, such as NIH GEO, EBI PRIDE, and ANL MG-RAST. Joint NASA/ESA discoveries made using GeneLab have begun and will continue to deepen our understanding of biology and advance the field of genomics (da Silveira et al., 2020; Overbey et al., 2019). A unique feature of GeneLab is that it has created a very successful collaborative workspace by means of four Analysis Working Groups (AWGs) in Plants, Microbes, Animals-Humans, and Multi-Omics, in which many of the Europe-based authors of this correspondence letter are active members. In fact, two AWGs are co-chaired by members of the European Space Agency (ESA) scientific community.

To support ESA member state scientists participating in GeneLab, to promote and support the use of Omics research by the ESA Space Biology community, and to study and implement future GeneLab based activities for ESA member state scientists, we have formed the Space-Omics ESA Topical Team (TT). The team includes members with expertise in space biology, bioinformatics, multi-omics, and spaceflight data experimentation. Examples of current activities of the TT include bi-lateral cooperation on future space biology experiments, co-authorship on original research, and bi-lateral exploration of incorporating human biology



datasets into GeneLab. Examples of potential future activities include establishing physical or virtual ESA supported GeneLab infrastructure, incorporating GeneLab-based experiments in new launch/operational platforms, partnering ESA ground and space based human biology experiments with GeneLab, and the organization of events and training sessions to integrate the ESA Space Biology Community Omics efforts.

Our TT will support the full integration of the interested ESA scientific community into the GeneLab NASA-led venture, while also exploring the opportunities of new ESA-led scientific ventures exploring Big Data and Omics research, as the global initiative *International Standards for Space Omics Processing* (ISSOP; <https://issop.space>) including JAXA scientists to optimize data processing and space biology experimental designs (Rutter et al., 2020; Manzano et al., 2020). Scientifically, the TT will engage in three broad areas of activity: (1) bi-lateral generation of new omics datasets for space biology, (2) bi-lateral participation in shaping omics approaches to space biology via GeneLab, and (3) Exploring how best to support the ESA scientific community in employing omics approaches to space biology. We envision

that this team will add new perspectives and scientific expertise to bioinformatics and omics-based space biology research, which will benefit space biology science in Europe and strengthen links and synergies with our colleagues at NASA GeneLab.

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