DMP du projet " Viral circulation and sharing in sympatric bat and rodent species living at the interface with humans and potentials risks of zoonotic spillover in southern Africa"

Plan de gestion de données créé à l'aide de DMP OPIDoR, basé sur le modèle "ANR - DMP template (english)" fourni par Agence nationale de la recherche (ANR).

Plan Details

Plan title	DMP du projet " Viral circulation and sharing in sympatric bat and rodent species living at the interface with humans and potentials risks of zoonotic spillover in southern Africa"
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Project Details

Project title	Viral circulation and sharing in sympatric bat and rodent species living at the interface with humans and potentials risks of zoonotic spillover in southern Africa
Acronym	VICTORIA
Abstract	Victoria project aims to better understand cross-species viral transmission and risks of emerging infectious diseases (EIDs) in southern Africa by exploring the circulation of three families of viruses within, but also between bats and rodents, two orders of small mammals known to play an important role in disease emergence, and zoonotic spillover. We hypothesize that viruses that could lead to EIDs naturally circulate within and between bat and rodent communities in Southern Africa, that viral cross-species transmissions between bats and rodents sharing the same ecological environment are more likely from bats to rodents, and that human populations living in close contact with these animals are exposed to these potential pathogens. To carry out this project, we have chosen as models three RNA viruses involved in interspecies transmission events from animals to humans with a major impact on human health**.** These viruses belong to the *Astroviridae*, *Coronaviridae* and *Paramyxoviridae* families. They are easily detectable in

animal excrement and their prevalence is important in bats and rodents.

The specific objectives will be to investigate communities of bat and rodent species living in sympatry as well as human populations living at a close interface in order to:

1. **Characterize diversity and prevalence of potentially zoonotic Corona-, Astro- and Paramyxoviruses in bat and rodent species sharing the same habitat,**
2. **Investigate viral sharing and transmission dynamics between these sympatric bats and rodents,**
3. **assess exposure of humans, and risks of spillover**

This project addresses the issue of EID risks related to small mammals in Southern Africa, a region that remains little investigated so far regarding this issue. Most importantly, in order to have a comprehensive understanding of EID, the project is based on an innovative strategy of multispecies investigation which focuses on viral circulation and sharing within and between two small mammal orders recognized to be of main importance for EID, but also on the link with human populations. It addresses the issue with a One Health perspective, involving intersectoral research (animal and public health)

Funding

- Agence Nationale de la Recherche : ANR-22-CE035-0011-01

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Partners

- Centre de coopération internationale en recherche agronomique pour le développement-ASTRE (UMR117) – CIRAD-INRAE, France https://ror.org/05kpkpg04
- Institut de recherche pour le développement-MIVEGEC-UMR 224 – IRD, CNRS, UM, France https://ror.org/05q3vnk25
- Centre for Viral Zoonoses, Faculty of Health Sciences, University of Pretoria, South Africa
- Universyty of Zimbabwe-Faculty of Veterinary Science, Zimbabwe
- University of Zimbabwe, Faculty of Medicine and Health Sciences, Zimbabwe
- University of Zimbabwe Centre for Applied Social Sciences, Zimbabwe

Research outputs :

1. Longitudinal monitoring of bat and rodent communities (Collection)
2. Detection and characterisation of potentially zoonotic viruses in bats and rodents (Dataset)
3. Characterization of human exposure and community perception of zoonotic risks (Dataset)

Contributors

Name	Affiliation	Roles
De Nys Hélène - https://orcid.org/0000-0002-2942-4531	CIRAD	• Data contact (WP-1)
Grosbois Vladimir - http://orcid.org/0000-0003-1835-1434	CIRAD	
Liegeois Florian - https://orcid.org/0000-0003-1048-0661	Institut de Recherche pour le Développement	• DMP manager • Data contact (WP-2, WP-3) • Project coordinator
Markotter Wanda - https://orcid.org/0000-0002-7550-0080	Centre for Viral Zoonoses, Faculty of Health Sciences, University of Pretoria	

DMP du projet " Viral circulation and sharing in sympatric bat and rodent species living at the interface with humans and potentials risks of zoonotic spillover in southern Africa"

1. Data description and collection or re-use of existing data

Longitudinal monitoring of bat and rodent communities

1a. How will new data be collected or produced and/or how will existing data be re-used?

***- Identification of sympatric bat and rodent species and characterization of communities*:**

Communities of small mammal species sharing the same habitat will be characterized through capture protocols designed to target a maximum of different bat and rodent species.

Bats will be caught using mist nets of various mesh sizes and heights and harp traps installed at the caves' entrance, roofs of houses or close to the roosting trees for Honde valley site. Bats will be captured from dusk onwards, up to midnight, in order to allow the capture of all species roosting in the caves which might have come out at different times for feeding. For each site, the same capture designs will be applied throughout field sessions to allow for comparison over time. Morphological measurements and traits as well as physiological data (age category, gender, reproductive status) will be recorded from captured individuals.

Capture mark-recapture approach using tattoos or microchips (PIT tags) will be used in order to account for recaptures and to allow estimation of species abundance. Cave bat population densities as well as size of E; helvum colonies will be estimated through direct counts. All animals will be released after sample collection. Species will be identified in the field based on morphology using species identification keys and confirmed by molecular analysis of a subset of individuals for cytochrome B fragments or COI and 12/18sRNA genes depending on existing genetic databases. Six voucher specimens (three male and three female) will be euthanized and preserved in 70% ethanol for species suspected not to be genetically characterized yet. Rodents will be caught using diverse live-traps (Sherman and mesh traps) adapted to animal behaviour and size according to protocols for field and laboratory rodent studies. Traps will be set homogenously, following a regular pattern, to cover the habitat within the caves, outside cave entrances or houses and beneath the *E. helvum* roosting trees. As for bats, physiological and morphological data will be collected. The capture-mark-recapture approach using PIT tags will be also used to account for recapture and virological monitoring. Species will be identified based on morphological traits and the use of identification keys as well as Cytochome B genetic analysis of a subset of individuals and six voucher specimens (three male and three female) kept for unknown species. Except for voucher specimens, all bats and rodents will be released at the capture site after sample collection. Community composition as well as species richness will be determined for each field session at every site.

- Biological sampling

For every site, each session will aim at collecting samples from 84 captured bats and 50 captured rodents (here referred to as semi-invasive sampling). Oral saliva swabs, rectal swabs (depending on animal size), blood, skin (wing punch for bats and tip of tail for rodents) will be sampled, as well as feces and urine in an opportunistic manner. Feces and swabs will be preserved in liquid nitrogen or using a home-made Nucleic acids stabilization solution (http://www.protocol-online.org/prot/Protocols/RNAlater-3999.html), blood will be preserved as dried blood spots on Whatman cards and skin and hairs will be preserved in 70% alcohol solution. Urine will be frozen in liquid nitrogen or preserved as Dried urine spot on Whatman paper. Given the expected prevalence of the *Corona-*, *Astro-* and *Paramyxoviruses* in both orders (2 to 20%) and the estimation of capture capacity per session, 1000 bats and 600 rodents will be sampled per site. Non-invasive sampling of fecal samples of bat colonies will also be carried out by setting plastic sheets under roosts (1800 samples per site). Each sampling team will comprise 6 persons: 1 team of three people (1 team leader, 2 assistants) will be in charge of bat capture overnight and the other team will be in charge of the daily rodent captures. All samples will be stored at -80°C at the laboratories until use

- **Study site and other data**

A detailed description of the study sites will be carried out, and for every field trip/season, fruit tree phenology, and observations on interactions with humans or other animals will be recorded. Capture effort and climate will be recorded daily during the field trips.

1b. What data (for example the kind, formats, and volumes), will be collected or produced?

The following data will be collected during the project for the WP-1:

- Data on capture effort for semi-invasive and non-invasive sampling (trap surface/number, time, …)(format excel, CSV) 10 Mo

- Number of individuals captured per species, Capture-Mark-Recapture data (format excel, CSV) 10 Mo
- Bat population counts (format excel, CSV) 10 Mo
- Study site description (format excel, CSV) 10 Mo
- Observations on human/animal interactions (format excel, CSV) 10 Mo
- Fruit tree phenology (format excel, CSV) 10 Mo
- Data on biological samples collected from captured bats (N=4000) and Rodents (N=2400): Rectal and salivary swabs, Blood (Dried Blood Spot), Hair, Skin, organs (=200) (format excel, CSV) 20 Mo
- Morphological measurements, traits and physiological data from captured bats and rodents: Age category, gender, reproductive status (format excel, CSV), 10 Mo
- Pictures (study site, Bats, Rodents, CYT B agarose gel, Format JPEG), 1To
- Data on bat feces collected by using non-invasive method (=1800) (format excel, CSV) 10 Mo
- Meteorological data: Temperature and humidity , weather at study sites (format excel, CSV), 10 Mo
- Nucleotidic and proteic acid alignements (fasta files), 100 Mo
- Phylogenetic trees (PDF, power point), 10 Mo
- General Database (REDCap-Research Electronic Data Capture), 100 Go
- Excel and CSV sheet: Victoria DB Bats, Victoria DB rodents, Victoria Seasonal field site data, Victoria daily field site data

Detection and characterisation of potentially zoonotic viruses in bats and rodents

1a. How will new data be collected or produced and/or how will existing data be re-used?

The objective of this task is: **1/ To identify** the different strains of *Corona-*, *Astro-* and *Paramyxoviruses* circulating in rodents and bats, **2/ To estimate prevalence** of the main strains for each site and sample session **3/ To determine** the genetic features of these viruses and more particularly the binding receptor domains allowing the attachment and fusion of the viral particles to their target cells **4/ To evidence**, according to their genetic characteristics and their phylogenetic relationship, the events of species jump between bats and rodents, **5/ To determine** and synthetize the antigenic determinants (epitope) or produce recombinant proteins needs for the realization of the task 3 and **5/ To train** the students attached to the project to advanced molecular and serologic techniques.

- Identification the different strains of *Corona-, Astro-* and *Paramyxoviruses* circulating in rodents and bats

Nucleic acids will be extract from all fecal samples and rectal swabs samples using an automatic extraction equipment (Kingfisher Duo Prime extractor) and 5X MagMax Pathogen RNA/DNA Kit. All samples will be subject to a reverse transcription step in order to obtain cDNA on which nested PCR system, for *Astro-* and *Coronavirus*, and hemi-nested PCR system, for *Paramyxovirus* will be process by using Pan-genomic primers allowing the amplification of each viral families. Positive PCR products well be agarose-gel purified and then sequenced using Sanger method. Sequence alignments will be realized using MEGA X software.

- Full genome sequencing and Recombination analysis

The sequencing and analysis of the complete genomes of the viruses of interest will allow us to determine the inter-species transmission events between different species of bats, rodents and between bats and rodents, to characterize the potential recombination events between the different viral strains and to genetic features such as antigenic determinants ad Receptor Binding sites. We will select different strains of the three studied viral families infecting different bat and rodent species.

Classical PCR systems using degenerated and specific primers will be set up and product PCRs will be sequenced by using both Sanger sequencing (Genome walking approach) and Next Generation Sequencing (Long read sequencing, MinION technology) methodologies. Design of primers will be done based on nucleic acid alignments of reference sequences. We will use a combination of six methods implemented in RDP5 (RDP, GENECONV, MaxChi, Bootscan, SisScan, and 3SEQ) to detect potential recombination events, and conservatively considered recombination signal detected by at least five methods. The beginning and end of breakpoints identified with RDP5 will be used to split the genome into regions for further phylogenetic analysis

Receptor Binding domains (RBDs)

In order to compare RBDs from the family viruses studied in the project with the known RBDs of *Astro-*, *Corona-* and *Paramyxovirus*, we will amplify the genes of interest of *Astro-*, *Corona-* and *Paramyxovirus* representing the genetic diversity we will observed after phylogenic analyses. Classical PCR systems using degenerated and specific primers will be set up and product PCRs (amplicon) will be sequenced by using both Sanger sequencing and Next Generation Sequencing (Long read sequencing, MinION technology and/or Illumina) methodologies. Design of primers will be done based on nucleic acid alignments of reference sequences. Putative RBDs obtained from our viruses will be compared to *Astro-*, *Corona-* and *Paramyxovirus* RBDs and more specifically to RBDs from human viral strains described in the literature. Additionally, protein structure comparison will be realized by using DaliLite server.

Antigenic determinants

Adaptive immunity is articulated by lymphocytes, more specifically by B- and T-cells, which are responsible for the

humoral and cell-mediated immunity. B- and T-cells do not recognize pathogens as a whole, but molecular components known as antigens. These antigens are recognized by specific receptors present in the cell surface of B- and T- cells. T-cells present on their surface a specific receptor known as T-cell receptor (TCR) that enables the recognition of antigens when they are displayed on the surface of antigen-presenting cells (APCs) bound to major histocompatibility complex (MHC) molecules. We will select about ten immunogenic epitopes per virus or group of viruses of interest using bioinformatics tools available online and by combining different methods (data-driven methods and T-Cell epitope Prediction). Peptides will be synthetized and lyophilized by a commercial company and then send in Zimbabwe and South-Africa. Additionally, we will also use recombinant protein such as the CoV or AstV spike proteins. Recombinant proteins will be produced in collaboration with the P2R platform (Nantes University: http://p2r-protein-facility.eu/en/home/).

1b. What data (for example the kind, formats, and volumes), will be collected or produced?

- Laboratory tests performed on bat and rodent samples and results (e.g. PCR results) (format excel, csv) 100 Mo
- Astrovirus, Coronavirus and Paramyxovirus nucleotidic sequences from bat and rodent samples (format excel, csv, Fasta, ABI, TXT, PDF), 500 Go
- Bats and rodents Mitochondrial DNA sequences (format Fasta, ABI, TXT, PDF), 500 Go
- Nucleotidic sequences will have a unique identifier corresponding to the sample ID and the organisme and gene, for example:

CHI (SITE)-001 (Sample Number) - AstV (Astrovirus)- RdRp (RNA dependent-RNA Polymerase)

- Raw sanger sequencing data (Chromatogram), 50 Go
- Metagenomic Data (fasta files), 1 To
- Pictures (PCR Agarose gels, 3D protein structures), 100 Go
- Nucleotidic and proteic alignments (fasta files), 100 Mo
- Phylogenetic trees (PDF, power point), 50, Mo

Characterization of human exposure and community perception of zoonotic risks

1a. How will new data be collected or produced and/or how will existing data be re-used?

The objectives of this work package are: **1/ To obtain** human blood samples for serological analysis**, 2/ To set up** serological assays with the Multiplex Bead Assay method (Luminex), **3/ To determine** whether human population has been in contact with zoonotic viruses, **4/ To identify at-risk behaviours for zoonotic transmissions from bats and rodents and assess** the perception of the infectious risk of human populations living in close contact with small mammals.

Human Blood sampling

Two sessions of human blood sampling will be conducted per site. These missions will be organized in the second year of the project at the same time as bat and rodent sampling missions. One during the viral peak period when bats are breeding (for example from December to March for the Magweto site in Zimbabwe) and one outside the breeding period. These periods of high viral circulation are conducive to interspecies transmission events. One hundred blood samples will be taken per session (200 in total per site). A preparatory mission will also be organized at each site to present the project to local authorities and residents of the study sites. The people targeted by this sampling will be adult >18 years old. People who have an activity in the cave (guano collection, religious ritual or hunting) and their families will be invited to participate in the study as well as randomly selected people who volunteer to participate in the study. A letter of consent, written in English and in the vernacular language, will be given to the volunteers. After verifying that the patient understands the study information, the physician will collect the patient's signature for informed consent. All the human samples will be destroyed at the end of the study. A team of two blood draw collectors will perform the sampling. All samples will be anonymized with a specific laboratory code for each site. Samples will be collected in 10 ml vacutainers EDTA blood collection tubes. Samples will be stored at 4°C until they are transferred to the laboratory where they will be processed and the plasma recovered by centrifugation. Plasma will be stored at -80°C in the laboratory.

Development of high throughput multiplex serological tests and screening:

Assays based on the Multiple Analyte Profiling technology (xMAP; Luminex Corp., Austin, TX) will be developed to screen human serum samples for antibodies against different viruses of interest that we will have characterised in the bat and rodent samples. Identification of viral antigens will be based on bio-informatic analysis of viral genetic information generated during this project (WP-2). Assays will be developed and carried out in South Africa (UP) and Zimbabwe (UZ) and standardized between the two laboratories. Human samples will be screened for bat/rodent viruses with the Luminex assays to investigate exposure to these viruses.

Briefly, Antigen determinant will be covalently coupled on carboxyl functionalized fluorescent magnetic beads (Luminex Corp., Austin, TX) with the BioPlex amine coupling kit (Bio-Rad Laboratories, Marnes-la-Coquette, France) according to the manufacturer's instructions. For each synthetic peptide-coupled bead set, we will use 2000beads/µl of assay buffer. Experiments will be done using on different plasma dilutions (1/100−1/1000) in order to determine the best signal to noise ratio. Diluted samples will be incubated with coupled beads for 16 h at 4 °C. Reactions will be revealed after incubation with abiotin-labeled anti-human IgG and streptavidin-R-phycoerythrin conjugate. Antigen-antibody reactions will be read on BioPlex-200 equipment (Bio-Rad, Marnes-la-Coquette. France) and the results will be expressed as median fluorescence intensity (MFI) per 100 beads.

The blood samples taken (DBS) from the animals for which we will have characterized the viruses of interest will serve as positive controls. Additionally commercial *Coronavirus* and *Paramyxovirus* positive controls will be used in order to validate our protocols. To calculate the cut-off, we will use the (Mean+3xSD) formula by calculating the mean of MFI of a panel of negative samples for each of the synthetic peptides tested. We will add to the value obtained three times the standard deviation. The result obtained will be considered as the cut-off for each antigen.

Sociological investigation:

A Mixed Method Research Methodology will be used to both explore and recommend strategies for reducing human behaviour and practices which might present a risk for spillover from small mammals to humans, as well as people's perception of health risks related to small mammals. Mixed research methodologies, comprising qualitative and quantitative components are largely recognized for their complementarity in understanding social phenomena by bring out both subjective and objective realities.

Quantitative data will be collected using a closed-ended questionnaire which will be distributed to a representative same of each case study site. The questionnaire will largely comprise cross-cutting questions, including variables such as socio-economic information of respondents (age, gender, education etc.,), livelihoods, trends, human behaviour, climate change, spatiality, temporality, impacts of human-bat-rodent interactions, disease incidence and burden; seasonality, institutional and organizational issues, among other important variables. The data collection process will be conducted using tablets and entered into the Survey Solutions computer software, which does not require constant access to internet, a big challenge in both rural Zimbabwe and South Africa.

Data analysis: Qualitative data will be analysed thematically and analysed using the NVIVO computer software. Qualitative data collected using Survey Solutions will be uploaded into Census and Survey Processing System (CSPro) which is designed to capture both large and small survey data.

1b. What data (for example the kind, formats, and volumes), will be collected or produced?

- Data on serological samples from human population (excel and CSV format) 100 Mo
- Serological tests and results from human samples (excel and CSV format), 100 Mo
- Questionaries, focus group and semi-structured interviews qualitative data (CSV, Excel, PDF and Doc format) 20 Go
- Astrovirus, Coronavirus and Paramyxovirus nucleotidic sequences (format Fasta, ABI, TXT, PDF), 50 Go

2. Documentation and data quality

Longitudinal monitoring of bat and rodent communities

2a. What metadata and documentation (for example the methodology of data collection and way of organising data) will accompany the data?

Different documents will be used:

- Data model (ER Diagram) (structural metadata)
- Descriptive metadata: geographical location, dates, collectors, Standard Operating Procedures (SOPs) (Victoria Protocols for field and laboratory studies, (SABRENet SOP manuals)
- General Database Structure (REDCap-Research Electronic Data Capture), Data dictionnary, Code Book
- Nomenclature of the documentation is in accordance with the one used at the University of ZImbabwe (Faculty of Veterinary Science) or at the University of Pretoria (Center for Viral Zoonoses)
- Nomenclature of the excel and CSV sheet

2b. What data quality control measures will be used?

Different control measures will be used according to the different data produced

- Standard Operating Procedures: these documents will be updated all along the project according to our field observations/experiences
- Database: Definition of domains and their constraints for the attributes, Double checking by the Data Manager and the technician assigned to this task.
- Checking the quality of pictures (clearness)
- CYTB Mitochondrial DNA analyses, PCR positive and Negative controls, Molecular ladder
- Quality of the Nucleic Acid sequences (Chromatogram) by using dedicated software (Geneious)
- DNA sequences quality will also be checked by using Basic Local Alignment Search Tool (BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi)

Detection and characterisation of potentially zoonotic viruses in bats and rodents

2a. What metadata and documentation (for example the methodology of data collection and way of organising data) will accompany the data?

- Data model (ER Diagram) (structural metadata)
- Descriptive metadata: laboratory, date, technician, ...,
- Standard Operationnal Procedure (SOPs) documentations (Laboratories protocols)
- General Database (REDCAP), Data Dictionaries, Code Book

2b. What data quality control measures will be used?

- Standard Operating Procedures: these documents will be updated all along the project according to our field observations/experiences
- Database: Definition of domains and their constraints for the attributes. Double checking by the Data Manager and the technician assigned to this task.
- Quality of pictures (clearness)
- Quality of the Nucleic Acid sequences (Chromatogram) by using dedicated software (Geneious)
- DNA sequences quality will also be checked by using Basic Local Alignment Search Tool (BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi)
- FastQ for metagenomic data
- PCR positive and Negative controls and molecular ladder

Characterization of human exposure and community perception of zoonotic risks

2a. What metadata and documentation (for example the methodology of data collection and way of organising data) will accompany the data?

- Standard Operational Procedure (SOPs) documentations (Laboratory protocoles)
- General Database structure (REDCAP), Data Dictionary, Code Book
- Consent letter template (English and vernacular langage)
- Questionary template and Interviewer’s instructions

2b. What data quality control measures will be used?

- Standard Operating Procedures: these documents will be updated all along the project according to our field observations/experiences
- Database: Double checking by the Data Manager and the technician assigned to this task.
- Quality of pictures (clearness)
- Quality of the Nucleic Acid sequences (Chromatogram) by using dedicated software (Geneious)
- DNA sequences quality will also be checked by using Basic Local Alignment Search Tool (BLAST: https://blast.ncbi.nlm.nih.gov/Blast.cgi)
- PCR positive and Negative controls
- Serology: Positive and negative controls

3. Storage and backup during the research process

3a. How will data and metadata be stored and backed up during the research?

Data and metadata will be stored and backed up by using IRD Dataverse (https://dataverse.org/).
Local Back up, every 24 hours, located at 3 differents and geographically distinct areas will be also set up by using Nas technology and 3To storage hard drive.

3b. How will data security and protection of sensitive data be taken care during the research

Only partners will have access to the data through secured collaborative space and shared Database. Accessibility of this collaborative space will be authorized by using a personnal password.

4. Legal and ethical requirements, code of conduct

4a. If personal data are processed, how will compliance with legislation on personal data and on security be ensured?

- Animal and human ethical clearances will be request from Zimbabwe and South Africa institutions (Ministries, Ethical committee etc..).
- For the human part of the project (questionnaries and serological analyses), samples will be anonymized.
- Management of Personal data will comply with the General Data Protection Regulation (GDPR)
- Nagoya protocol will be followed.
- Consent form (in English and vernacular languages) will document the voluntary approval of participants.

4b. How will other legal issues, such as intellectual property rights and ownership, be managed? What legislation is applicable?

Intellectual property rights and ownership will be managed according to:

1/ Zimbabwean and South African legislations according to the source of the collected samples.

2/ The Research Agreement signed between the parties:

Research Agreement between IRD and University of Pretoria:

Article 11 – Intellectual property

11.1 – Proprietary Knowledge

The Proprietary Knowledge of one Party that is made available to the other Party for the purposes of the Study shall remain that Party's exclusive property and must not be published in any form whatsoever without the explicit agreement of the Party that holds the relevant rights.

Each Party agrees not to reuse the Proprietary Knowledge of the other Party for any purpose other than the purpose for which it was provided to them.

If the direct or indirect use of the Results by one of the Parties or by a third party requires the use of the Proprietary Knowledge of the other Party, the latter shall endeavour, subject to the rights granted to third parties, to allow such use. The terms and conditions under which the Proprietary Knowledge is to be used must then be contractually agreed on a case-by-case basis.

Research Agreement between IRD and University of Zimbabwe:

1. **INTELLECTUAL PROPERTY**

10.1 Any Background Intellectual Property belonging to either Party before or after the commencement of the agreement will belong to that Party and the other Party will not have a claim against such Background Intellectual Property, which may include, but are not limited to thoughts patents, patent applications, inventions, discoveries and improvements, copyright in documents, computer software, drawings, designs, operational analysis, technology, course material and know-how and written material, including course material of whatever nature compiled for the purposes of this research. The ownership of any Background Intellectual Property owned by any party prior to the commencement of this Agreement shall remain vested with that party.

The Results of the Study, whether protectable or not under intellectual property law, are jointly owned in equal shares by IRD and UZ.

All Foreground Intellectual Property shall be jointly owned by the Parties in equal shares and the Parties. If the Results of the Study are likely to be subject to protection under intellectual property law, and especially to filing a patent application:

- the Parties shall have a period of three (3) months to decide the modalities of their protection, in particular by taking out one or more patents;

- unless the Parties mutually agree to file the application on behalf of one of them, the title to intellectual property shall be jointly registered in the names of IRD and UZ.

A co-property agreement will be drawn-up as soon as possible to:

- Identify the intellectual and financial contributions of each Party;

- Set out the conditions of the condominium;

- Establish the procedures for the management of intellectual property and valorization.

As long as this agreement has not been reached, no Party may take the initiative of direct or indirect industrial or commercial use of these Results.

The Parties shall bear equally the costs relating to the protection of these common Results, unless the condominium rules state otherwise.

If for any reason either Party should waive to apply, to pursue an issue or maintain one or other of these intellectual property rights, it will inform the other Party timely by registered letter with recorded delivery, so that this Party could file on its own name and at its sole expense, or continue the proceedings for grant or maintain the rights in force.

The Party which has withdrawn undertakes to execute any and all documents required to enable the other to become sole owner of the right in question.

In addition, the Parties undertake:

- that the names of authors and/or inventors are listed (unless they object in writing), consistent with applicable laws, in the applications that either Party will file;

- that their respective staff, named as author or inventor, gives any signature and perform all the necessary formalities for filing, maintenance and defence of such rights;

- to assume the responsibility for fair compensation, in compliance with the applicable laws, for their employees who participated in obtaining the Result subject to intellectual property right.

10.2 Both Parties acknowledges that the Intellectual Property Rights from Publicly Financed Research and Development will be governed according to government or funder requirements, regulations and guidelines.

10.3 Use for research

Each Party may use freely and free-of-charge the Results of the Study for its own research needs.

10.3.1 Use for industrial or commercial purposes

The Parties, which share ownership of the Results of the Study, may negotiate and conclude with a third party under the conditions laid down in the condominium agreement, any license agreement for industrial and/or commercial use of these Results.

10.4 - Use of prior knowledge

If the direct or indirect use of the Results of the Study by either Party requires the use of Previous Know-How or previous patents owned in part or in whole by the other Party, the latter endeavours to facilitate this operation, subject to the rights possibly granted to third parties. The conditions of use of these prior rights are settled contractually on a case by case basis.

4c. What ethical issues and codes of conduct are there, and how will they be taken into account?

According to ethical rules defined by local (Zimbabwe and South Africa) and french regulations:
- National Animal Research Ethics Council (NAREC) – Zimbabwe for animal handling and sampling, testing
- Medical Research Council of Zimbabwe (MRCZ) – Zimbabwe for human sampling, testing and social study
- University of Pretoria Research Ethics Council – South Africa

France:
The project will be submitted to the INRAE-CIRAD-IFREMER-IRD Consultative ethical committee.

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5. Data sharing and long-term preservation

5a. How and when will data be shared? Are there possible restrictions to data sharing or embargo reasons?

All data generated by the project will be shared in repositories as allowed by legal and ethical regulations.
No data will be public until the valorization of results and the acceptance of all involved project partners to release the data.
Nucleotidic Acid sequences will be deposited in NCBI-Genbank (https://www.ncbi.nlm.nih.gov/genbank/) and will be freely available to the research community

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5b. How will data for preservation be selected, and where data will be preserved long-term (for example a data repository or archive)?

The data generated during the Victoria Project will be conserved on our servers for a duration of 5 years from the end of the project.
In addition, data and metadata will be stored and backed up by using IRD Dataverse repository (https://dataverse.ird.fr/)

5c. What methods or software tools are needed to access and use data?

The shared data will rely on open formats and will not require specialized software CSV and Text format will be mainly used and data could be used using dedicated and free software (Libreoffice, CSV viewer for example)

5d. How will the application of a unique and persistent identifier (such as a Digital Object Identifier (DOI)) to each data set be ensured?

A digital Object Identifier (DOI) will be attributed for each Data set deposited on the IRD Dataverse (
institutional data repository “DataSuds”, which is powered by the Dataverse open-source software)

6. Data management responsibilities and resources

6a. Who (for example role, position, and institution) will be responsible for data management (i.e. the data steward)?

Florian Liégeois, Principal investigator, Researcher at IRD:
- DMP Update, Database management, Quality control
Hélène De Nys, Scientific Coordinator in Zimbabwe, Researcher at CIRAD.
- Database management, Quality control
Wanda Markotter, Scientific Coordinator in South Africa, Head of Centre of Viral Zoonoses, University of Pretoria.
- Database management, Quality control
PHD student
- Data Acquisition, Database management

6b. What resources (for example financial and time) will be dedicated to data management and ensuring that data will be FAIR (Findable, Accessible, Interoperable, Re-usable)?

Part time technician dedicated to the database management, 0.3 FTE.
Principal investigator and Scientific coordinators