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RAPID: COVID-19 induced cessation of ecotourism and supplemental feeding: Implications for wildlife physiology, reproduction, and the microbiome

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Data Management Plan

1. Types of data, samples, and other materials to be produced

Three types of data will be generated by this project:

- a) Field measurements of habitat characteristics, animal morphometrics, and capture/recapture histories will be recorded on paper and transcribed into the computer on a daily basis. All generated data will be entered in Microsoft Excel spreadsheet format and uploaded onto BOX.com. Box.com is a cloud storage system used by Utah State University. Files are backed up nightly at multiple sites. Box.com ensures data integrity, includes version control, and is password controlled, encrypted and HIPAA compliant. We also have csv and dbf format capabilities available upon request for future data sharing. This data format is commonly used in most physiology labs and facilitates ease of data interpretation by others as well as data sharing. The format of spreadsheet data can easily be changed and related to R or SAS code.
- b) Blood samples collected in the field will be placed in individually marked microcentrifuge vials (label includes: species, individual, and date) and kept on ice until transported back to and stored in the laboratory. Samples are centrifuged to separate red blood cells from plasma with each stored separately. We will also maintain a digital record of all blood and tissue samples retained in the laboratory. Blood cell and plasma samples will be maintained in a -80C freezer in the laboratory for no less than 5 years following collection. Resulting data will be scanned and archived in BOX after the data have been transcribed into spreadsheets within BOX.com and checked for accuracy. BOX.com is backed up to the cloud daily, and provides version control.
- c) Sequence data from DNA sequences will be received from sequencing facilities as digital files in the FASTQ format via secure file transfer protocols (SFTP), and kept on the lab-owned storage space at the Utah Center for High Performance Computing (UHPC). The data storage nodes require authentication for access, and data transfers are encrypted. All team members will be able to access these data upon request. This space is backed up to alternating sets of tapes stored in a separate location on a quarterly basis. This space is cloned to a Google Drive with unlimited space on a weekly basis.

2. Standards to be used for data and metadata format and content

Findability - All data and metadata generated from this project will persist with unique identifiers in the National Center for Biotechnology Information Sequence Read Archive (NCBI SRA), in the Dryad Data Repository, or USU Digital Commons. Data can be easily searched, accessed, and cited from each of these repositories.

Accessibility - Data and metadata will be openly accessible at the NCBI SRA, Dryad Data Repository, or USU Digital Commons. Data may be embargoed until publication or 3 years after the end of the funding period, whichever comes first.

Interoperability- The project "Open Science Framework" Wiki includes instructions on standards for file naming, spreadsheet organization, file management, and coding, and these will be based on recommendations from the USU Research Data Management Systems. Archived data, will conform to metadata standards of each repository. Both Dryad and Digital Commons repositories are based on the Dublin Core metadata standards.

Reusability- Each of the archival repositories we have selected perform validity checks and version control, thus enhancing long-term reusability. Metadata will accompany all data.

3. Policies for access and sharing

Data will be disseminated using the following methods:

- a) Upon completion of the study, data related to published articles will be posted on Dryad Data Repository or USU Digital Commons. These are repositories of data underlying peer-reviewed manuscripts in the biological sciences. These repositories allow scientists to validate published findings, explore new analysis methodologies, repurpose data for research questions unanticipated by the original authors, and perform synthetic studies.

- b) All sequence data from the research will be publically and permanently accessible in the NCBI SRA.
- c) Investigators will present data and discussion of results at national and international meetings in the fields of physiology, ecology, conservation, tourism, and natural resource management.
- d) Investigators will publish results in peer-reviewed journals in the fields of physiology, ecology, conservation, tourism, and natural resources enabling broad distribution of the data across disciplines. Papers will also be uploaded to ResearchGate or equivalent.
- e) Following publication, the PI and co-PI may also report findings on their laboratory/institution websites. This will expose this and related work to the general public and colleagues. Any other relevant auxiliary data will be deposited in USU digital commons.

4. Policies and provisions for re-use, re-distribution, and the production of derivatives

All research products will be freely distributed in the repositories described above. There are no privacy, copyright, or confidentiality issues associated with the project data. Specifically, following publication of results, the PI will allow access to any remaining blood/tissue samples collaborators and researchers with an established track record or suitable references.

We will also provide a synopsis of the work and the data supporting it to the Bahamian government, The Bahamian National Trust, the ecotourism operators, the IUCN Species Survival Commission's Iguana Specialist Group, and the International Iguana Foundation. Drs French and Knapp are both invited member of the Iguana Specialist Group and board members of the International Iguana Foundation. The researchers will be available to work with these groups to best use the data for tourism planning, marketing, and decision making. The data will also be helpful in informing policy related to potential regulation of iguana tours and feeding behavior. Similar studies that have looked at the intersection of tourism activity, such as whale watching tours, and animal behavior have been instrumental in regulation of tour operators to mitigate negative impacts on animals.

5. Plans for archiving data, samples, and other research products

Dr. French will be responsible for retaining all field physiological data and samples collected for the proposed studies. Dr. Knapp is responsible for archiving all measurement and population data. Dr. Kapheim will be responsible for archiving all sequence data.

Specifically:

- a) Field Measurement Data: Copies of all data generated are saved permanently in three different locations: 1- Original hard copies are retained in laboratory notebooks (for physiological and morphometric data). 2- All electronic data will be organized by date and study number and stored on hard drives and on Box.com. 3- We will also use online back-up and storage programs, which also facilitate data sharing in the future. Finally, all resulting data will be permanently maintained on hard drive and also on network storage which, following initial publication, will assist data sharing with other interested parties.
- b) Blood samples: Once initial processing is complete, samples will be transferred to cryogenic vials to prevent evaporation and stored in an -80°C padlocked freezer until future need. These vials will be kept in clearly labeled sample boxes in chronological order and by study number for organization and easy relocation. The freezer has a backup alarm to protect and preserve samples. Once blood samples are analyzed, resulting data will be entered into a database that can be related to the field-based studies. Samples will be maintained in the -80C freezer for no less than 5 years following collection.
- c) Sequence Data: All left over extracts from DNA samples will be archived and stored in an -80°C padlocked freezer until future need and retained for no less than 5 years, as described above under 2.b. Resulting sequence data will be received as digital files in the FASTQ format via secure file transfer protocols (SFTP), and kept on the lab-owned storage space at the UHPC. Sequence data and metadata will be openly accessible at the NCBI SRA.