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Research Article,

Exploratory Tool for Radiation Exposure from Spaceflight: Rad-Bio-App

Dr Debopriya Ghosh[1], Dr Ekta Verma[2], Mr.Romel Kumar Ghosh[3], Dr.Tim Anderson[4]

[1]Senior Resident, Department Of Physiology, University College of Medical Sciences, New Delhi
[2]Department of Paediatrics, All India Institute of medical Sciences, Gorakhpur, India
[3]University of Calcutta, Kolkata, India
[4]Graduate Student, University Of Cinciniati, Usa

Abstract:

Spaceflight concurrently subjects biology to a variety of different stressors in addition to microgravity. For instance, ionising radiation conditions that organisms encounter in space differ significantly from those they typically encounter on Earth in terms of both quality and quantity. However, accessing and comprehending data on radiation exposure during space missions is sometimes difficult, which hinders research into how radiation affects organisms in the particular context of spaceflight. We created the Rad-Bio-App to aid with this problem. The user may examine these experiments both in terms of their radiation exposure and via their other metadata and outcomes using this web-accessible database, which imports radiation metadata from experiments preserved in NASA's GeneLab data repository. In order to help radiation biologists and non-specialist researchers view and comprehend the effects of ionising radiation on diverse biological systems in the context of spaceflight, Rad-Bio-App offers an intuitive, graphically driven environment.

Keyword: Space Biology, Omics, Metadata, Standardization, Genelab, ISSOP.

Introduction:

The environment in space presents organisms with a distinctive set of difficulties. For instance, the isolation brought about by the large distances travelled and the restricted environment of spacecraft for humans all have a significant influence on the physiology and psyche of the crew. Many of these impacts are being investigated in Earth-based analogues, such as the Scientific International Research in Unique Terrestrial Station missions1,2 and the Hawaii Space Analog and Simulation. Some aspects of space, however, are difficult or impossible to duplicate on the surface of the Earth, necessitating exploration through the comparatively seldom chance of a spaceflight experiment. Examples include prolonged exposure to microgravity and increased ionising radiation, both of which are beyond the experience of terrestrial life and are now very difficult to simulate on the surface of the Earth. In spite of this, it is still unclear how their separate and combined impacts on biology affect how organisms adapt to live in space.

Because of the atmosphere's radiation-shielding properties and the magnetosphere's capacity to redirect radiation away from the planet, Earth's organisms have been mostly shielded from space radiation for much of its history. Despite the fact that terrestrial life is exposed to UV radiation from the Sun and natural background radiation from geological sources, this exposure is relatively low compared to space, with an average annual dose equivalent per person in the US of around 6 mSv3, depending on altitude and soil composition (e.g., the presence of minerals that produce radon gas). The radiation exposures in deep space will be substantially greater and contain highly ionising single particles that are not often observed on Earth. Based on data from the Radiation Assessment Detector (RAD) on the Mars Science Laboratory (MSL) during its cruise phase from Earth to Mars and the measurements it made on the Martian surface, the crew on a

roughly 1000-day mission to Mars, assuming "quiet" periods of solar activity throughout, would experience an increase in the amount of radiation that would be emitted from the planet. 360 mGy of the total dosage are absorbed, with the majority coming from highly ionising galactic cosmic ray (GCR) ions4,5. This is comparable to the absorbed background dosage over several decades on Earth, but, as already mentioned, it comes from a totally different radiation spectrum and is administered at a very different dose rate. It is difficult to generalise from terrestrial models to the spaceflight environment since all of these elements are likely to have an impact on the specific effects that radiation exposure will have on the crew of such a trip.

In fact, it has been demonstrated that exposure to space radiation has greater harmful effects in tissues than comparable ionising radiation doses on Earth, with, for example, up to 40 times higher biological efficacy in inducing Harderian gland tumours in mice6. Radiation exposure in animals can cause a variety of cellular and microenvironmental consequences, such as chronic inflammation, tissue deterioration, and compromised nerve function, in addition to the development of cancer (e.g., refs. 7,8). In fact, radiation has an impact on all living things. Animals, microorganisms, and plants all experience different cellular events as a result of radiation, such as DNA damage, oxidative stress, and changes in metabolism9,10. Radiation tolerance varies among species, and within a species, genetics can influence a person's radiation response11–14. As an illustration, bacteria of the species Deinococcus can withstand radiation doses that are far higher than those that would be fatal to humans15. The influence of the spaceflight environment, such as surviving in microgravity, which itself affects an organism's radiation response, further complicates the prediction of such consequences (e.g., refs. 16–18). Assessing the dangers of radiation exposure to crew members on lengthy, deep space missions is highly difficult19,20 due to the complexity of the potential biological impacts and the relatively few possibilities to conduct direct spaceflight studies. However, it becomes more crucial to address the topic of how various species react to the impacts of greater space radiation exposure and the possibility of interactions with, for example, the micro-gravity of spaceflight, as the length and distance of spaceflight missions rise. Radiation exposure data from a lot of biology-focused spaceflight experiments have not yet been published, and even when they have, they are sometimes difficult to access. The NASA GeneLab project, which serves as a repository for genomic, transcriptomic, proteomic, and metabolomic data from studies conducted in space or subjected to simulated space stressors, has identified this gap.21–23 The GeneLab data repository aggregates relevant metadata into a freely available database known as the GeneLab Data System together with the raw omics datasets (GLDS21,22). The network of molecular reactions to space settings may then be explored as a function of the experimental conditions listed in the metadata by mining GeneLab's omics data. The majority of the radiation information connected to GeneLab's spaceflight-related datasets24 has now been compiled. In other words, the GLDS now offers the data and information necessary for drawing general conclusions regarding radiation impacts in various taxa and across various sets of spaceflight studies. In order to allow the scientific community to use unique tools to view and analyse this data in ways that complement those offered by GeneLab's own data visualisation site, the GeneLab Application Programming Interface (API) also makes these data accessible to external web apps. In the work discussed here, we introduce the Rad-Bio-App (https://astrobiology.botany. wisc.edu/astro-rad-bio-app), one such bespoke visualisation tool. To give researchers an interactive graphical interface via which they can examine, filter, and compare radiation dosimetry and other information throughout the GLDS, Rad-Bio-App takes use of the "FAIR-ness" standards and extensive data curation of the GLDS25. The user can define datasets with possibly common radiation effects or investigate connections between radiation exposure and a range of space-related experimental circumstances using Rad-Bio-reiterative App's filtering capabilities. Then, utilising a number of bioinformatics-related technologies, these datasets serve as targets for more in-depth investigations. Design principles and objectives of the Rad-Bio-App

The Rad-Bio-main App's objective is to enable users to create curated, filtered lists of omics datasets from the GeneLab data repository, which can subsequently be investigated for potential radiation-related reactions. As a result, tracing the provenance of such data is crucial and at the core

of the Rad-Bio-data App's structure, which is seen in Fig. 2. The Space Shuttle, the International Space Station (ISS), satellites (including the Russian Bion and Foton spacecraft), and the Chinese Shenzhou spacecraft are among the sources of these spaceflight datasets. Data from studies using terrestrial radiation sources, such as particle accelerators and gamma, x, and neutron sources, are known as ground data. We have also imported data from the Cosmic Ray Telescope for the Effects of Radiation (CRaTER) instrument on the Lunar Reconnaissance Orbiter (LRO)27, the RAD instrument of the Mars Science Laboratory4,5,28, and the Lunar Lander Neutrons and Dosimetry (LND) experiment mounted on the Chang'E 4 spacecraft. These data include orbital and surface data from the Moon, from the journey from Earth to Mars, and from the Martian surface. Data on radiation in lunar orbit and LND for the lunar surface are provided by CRaTER. RSMs (radiation survey metres) 32. Data on radiation in lunar orbit and LND for the lunar surface are provided by CRaTER. The RAD monitored radiation exposure while travelling to Mars and while standing on the surface of Mars. The lists of GLDS datasets that emerge, chosen for certain radiation exposure characteristics, then provide the opportunity to further query the linked omics data within GeneLab, using either GeneLab's visualisation portal capabilities or other customised ways (e.g., for plants, exploration within the TOAST database33). With these methods, it is possible to compare the molecular fingerprints left by trials with similar or dissimilar radiation exposures and to determine if other experimental variables may have an influence on the responses. In order to better understand how biology reacts to ionising radiation exposure in the context of spaceflight and to detect space radiation circumstances that are presently not being modelled on Earth, the scientific community should use the Rad-Bio-App. It is crucial to point out that users of the GeneLab website may search for omics datasets associated with particular radiation metadata classes, including radiation type, energy, dosage, and dose rate. These capabilities are enhanced by Rad-Bio-App by expanding the scope and depth of the searchable giving interactive functionality to apply quantitative filters concurrently across all datasets and radiation information. To illustrate the value of putting such additional capabilities in place: There is a lot of information from ground-based investigations on a radiation source that is available for operational reasons. a variety of different creatures at the NASA Space Radiation Laboratory (NSRL) at Brookhaven National Laboratory were exposed to iron ions. As a result, by contrasting studies with comparable irradiation parameters, these databases might potentially yield a lot of information. A knowledgeable user would know to look for this kind of radiation exposure to combine this large number of data, a task that GeneLab's gateway for visualisation. Through straightforward study of the graphical representation of the aggregate terrestrial radiation data, a biologist who is somewhat new to the subject of space radiation might use the Rad-Bio-App to immediately identify iron as a radiation type that is rich in datasets (Fig. 3). They might also quickly determine whether these datasets contain the species of relevance to them. By enabling researchers who do not have a background in radiation biology to start incorporating potential radiation impacts into their studies and experimental plans, Rad-Bio- App should also assist to increase access to and utilisation of these types of data. The radiation data's features within Rad-Bio-App Galactic cosmic radiation (GCR), which originates beyond the Solar System, and solar-derived particles and energy make up space radiation34. As a result, Rad-Bio- App offers filtering capabilities to make some of these complexities easier to explore. Protons and electrons make up the majority of the solar particle flow, which has energy up to around 100 keV. However, rare solar particle events can accelerate these particles to greater energies (about 1–10 MeV35). GCR can be considerably more energetic (over 100 MeV/nucleon), and it is made up of protons and heavier ions that are expelled from supernovae. Secondary particles may also be produced as a result of nuclear or electromagnetic interactions between such primary radiation and other materials, such as the spacecraft's hull or shielding. Protons, neutrons, and light charged pieces are some of these secondary particles. These particles have the potential to penetrate deeply and, like solar particles and GCR, cause biological harm6. The Rad-Bio-App enables data filtering for specific energy and dosages and, for terrestrial investigations with well-defined radiation sources, by the radiation quality to assist address this complexity in the spectrum of the types of radiation that may be present in an experiment

(e.g., alpha, Fe nucleus, proton, etc.). The energy that radiation can supply over a distance travelled (its linear energy transfer, or LET, which is commonly given in kiloelectron volts per micrometre; keV/m) is another important property in connection to impacts on biological systems. Protons and electrons are examples of low LET radiation, which is broadly defined to include particles with less energy than 10 keV/m. In contrast, high LET radiation is made up of energetic nuclei with more penetrating power and, as a result, a higher potential to harm biological molecules36. However, even low LET radiation may easily impair biological functions by causing oxidative stress and DNA damage37,38. So, when the LET of the radiation quality is known, the Rad-Bio-App allows filtering on that information. The difficulty of reproducing the range of space radiation conditions in the lab, whether on the ground or in Low Earth Orbit, is another significant obstacle to the research of the effects of space radiation on biology (LEO). It is crucial to consider the implications of this issue when a researcher draws conclusions from Rad-Bio-App-based analysis. In order to simulate the expected radiation exposure in space, particle accelerator facilities on Earth, like the NSRL, can deliver low absolute doses, but these must typically be delivered acutely, that is, at dose rates on the order of Gy/min as opposed to the typical rates of hundreds of Gy/day that are experienced in Space. Furthermore, exposures in these ground-based investigations were previously restricted to a single particle type at a single energy, but, as was previously mentioned, space radiation comprises a complex mixture of radiation kinds. When known, Rad- Bio-App offers filters for dose rate and particle kinds to assist put these space radiation analogue experiment studies into perspective. Fortunately, terrestrial facilities are developing more advanced mixed field capabilities that promise to more precisely imitate the range of particles evoking space radiation effects, even if they are still restricted to rather high dose rates. However, it is still difficult to do accurate analogue studies for space radiation on Earth, therefore it is important to keep these problems in mind while conducting Rad-Bio-App evaluations. When using the Rad-Bio-App to compare datasets, it is crucial to be aware of how the location affects the radiation environment. Orbiting spacecraft provide dose rates that are more relevant for studying the impacts of space on life. Because of this, radiation exposures in low-Earth orbit (LEO) will likely have a much higher proton contribution than will exploration missions travelling to the Moon and beyond, even though particle types are typically not recorded for experiments conducted in spaceflight (Rad-Bio-App classes these as "Mixed" radiation). Future missions like Artemis39, Lunar Gateway40, and BioSentinel41 offer to deliver biological data that operates outside of these confusing LEO effects. When data from these new facilities and missions become available, the GeneLab data system and Bio-Rad-App are both built to easily incorporate it in order to more accurately align upcoming investigations to the gamut of expected space radiation profiles. The Rad-Bio-App exploration environment is designed with the help of the Qlik database management system (Qlik Technologies Inc., King of Prussia, PA, USA). Data collected by the RaD-X high-altitude balloon mission, CRaTER, the RAD, the LRD, and on Apollo flights have been combined with radiation data from NASA's GeneLab data repository21,23. The Qlik software engine was then used to manually integrate these datasets and related metadata together to create a searchable relational database. In order to show datasets as a straightforward graphical user interface centred around data-centric dashboards, Qlik offers customisable interactive representations of datasets. There are built-in data filters that enable users to quickly narrow searches and comparisons by, for example, organism, radiation type, or mission. These filters then spawn to all other datasets and analysis dashboards, enabling users to repeatedly narrow their searches and comparisons across the breadth of all the data within Rad-Bio-App as described below. Dashboards for using the Rad-Bio-App Rad-Bio-App is accessed through a main menu or index page that displays icons and brief explanations of the pages or dashboards they connect to. Each dashboard makes it easier to obtain a certain type of radiation data and provides visualisation and filtering capabilities so that users may easily study those datasets. The researcher can search datasets by amount of radiation exposure using dashboard #1. A summary of the typical radiation dosage that each creature received throughout an experiment is displayed to users. Within the GeneLab data repository, indexed to the pertinent dataset. Further filtering of these radiation data is possible based on information elements including radiation kind,

radiation source, and exposure levels. The user may locate datasets by the kind of radiation from various sources using Dashboard #2. In this dashboard, a substantial number of datasets are categorised as LEO experiments (such as the International Space Station and the Space Shuttle), whereas radiation data relating to terrestrial Experimentation enables, for instance, the choice of the desired particle (for instance, Fe at 1 GeV/n). The Rad-Bio-App offers further filtering of these datasets based on characteristics like organism and method of analysis used to evaluate biological response (e.g., transcriptomics, genomics, and proteomics). The third dashboard enables users to concentrate on space studies, which often have significantly lower dose rates than trials on Earth and represent chronic exposure lasting days to weeks. Consequently, the dashboard opens to a graph showing radiation doses as a function of time. These space-related sub-selections are available. filtering experiments for things like mission, dosimeter, and flight hardware. The precise types of particles causing the radiation exposure in the majority of spaceflight experiments are not measured, which is why, as mentioned above, they are all grouped together as "Mixed" radiation exposures on this dash- board, in contrast to terrestrial radiation experiments that use defined radiation sources. As a result, in dashboard #3, the filter for radiation source or group is based on the space location where the measurement was made (such as LEO), rather than a specific radiation type, as was possible for the terrestrial research in the prior dashboard. A comparison of maximum, lowest, and average radiation doses for lunar orbit, lunar surface, Martian surface, and Earth-to-Mars transit against the plethora of spaceflight and terrestrial biological studies accessible at NASA's GeneLab data repository is shown in dashboard #4. Due to the extensive amount of data collected, factors like powerful solar particle events, which occur when the Sun releases extraordinarily high amounts of radiation for a brief period of time, may have an influence on average readings for these Moon-space and Mars-space measurements. Therefore, Rad-Bio-App displays a number of "average" exposure rates for the lunar and Martian datasets in addition to maximum and lowest exposures. Both measurements taken from periods during which these events did not occur and values with high intensity stochastic occurrences included are included in these averages. We also include average values from the RAD's Si detector's Si data that have been adjusted for radiation penetration into water for the Martian data. Compared to the Si detector's raw output, the latter measurement offers a more accurate approximation of how radiation is probably interacting with biology. This adjustment should only be used as a rough approximation because it is based on a computation from the Si detector data using a dosage conversion factor5. Dashboard Glossary: Last but not least, the App also includes a glossary of words on the main dashboard index page. The Rad-Bio-App homepage also provides access to a video lesson that guides potential users through using some of the App's fundamental features. Testing radiation biology on the surface of the moon The Rad-Bio-App is made to provide researchers quick access to information on the radiation environment of a specific study and to make it simple to compare datasets in order to get new knowledge. We have utilised Rad-Bio-App as an illustration to investigate potential consequences. Of the radiation present on the moon. Therefore, it is vital to consider how radiation may impact life in these circumstances as the spaceflight community's horizons start to broaden to encompass crewed trips to the Moon and eventually Mars. But up until now, other from the 27 Apollo astronauts who visited the Moon and the brief seedling germination experiment carried out by China's Chang'E-4 mission29, 30, we haven't been able to send any other spacecraft beyond Earth. Have no knowledge of how biology functions in the lunar environment. How can forecasts be made regarding the radiation impacts to guide upcoming missions to this location? Rad-Bio- App integrates data from astronaut dosimetry on Earth, the Chang'E-4 lunar lander, and direct radiation measurements taken by CRaTER as it orbits the Moon. Lunar missions In order to filter the variety of LEO spaceflight and terrestrial data from NASA's Genelab repository for radiation doses near to those anticipated for the lunar surroundings. In a nutshell, we assumed that the average mixed lunar surface radiation dose rate from the LRD detector on Chang'E-4 (0.55 mGy/day) would broadly encompass a plausible lunar radiation dose rate and established limitations of 2x 0.5x (i.e., looking for 1.1 to >0.25 mGy/day). Additionally, Rad-Bio-App demonstrated that the associated datasets cover 10 distinct species. In this instance, we took use of

the synergy that may exist between the carefully curated data repository at GeneLab and the quick dataset surveys made available by Rad-Bio-App. Therefore, searching the GeneLab data repository indicated that majority of the research found in the aforementioned analysis used flight samples as opposed to a corresponding ground control for gene expression analysis. The majority (15) of these research, which used microarray or RNAseq technologies to analyse the expression of the complete genome, were conducted on mice, as demonstrated by Rad-Bio-App. Cross-referencing to GeneLab's visualisation portal also indicated that the majority of these datasets had been processed using GeneLab's RNAseq or uniform microarray software pipelines (Overbey et al.42). In other words, these datasets have undergone the same computational pre-processing within the GeneLab data system, and the analysed findings on differential gene expression have been deposited and made publically available for download. Briefly stated, these analytical pipelines used the R/Bioconductor software package for the microarray analysis whereas the GeneLab studies were carried out in the Galaxy software environment43. RNA-seq with Limma44 and STAR (v2.7.1a45) and RSEM (v1.3.146). On the Genelab website22, you can find further details about the processing, links to the analytical scripts utilised, and the processed datasets that have been posted. Comparisons between datasets are significantly more reliable when the same analytical procedures are used for each dataset. investigations, and the open access to the results that have been deposited substantially expedites and streamlines further exploration. After that, these analyses gave us target datasets from the GeneLab data repository to investigate for typical molecular traces from life exposed to radiation dose rates comparable to those we would anticipate on upcoming lunar missions. It is important to highlight that comparing microarray and RNAseq datasets might be difficult to carry out and analyse since there is a chance that artefacts could be produced when combining results from these various analytical approaches (e.g., ref. 47). Therefore, we concentrated on five RNAseq datasets originating from the same mission: Rodent Research 6 (RR6)48 in order to maximise the robustness of our subsequent studies. These RR6 datasets were processed using the GeneLab RNAseq pipeline and came from five distinct tissues: dorsal skin, thymus, spleen, colon, and lung, respectively (i.e., GLDS 243, 244, 246, 247, and 248). Multiple controls were used in these datasets: either tissues were taken from slaughtered animals and subsequently preserved (i.e., euthanasia), or where the entire animal was initially frozen (to later be dissected by simultaneously with carcasses kept in space by (thawing) astronauts (i.e., carcass). Animals sacrificed right before the mission (base control) as opposed to those sacrificed on the ground concurrently with the operation served as another element separating distinct controls. The researcher can search datasets by amount of radiation exposure using dashboard #1. A summary of the typical radiation dosage that each creature received throughout an experiment is displayed to users. Within the GeneLab data repository, indexed to the pertinent dataset. Further filtering of these radiation data is possible based on information elements including radiation kind, radiation source, and exposure levels. The user may locate datasets by the kind of radiation from various sources using Dashboard #2. In this dashboard, a substantial number of datasets are labelled as LEO experiments (such as the ISS and Space Shuttle), whereas radiation data relating to terrestrial testing enables, for example, choosing the desired particle (such as 1 GeV/n Fe). On this dash- board, they are categorised as "Mixed" radiation exposures. As a result, in dashboard #3, the filter for radiation source or group is based on the space location where the measurement was made (such as LEO), rather than a specific radiation type, as was possible for the terrestrial research in the prior dashboard. A comparison of maximum, lowest, and average radiation doses for lunar orbit, lunar surface, Martian surface, and Earth-to-Mars transit against the plethora of spaceflight and terrestrial biological studies accessible at NASA's GeneLab data repository is shown in dashboard #4. Due to the extensive amount of data collected, factors like powerful solar particle events, which occur when the Sun releases extraordinarily high amounts of radiation for a brief period of time, may have an influence on average readings for these Moon-space and Mars-space measurements. 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included in these averages. We also include average values from the RAD's Si detector's Si data that have been adjusted for radiation penetration into water for the Martian data. Compared to the Si detector's raw output, the latter measurement offers a more accurate approximation of how radiation is probably interacting with biology. This adjustment should only be used as a rough approximation because it is based on a computation from the Si detector data using a dosage conversion factor. The Rad-Bio-App homepage also provides access to a video lesson that guides potential users through using some of the App's fundamental features. Testing radiation biology on the surface of the moon The Rad-Bio-App is made to provide researchers quick access to information on the radiation environment of a specific study and to make it simple to compare datasets in order to get new knowledge. We have utilised Rad-Bio-App as an example to investigate potential radiation impacts on the lunar environment. Therefore, it is vital to consider how radiation may impact life in these circumstances as the spaceflight community's horizons start to broaden to encompass crewed trips to the Moon and eventually Mars. We currently have little information on how life functions in the lunar environment, with the exception of the 27 Apollo astronauts who visited the Moon and the brief seedling germination experiment conducted by China's Chang'E-4 mission29,30. How can forecasts be made regarding the radiation impacts to guide upcoming missions to this location? Rad-Bio-App integrates data from astronaut dosimetry from the Apollo missions as well as direct radiation measurements taken by CRaTER as it orbits the Moon, the Chang'E-4 lunar lander, and other sources. In order to filter the variety of LEO spaceflight and terrestrial data from NASA's Genelab repository for radiation doses close to those anticipated for the lunar environment, Rad-Bio-App was developed. In order to do this research, we looked at the lunar surface environment and utilised direct measurements of the radiation taken by Chang'E 4 to see whether any datasets in the GeneLab data repository may provide insight into how biology might behave in this radiation environment. In a nutshell, we assumed that the average mixed lunar surface radiation dose rate from the LRD detector on Chang'E-4 (0.55 mGy/day) would broadly encompass a plausible lunar radiation dose rate and established limitations of 2x 0.5x (i.e., looking for 1.1 to >0.25 mGy/day). Additionally, Rad-Bio-App demonstrated that the associated datasets cover 10 distinct species. In this instance, we took use of the synergy that may exist between the carefully curated data repository at GeneLab and the quick dataset surveys made available by Rad-Bio-App. Therefore, searching the GeneLab data repository indicated that majority of the research found in the aforementioned analysis used flight samples as opposed to a corresponding ground control for gene expression analysis. The majority (15) of these studies were conducted on mice, and investigations of whole-genome gene expression were carried out using either microarray or RNAseq technologies, as was easily demonstrated by Rad-Bio-App. Cross-referencing to GeneLab's visualisation portal also indicated that the majority of these datasets had been processed using GeneLab's RNAseq or uniform microarray software pipelines (Overbey et al.42). In other words, these datasets have undergone the same computational pre-processing within the GeneLab data system, and the analysed findings on differential gene expression have been deposited and made publically available for download. It is important to highlight that comparing microarray and RNAseq datasets might be difficult to carry out and analyse since there is a chance that artefacts could be produced when combining results from these various analytical approaches (e.g., ref. 47). Therefore, we concentrated on five RNAseq datasets originating from the same mission: Rodent Research 6 (RR6)48 in order to maximise the robustness of our subsequent studies. These RR6 datasets were processed using the GeneLab RNAseq pipeline42 and came from five distinct tissues: dorsal skin, thymus, spleen, colon, and lung, respectively (i.e., GLDS 243, 244, 246, 247, and 248). Multiple controls were used in these datasets: either tissues were taken from slain animals and then preserved (i.e., euthanasia), or the entire animal was first frozen (to be dissected later by thawing), all while astronauts preserved the carcasses in space (i.e., carcass). Animals sacrificed right before the mission (base control) or animals sacrificed on the ground concurrently with an astronaut mission (ground control—GC) were another difference between various controls. These experimental variables' effects on gene expression have recently been discussed49 and are explained in depth. In the pre-processed datasets uploaded at GeneLab,

these five distinct tissues gave 10 flight-to-basal-control and five flight-to-GC comparisons; hence, we obtained the gene expression data for these 15 comparisons from the GeneLab data repository for additional analysis. The RadAtlas, a tool that compiles gene expression profiles of radiation-associated and radiation-responsive genes culled from the ground-based literature, was the object of our next investigation. Which of the genes identified as being transcriptionally sensitive to radiation in that tool also shown transcriptional changes in the mouse spaceflight RNAseq datasets described above? We obtained the aggregated data from the RadAtlas and inquired. After that, we narrowed down the list to only those genes that had a 2-fold or greater agreement in either suppression or induction in spaceflight across at least four mouse datasets. We added the additional condition that no dataset displayed a conflicting result in order to strengthen the filtering process. Specifically, none of the other datasets indicated repression at the 2-fold threshold if four or more datasets showed induction of a single gene. With the use of thresholding, we were able to separate potential common radiation response genes from those that had weak or erratic responses. The functional classifications (ontologies) connected to these gene sets were then shown using the gene network annotation and analysis programme Metascape. This list demonstrated enrichment in characteristics including DNA repair, cell cycle regulation, T-cell apoptosis, and more, giving candidates for further investigation of potential radiation effects in the spaceflight environment by, for example, focused flight testing.

Conclusions:

As a conclusion, we have presented the Rad-Bio-App, a data mining visualisation tool that enables the quick identification of omics datasets that have been deposited in the NASA GeneLab data repository and are relevant for a particular spaceflight radiation scenario (such as a trip to Mars or the surface of the moon) or specific radiation exposure characteristics. We found a number of tests carried out on the ISS with comparable radiation profiles by using this technology to test a lunar mission scenario. The Rad-Bio-App should become a more potent tool to help hasten assessment of the effects of Space radiation environments on living entities as more researchers enter datasets into GeneLab related to spaceflight and radiation exposure that explore the effects of, for example, species, genetics, gender, and age.

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