



THE PASET AFRICA REGIONAL SCHOLARSHIP AND INNOVATION FUND

Project Proposal Template RSIF Junior Investigator Research Award (JIRA)

Project Title	Hunting for Emerging and Re-emerging Viruses with Potential for			
	Zoonotic Transmission Using Metagenomics; Diagnostics			
	Preparedness for Pandemics			
Project Acronym	HEDPA			
Project Leader/ Lead	Emmanuel George Kifaro			
Applicant				
Details of Administering	Sokoine University of Agriculture			
Organization				
Project Duration	2 Years			
Project Budget (RSIF component)				
Partners	Tanzania Wildlife Research Institu	ute (TAWIRI), Tanzania		
Partners (Name and	Name of entity and project	Address/ contact email		
Address) team member				
	1. Dr. Mikidadi Mtalika (BVM,	Tanzania Wildlife Research		
	MSc)	Institute		
		Box 661 Arusha		
	mickyissa@gmail.com			
Project Team	Name	Title/ Affiliation & Contact email		
Composition	1. Emmanuel George Kifaro	Department of Microbiology,		
	(Ph.D.)	Parasitology and Biotechnology,		
		Sokoine University of Agriculture.		
		Box 3019, SUA, Morogoro,		
		Tanzania.		
		emmanuel.kifaro@sua.ac.tz		
	2. Emma Peter Njau (Ph.D.)	Department of Microbiology,		
		Parasitology and Biotechnology,		
		Sokoine University of Agriculture.		
		Box 3019, SUA, Morogoro,		
		Tanzania.		
		emmanjau.en@gmail.com		
	3. Prof. Philemon Wambura	Department of Microbiology,		
		Parasitology and Biotechnology,		
		Sokoine University of Agriculture.		
		Box 3019, SUA, Morogoro,		
		Tanzania.		
		and the second second second		
		<u>pwambura@sua.ac.tz</u>		





Dear Applicant,

Please, read these instructions for writing the proposal carefully.

1. General remarks

- a. The proposal should not exceed 15 pages including references written in English or French.
- b. Use Times New Roman, font size 12, single spacing, normal margins, portrait orientation
- c. The following documents must be attached to the online application system:
 - i. A complete project proposal
 - ii. The Project result matrix and Workplan (See template provided)
 - iii. Budget (See template provided)
 - iv. Official letters of support from the Administering Organization and partner organizations
 - v. CVs for applicant and Partner
 - vi. Personal Statement (outlining vision for your career growth)
 - vii. Recommendation Letter from AHU indicating the applicant has met requirements for graduation/ graduated
- d. The online system will accept the following file types: .doc, .docx, .pdf, .rtf, .zip, .rar, .xls, .jpg, .jpeg, .png, .bmp, .tif. The maximum file size accepted for any single file is 5 MB
- e. The deadline for submission of proposals is on an on-going basis. Until all grants are allocated.





1. Project Overview

Provide a ½ page summary of the project, keep it simple and avoid technical language (if possible), summarize the project aims and how they will be achieved, significance, expected outcomes, and national/community benefits of the project. This summary will be used for communication with external stakeholders and be published on the RSIF website

Climate plays a key role in influencing global human and livestock health. Over the years, however, there has been increased global climate change. Although climate change is induced by several factors, human activities remain crucial. The climate change coincides with the cases of emerging or re-emerging vector-borne viral zoonotic diseases (Filho et al., 2022). Indeed, efforts toward the control of infectious diseases have been invested in either direction but are not holistic. Usually, studies are independently focused on either wildlife or domestic livestock with a bias toward a specific pathogen. Notably, no deliberate holistic studies in both wildlife and domestic life are regularly conducted. For instance, although so far Crimean Congo Hemorrhagic fever (CCHFv) and Marburg virus disease (MVD) are the only reported re-emerging zoonotic infectious diseases between these two countries, it's highly probable that some cases and other pathogens have gone unnoticed. The rationale is that we do not understand most of the hot spot areas and viruses circulating in different arthropods, wild animals, and other hosts. Yet cross-transmission of viruses, bacteria, and fungi from different hosts to humans, domestic, and wild animals can occur causing significant health and food security effects. For this reason, it's not possible to quickly predict and detect emerging or re-emerging zoonotic diseases and institute proper control measures. In this study, we aim to generate baseline data on the possible hot spot areas and the profile of zoonotic viruses circulating in bats and rats in communities where these animals are used by humans for different economic or nutritive purposes at the wildlifefarm-forest interfaces in Tanzania. Building on these data, we will be able to boldly speak out of the potential hot spot areas, the inventory of the circulating pathogens, and the potential risk for the occurrence of emerging or re-emerging zoonotic disease outbreaks in the region. We additionally, will develop a molecular assay to facilitate prompt detection of the suspected viral pathogens of significant human and food security importance to enhance the livelihood and global health agenda.

2. Introduction and problem statement

Describe the motivation and focus of the proposed project. Include information about the recent international progress in the field and the relationship of this proposal to similar ongoing work. Analyze context of the problem addressed and gap to be addressed. (max 1.5 pages).

The project has gained its motivation from the information that newly emergent diseases have been found to strongly correlate with specific geographic areas (Amazon, Congo basin, Gangetic region and the Southeast Asia region), specific animal species or hosts (rats, bats and non-human primates), specific microbial agents (RNA viruses including retroviruses, Influenza viruses, Filoviruses and Corona viruses) and high-risk populations (hunters, miners, bush meat traders, wild honey collectors, traditional herbalists and people that co-exist with wildlife) (Wang & Anderson, 2019; Letko *et al.*, 2020). These are therefore referred to as "HOT SPOTS" for the emerging pandemic threats and should provide the basis for targeting surveillance (Lessler *et al.*, 2017). From the recent international research progress, similar works are ongoing in other geographical areas including the Amazon, Gangetic region, and





the Southeast Asia region. Screening for microbial agents from specific animal hosts and animal species is also evidenced by the increased number of global publications reporting on the same. This project will be adding material to the international scientific community by unveiling some information from Tanzania.

Tanzania is located in the tropics along the same latitude of the Congo basin and directly sharing borders with the Congo basin countries. Consequently, the regularity of relations between people, domestic animals, and wildlife is increasing leading to prospects for new diseases to emerge. Given the high increase in global travel and trade, these interactions can easily drive a pandemic. Moreover, the rich ecosystem in the two countries entertains the specific animal species and hosts, disease vectors, and microbial agents tagged for the emergence of pandemics (Tazerji et al., 2022). For instance, the outbreak of the first Marburg fever associated with bats originated from Uganda (Knust et al., 2015; Siya et al., 2019; Africa CDC, 2023). Similarly, Ebola disease virus outbreaks have been associated with several animal reservoirs including bats, primates, and rodents (rats, mice) (To et al., 2015), while the first Lujo virus cases in South Africa was associated with rodents (Briese et al., 2009). In addition to this, some practices such as the use of wild birds and bat manure for agriculture (Sakoui et al., 2020; Dimande et al., 2023), the high consumption of wild animals including rats as a source of protein (Hoffman & Cawthorn, 2012), and the increased demand for traditional medicines from the forests with some traditional concoctions known to contain animal remains and excretes such as urine and feces (Vats & Thomas, 2015; Du et al., 2019), puts this population at a higher risk of viral epidemics from the novel and reemerging viral diseases.

Focusing on the project's intention, rats and bats, including their oral fluid and feces will be screened for the presence of the novel viruses of zoonotic importance. There will also be a development of a molecular assay to facilitate prompt amplification and detection of the suspected viral pathogens in case of viral epidemics.

3. Objectives, Expected Outcomes and Outputs

Describe the expected outcomes of the proposed project and potential applications of the expected results. Provide outcomes that can be measured quantitively (1 Page)

General objective

To identify, characterize, and design a specific molecular assay for the novel and/or reemerging zoonotic viruses of human and food security importance, circulating in different potential hosts harboring these viruses that include bats and rats at the farm-wildlife-forest interface in the selected districts of Tanzania.

Specific objectives

- 1. To explore the availability of potentially lethal viral pathogens from selected animal hosts including bats and rats in the selected districts using metagenomics.
- 2. To characterize the specific zoonotic viruses identified that carry the potential of human, and animal health, and food security importance.
- 3. To design and validate molecular-based assay specific for the identified virus(es) as diagnostic preparedness for prompt response in case of emergence.
- 4. To assess the impact of climate change and the distribution dynamics of bats and rats' populations in selected sampling areas.





Expected Outcomes and Outputs

At the end of this proposed project, we expect to have several research outcomes and outputs. Apart from contributing to increasing the body of knowledge, understanding, and expertise of the subject to research members, collaborating institutes, and the globe; the generated data from this research work will also open up new areas for research, leading to genuine hypothesis on the rational control strategies for infectious diseases, improved food security and global health to human and animals. Here are the three major outcomes from each of the specific objectives and their research outputs;

- 1. Better understanding and increased expertise in viral discovery research using cuttingedge genomics technologies;
 - List of novel and/or re-emerging viruses from the two regions associated with bats and rats.
 - Identified potential risks of viral shedding from the two animal species for both human health and food security.
- 2. Increased knowledge and understanding of the biology of the novel and/or re-emerging viral pathogens in the country.
 - The project will contribute to capacity development to 1 PhD and 2 MSc graduates from the collaborating institutes.
 - A minimum of three peer-reviewed journal papers will be published.
 - Well-established research partnership between project members and students in collaborating institutes.
- 3. Availability of ready-to-use molecular based assay (PCR, or sequencing based) to facilitate prompt detection and discrimination of the suspected viral pathogens in case of viral epidemics is an important tool as part of preparedness to control pandemics.
 - Enough expertise in designing, optimization, and validation steps for PCR and Sequencing-based methods for future novel pathogen detection.
 - Enough capacity and expertise in handling big genomic data at SUA and TAWIRI (data cleaning, analysis, presentation, and interpretation), as part of preparedness activity for prompt diagnostic response in case of emergence.
 - A well-validated PCR-based assay(s)/Nanopore-based direct sequencing for emerging/re-emerging viral pathogens.
- 4. Highlights of the effects of climate changes and natural habitat destruction as a driver for zoonosis will be understood;
 - Specific climatic and environmental features, and human activities contributing to high/low bats and rats' populations in specific sampling sites related to climate change will be revealed.

Methodology

Outline the design, tools and methods to be used to execute the proposed project, demonstrate that they are adequately developed, well integrated and appropriate to the aims of the proposed project. (1.5 Pages)

Study area

Samples will be collected from selected districts in Tanzania. The districts in Kagera region bordering Uganda and the districts in Mtwara region, southern Tanzania. Kagera region had





experienced human Marburg virus infection transmissions with no clear evidence of the viral origin, while Mtwara region represents bat and rats eating communities.

Sample size

As a pilot study, we expect to sample approximately 700 bats and rats (approximately 1400 specimens) from wildlife (bats, wild rodents, selected mammals) and domestic animals (cattle and goats) from the two regions as a cross-sectional study design.

Sample collection

All materials will be handled as biological hazards, and all necessary biosecurity measures will be taken during sample collection, transportation, and analysis. Blood, oral fluids/swabs, and stool samples will be collected from different wildlife (bats, wild rodents, and selected mammals) and domestic animals (cattle and goats) from the study area. From each, blood, oral swabs, and stool samples will be collected for this study. Oral swabs and stool samples will be collected in viral transport media to enhance viral viability for identification. All samples will be kept, and transported in a cold chain to the molecular biology laboratory, College of Veterinary Medicine and Biomedical Sciences, Sokoine University of Agriculture and Kilimanjaro Christian Research Institute (KCRI), for laboratory investigations.

Sample analysis

Nucleic acid extraction

Viral nucleic acid from all the samples will be extracted using PureLink™ Viral RNA/DNA Mini Kit. Invitrogen™, Waltham, Massachusetts, USA. According to manufacturer instructions. Samples will be quantified by nanodrop (Thermo Fisher Scientific, Waltham, MA, USA).

Metagenomics analysis and bioinformatics

The enriched NA samples will be sub-submitted for metagenomic sequencing. Library preparation will be prepared using Oxford Nanopore Technology (ONT) (MinION Mk1C) ligation sequencing kit (SQK-LSK109). The sequencing platform will be deployed for metagenomics analyses to identify viral species found in different bat and rat specimens using the random oligos, according to the manufacturer's recommendations for the specific flow cell used for sequencing. The obtained sequence reads will be subjected to quality control analysis. This will entail removing redundant and duplicate sequences and trimming adaptors and host DNA. Using de novo assembly, the trimmed sequences will be aligned to the known virus genome sequences to obtain contiguous sequences (Contigs). The contigs will be submitted to NCBI Blast Local Alignment Search Tool (BLAST) where sequences are compared to the known virus genomes. Sequencing data will be analyzed using different bioinformatics tools to identify novel and existing viral species. The analyzed data will then be used for peer-reviewed publications and as part of training for capacity building for SUA and TAWIRI members to initiate the bioinformatics data unit station and for training purses.

Specific objective 2

Virus-specific characterization will be conducted using a similar device (MinION Mk1C), where whole genome sequencing will be conducted using virus-specific overlapping oligos. Partial DNA sequencing will be performed on all the viral isolates based on the quality of the whole genome sequencing data. All the oligos will be designed in collaboration with the partner institute. All the sequencing data obtained will be saved and shipped to the Kilimanjaro Christian Research Institute (KCRI), for sequence data analysis, and interpretation.





ONT sequence data analysis

The data analysis of the ONT sequenced reads of the raw fast5 files will start with base-calling using Guppy version 5.0.7 (Oxford Nanopore Technologies) in super high-accuracy mode on a GPU server. Statistics will be obtained from the base called reads using NanoPlot version 1.36.2 for quality assessment. The reads will further be filtered to retain only those with a quality higher than 7 using NanoFilt version 2.8.0. The output fastq files will be uploaded to BugSeq (version 1.1) for metagenomics classification (Gauthier *et al.*, 2021; Buytaers *et al.*, 2022).

Specific objective 3

Virus-specific primer/probe sequences will be designed using appropriate bioinformatics tools such as the PrimerQuest - design qPCR assays (Integrated DNA Technologies (IDT), Inc. Iowa, USA) for the discovered potentially lethal viruses from objectives 1 and 2 above. Virus-specific qPCR and RT-qPCR assays will be optimized and validated at SUA, Tanzania. The Applied Biosystems 7500 Fast Real-Time PCR System (Thermal Fisher Scientific Inc. USA), and MinION Mk1C will be used to test and validate the developed assays.

Specific objective 4

Metadata will be collected through questionnaires and observation studies will be combined with data obtained from specific objectives 1-3 while considering the climatic changes and the variations of bats and rats' populations as an element of climate change.

5. Description of activities

Describe the main activities to be executed to achieve the expected outcomes and outputs. (2 Pages)

Activities for objective 1; SUA laboratory

- Project preparation meetings and research permits acquisition.
- Six weeks will be used for field sample collection from both regions, three weeks per each region. The samples will be temporarily stored in cold boxes/or canisters in liquid nitrogen, and transported to nearby veterinary laboratory agencies before are shipped to DVMPB, SUA for analysis.
 - 1. Whole blood samples will be separated to obtain serum before being shipped to the laboratory.
 - Oral swabs and stool samples will be directly collected into virus transport media (VTM), to enhance the virus viability, and reduce the chances for rapid degradation of the matrices and the analytes (Viral nucleic acids).
- A one-week hands-on training on the operation and application of the ONT-MinION Mk1C sequencing platform. This will be done at the molecular laboratory, SUA by the Application Specialist from ONT Agency Company in Tanzania.
- The initial training on ONT sequencing data handling and analysis will be conducted at the molecular laboratory at SUA, by the application specialist from ONT Agency Company personnel. This will assist researchers in competently determining quality sequencing results from the MinION Mk1C, and where necessary performing troubleshooting and corrective actions in case of low-quality output results.
- Samples will be analyzed at the DVMPB molecular biology laboratory after the hands-on training. In this case, oral swabs and stool samples will be utilized. Samples will be pooled (up to 10) before they are analyzed. The pooling of samples will





depend on the sample type and location. Nucleic acids will be extracted and direct sample sequencing performed according to the manufacturer's recommendations.

- In-depth data analysis and interpretation of raw metagenomics sequences will be conducted at KCRI.
- Manuscript writing and submission

Activities for objective 2; SUA and KCRI laboratory

For all novel and re-emerging viruses of human or food security importance obtained from objective 1 above; will be considered for detailed analysis to investigate their genetic characteristic and relatedness with closely related viruses.

- We will design sequencing primers specific for each of either novel or re-emerging viruses of interest for partial and whole genome sequencing. Overlapping primers specific for each virus will be designed and ordered to be utilized for whole genome sequencing using the MinION Mk1C sequencing platform at DVMPB, SUA.
- In case partial DNA sequencing becomes important to be conducted, the DNA samples will be sent to a commercialized company for sequencing using the Sanger Sequencing platform at SUA.
- Similar samples will be used for 2 weeks of capacity-building training for SUA and TAWIRI members on sequencing data analysis, interpretation, and presentation at KCRI or any other identified institution with such a capacity based on space and resource availability.
- Manuscript writing and submission

Activities for objective 3; SUA laboratory

For any potential novel or re-emerging discovered viruses from objectives 1 and 2 above; we have to design a molecular-based assay for easy detection of the virus in case of emergency. The assay will facilitate healthcare workers and researchers to make prompt diagnoses and decisions marking on the control strategy during disease epidemics.

- We will design and order from the manufacturer's diagnostic primers for the novel or re-emerging viruses for either PCR or RT-PCR assay based on the virus type.
- We will optimize and validate the designed assay using the Applied Biosystems 7500
 Fast Real-Time PCR System (Thermal Fisher Scientific Inc. USA), available at the
 molecular laboratory at DVMPB, SUA.
- Manuscript writing and submission.

Activities for objective 4; SUA, NALIRI laboratory and the field stations

- We will design and administer structured questionnaires and observational studies to selected households and owners of animal shelters to capture presence of distinct features of climatic changes related to bats and rats' population dynamics over times.

6. Overall Socio-economic impact and commercial relevance

Describe the envisaged economic and societal impact of your project especially in relation to the national and regional development plans of SSA. Highlight any commercial potential/business linkage of your proposed idea. (1 page)

The proposed project will contribute to the improvement of surveillance activities technologies and diagnostic capacity of emerging and re-emerging viral diseases in the region and contributing to prompt control measures for the spread of infectious agents. Identification of the pathogens inventory circulating in the study area and beyond, will raise public health awareness on the proper use of the bats manure and wild rats for





consumption. People, will be aware of the health hazards carried by these animal species, that will lead to improved human and animal livelihood and food security. Both human and livestock viral diseases cause negative socio-economic impacts on the income of livestock farmers and, in particular, the livelihoods and food security of the most vulnerable rural communities, notably of women. The project will also contribute towards national and regional control of such debilitating viral diseases by early warning signs detection to block global pandemics. Therefore, identification and continua surveillance activities of zoonotic diseases and rapid detection during epidemics in the region will help the joint control of the disease in the region hence improving the livelihoods and nutritional security in our communities, while contributing to the national Gross Domestic Product (GDP). The molecular diagnostic assay (PCR) designed and validated under this project will also contribute in testing human and animals to early disease detection and continual surveillance activities.

7. Development Gender Considerations

Describe how your project has incorporated gender issues and the likely impact on women and men (1 Page)

The project will take into consideration gender equity before and during the execution of the project. The study will take into account the potential differences between males and females in terms of their special roles. Specifically, the project team has included both men and women in a 50/50 ratio, however, the proportion might change based on the quality of the MSc student we will engage with. The senior team members who are considered mentors are females. This is to say, we have ensured equal opportunity for capacity building and networking in this proposal, linking individuals from different institutions with different expertise. In the implementation of the project, gender will highly be considered during sample collection and data acquisition. Both, male and female individuals found in places for data collection will be given equal chances to explain what they understand on the negative health effects of either using bats/rats by-products for economic purposes or for consumption. Data related to social norms and institutions in farming communities, women's and men's indigenous knowledge and survival-both for self and farming communities, gender division of labor- and any shifts in the practices and norms e.g who does what and why or why not? In order to successfully explore those roles, the project will specifically include both female and male involved in manure collection, or capturing and selling these animals for food and different activities along the value chain. The investigations of infectious diseases will inform the impact of gender dynamics in improving prevention, and control of infectious diseases. Therefore, gender involvement in this project will be considered during project planning, execution, implementation, monitoring, evaluation, and project close-up. This will also be in-line with the SUA gender policy on research where it proposes to mainstream gender issues in all research activities and researchers must strive to generate gender-disaggregated data and gender sensitive technologies.

8. Mentoring and Capacity Building of MSc Students

Indicate if your project will integrate any MSc students. Indicate the number of students and suggested topics for their study, where applicable





The project will mentor one Ph.D. by thesis and two MSc students by course work and research registered in MSc in One Health molecular biology or Molecular biology and Biotechnology and does not have research funds at the DMPB, Sokoine University of Agriculture, Tanzania. The Ph.D. student will be full time, while the MSc students will work on a daily basis for the project during their second year of studies. The student will participate in all the four objectives, from sample collection, and sample and data analysis, to manuscript writing. The manuscripts will contribute to their thesis development according to SUA regulations. "Hunting for emerging and re-emerging viruses with potential for zoonotic transmission using metagenomics". The MSc students will work on; 1 MSc student "Genetic characterization of the novel virus(es) with potential for zoonotic transmission"; 2 MSc "The design and validation of molecular-based assay(s) specific for the identified virus(es) for prompt diagnostic response in case of emergence".

To enhance capacity building and transferable skills among team members; the mentor, Prof. Wambura will be a focal person to ensure smooth run of the project in scientific context. He will be an overall advisor for the lead applicant and the research team as well as for the Ph.D. student. The two MSc students will be under immediate supervision of the Ph.D. student, and the other team members. The students and research team members will acquire more transferable skills by attending different courses organized by the University or other stakeholders. Furthermore, the Ph.D. student and other members of research team will attend a special training on handling big genomic data (Bioinformatics), as part of capacity building at SUA, to upgrade training and genomic diagnostics capacity for prompt response to pandemics.

9. Risk Analysis

Describe the potential physical, environmental, political, economic, and social risks that may be encountered during project implementation and proposed mitigation plans. This should be submitted

During sample collection in the field, there is a possibility that researchers and assistants be exposed to infectious disease agents which can cause serious disease conditions and possibly spread the disease to the community at large leading to an epidemic with serious health and economic effects to the community and the government. The risk will only be mitigated by strict follow-up of the guidelines and standard operating procedures for collecting and handling biological samples from animals with the potential for infectious disease transmission to other species.

During sample analysis in the laboratory, there is a risk for laboratory personnel and environmental contamination with biological agents from the field samples. Following a lack of safety reagents (e.g. disinfectants such as 70% alcohol and sodium hypochlorite); and equipment (e.g. autoclave and biological safety cabinet II), failure to follow safety precautions and laid down guidelines might lead to transmission of the agents from the laboratory to the environment causing serious health effects. Similarly, the risk can only be handled by ensuring all appropriate biosafety materials and reagents are available during sample analysis, as well as all the guidelines for handling biological hazards and waste management are correctly followed and adhered to.

10. Ethical Considerations

Briefly describe the ethical issues that your project is likely to present during implementation, and how you plan to obtain the necessary ethical approvals. (0.5 Page)





The study will involve the collection of samples from wild animals; bats and rats to be more specific from the two previously named regions, where both invasive (whole blood) and noninvasive (stool) samples will be collected. These specimens pose a great risk of infectious disease exposure to the researchers and the community if biosafety and security aren't carefully considered. Ethical approvals will be sought from the Ethical Committee of Research and Publication of the Sokoine University of Agriculture, Morogoro, Tanzania, and the Tanzania Wildlife Research Institute (TAWIRI). All personnel handling or sampling animals will wear appropriate Personal Protective Equipment (PPE) and practice appropriate biosafety practices to avoid spreading infection from the sampled animals to humans, and from one area to the other. This includes wearing dedicated clothing (e.g. coveralls and rubber boots) that can be removed and/or discarded once fieldwork or laboratory work has been completed. Nets and traps will be used to capture bats and rats respectively. Capture animals will be manually restrained for sample collection; no drugs will be used for restraining study animals. Animal restraining and sample collection will be performed by trained veterinary officers. All research activities will be conducted in compliance with the established national and international protocols, and research ethics for animal handling.

11. Partnerships

Briefly explain the collaborative partnerships within the proposed project. Explain the **role** and specific contribution of each partner. (1 Page).

The current research partnership between SUA and TAWIRI aims to establish active viral hunting research activities, and capacity building in the region using cutting-edge molecular technologies. SUA will host the project, in the Department of Veterinary Microbiology, Parasitology, and Biotechnology (DVMPB) laboratories. The Department has experience and expertise in infectious disease surveillance activities of both humans and animals. The department also is equipped with experienced researchers for different pathogens, in a wide range of research topics, from immunology, bacteriology including drug resistance, virology, and molecular studies including genomics. Among others, African swine fever, Peste des petits ruminants, Dengue fever, Rift Valley fever, and foot and mouth disease have been in continual research grants for years, with well-established laboratory facilities for research activities. As part of capacity building, apart from other project activities, the project will support one MSc student who will be registered at SUA for dissertation development. The DVMPB will host the major part of the project research activities, and the direct supervision of the student. All the collected samples will be kept at DVMPB, and all sample analyses will be conducted at the molecular laboratory in the same department. TAWIRI comes in as a partner institution with Dr. Mikidadi as a focal person. The TAWIRI will provide capacity and expertise in study areas and sample collection. TAWIRI is a local partner institution, located in Northern Tanzania, with a mandate to lead all research activities related to wildlife.

12. Budget and Matching Funding Support

Indicate the total proposed budget, clearly highlighting the matching funds. Complete the consolidated detailed budget as per the budget template provided.

Matching Funding: State if there is any matching support (either in-kind or in-cash or both) by the university or partners, the sources of the support, and how these will benefit or add value to the project.

13. Publications





Highlight the publications made by the lead applicant and the collaborating partner, you may provide relevant links) (0.5 page)

Lead applicant (Emmanuel George Kifaro, Ph.D.)

- i. https://doi.org/10.56367/OAG-038-10484
- ii. https://doi.org/10.3390/diagnostics13020261
- iii. https://doi.org/10.1007/s13206-022-00065-0
- iv. https://doi.org/10.1186/s13104-017-2883-3
- v. https://doi.org/10.1089/aid.2017.0025
- vi. https://doi.org/10.1093/jac/dku087
- vii. http://dx.doi.org/10.4102/ojvr.v81i2.717

Emma Peter Njau (Ph.D.)

- i. https://doi.org/10.1038/s41598-021-92593-2
- ii. https://doi.org/10.1111/tbed.13747
- iii. https://doi.org/10.1007/s11250-014-0628-z
- iv. http://www.suaire.sua.ac.tz/handle/123456789/4674

Prof. Philemon Wambura

- i. https://doi.org/10.1023/A:1005173232204
- ii. https://doi.org/10.1111/tbed.12200
- iii. https://doi.org/10.1016/j.aaf.2020.05.003
- iv. https://doi: 10.1016/j.heliyon.2019.e02220
- v. https://doi.org/10.1016/j.aqrep.2020.100300
- vi. https://doi.org/10.1155/2019/3768948
- vii. https://doi.org/10.1016/S0167-5877(99)00089-6
- viii. DOI: https://doi.org/10.4142/jvs.2007.8.3.303
- ix. https://doi: 10.1007/s00705-006-0898-5
- x. https://doi.org/10.24105/2157-7560.10.401
- xi. https://doi.org/10.4269/ajtmh.18-0798
- xii. https://doi.org/10.4102/ojvr.v86i1.1683
- xiii. https://doi.org/10.1371/journal.pntd.0006931
- xiv. https://doi.org/10.4172/2157-7560.1000394
- xv. https://doi.org/10.1016/j.heliyon.2017.e00428
- xvi. https://doi.org/10.9734/JAMB/2017/36036
- xvii. https://doi.org/10.9734/BBJ/2016/20150
- xviii. https://doi.org/10.9734/AIR/2015/13382
- xix. https://doi.org/10.4102/ojvr.v81i2.729
- xx. https://doi.org/10.4102/ojvr.v81i2.728
- xxi. https://doi.org/10.4102/ojvr.v81i2.736

Partners

Dr. Mikidadi Mtalika (BVM, MSc)

i. https://www.suaire.sua.ac.tz/handle/123456789/2949

14. References

List the references. (1 Page)

- Africa CDC (2023). Republic of Tanzania declares Marburg Virus Disease (MVD) Outbreak https://africacdc.org/news-item/republic-of-tanzania-declares-marburg-virus-disease-mvd-outbreak/ Cite visited on 31st October 2023.
- Briese, T., Paweska, J. T., McMullan, L. K., Hutchison, S. K., Street, C., Palacios, G., Khristova, M. L., Weyer, J., Swanepoel, R., Egholm, M., Nichol, S. T., & Lipkin, W. I. (2009). Genetic detection





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Annex 1.

ENVIRONMENTAL AND SOCIAL SAFEGUARDS

PRE-SCREENING TOOL

All projects receiving funding from RSIF must adhere to the Environmental and social safeguard Framework of the World Bank. Screening and categorization of projects is one of the key delivery requirements of the World Bank's Social and Environmental Safeguard Framework. This prescreening tool will assist the RSIF RCU fulfill this requirement by identifying potential social and environmental risks and their significant and determine the level management required to address the potential risks and impacts. A more detailed assessment will be done to successful projects at the time of award that will inform the design of tools and mitigation plans to provide guidance to the implementation of quality projects and meet the requirements of the World Bank Environmental and Social Safeguard Framework.

a. Grievance Redress Mechanism

No		Response
1	Does the University have a grievance redress mechanism?	Yes, the university has a
		grievance redress
		mechanism
2	Describe the University's grievance redress mechanisms related to grant/	The University resolves
	projects and partnerships and the remedial processes	grievances through
		administrative meetings
		of the affected
		grant/projects and or
		partnerships and the
		remedial processes. For
		projects/grant that will
		result in large-scale
		grievances, the national
		administration meetings
		are also contacted to
		reach resettlement.
		Normally the grievance
		is registered to the
		University
		administration through
		any channel such as
		phone, letter, email or
		meeting). Then the
		University will hold
		meetings to resolve the
		grievance in place via
		the Directorate of
		Postgraduate Studies,





Research, Technology
Transfer and Consultancy.

b. Social Safeguard

No		Response
1	Describe any negative social and economic impact the project may have on the community e.g (providing access to community development resources and project benefits	This project will provide awareness to the community on the potential existence of lethal viruses in bats and/or rats which can be transmitted to human and animals and cause significant health hazards and to impair food security. The project will suggest the best use of bats manure for crop production, or consumption of bats and rats for nutrition purposes.
2	Briefly describe in the space below how the Project is likely to improve gender equality and women's empowerment in ASET field	This project is likely to improve gender equality and women's empowerment through project supervision and mentorship. Two of the project members are women experts in the field of viral research of food security importance.

c. Environmental Safeguards

No		Response
1	Does the University have an environmental management policy?	The management and
		coordination of
		environmental issues in
		Tanzania is mandated
		by the National
		Environmental
		Management Council
		(NEMC), which was
		enacted by the
		Parliament of the
		United Republic of



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_		1
		Tanzania (The
		Environmental
		Management Act,
		2004). SUA adheres to,
		and observes, not only
		the provisions stated in
		the Act that established
		the NEMC but also
		implements all projects
		and activities in
		accordance with the
		National Environmental
		Policy.
2	What are the expected environmental impacts out of the proposed	The possible effect is
	project activities?	the ecological
		disturbance of the bat
		population in the
		sampled places.
3	How will the above impacts be mitigated?	Proper use of sampling
	·	nets and adhering to
		the developed sampling
		protocols will be strictly
		followed.