



PREPARE4VBD newsletter

December 2024

Newsletter #5

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News and Views from the Coordinator

It is again the end of yet another year, and a third year has now gone by for the PREPARE4VBD project. In 2024

we rounded another important milestone, as we in August 2024 completed another 18 months period (RP2), now embarking on the third and last reporting period. In 2024 a lot of work has gone into the 2nd periodic reporting, both the technical and financial reports, deliverables, and the recent online review meeting with our EU Project Officer and two external reviewers on November 22nd. Overall, the project has made significant strides in 2024. Numerous publications, presentations, and stakeholder engagement

activities have been completed. The project website has been updated with new resources and a blog (which you can read more about in this issue) A major research highlight is the successfully conducted massive, cross-country vector snail warming experiments to elucidate impacts of climate change on fascioliasis across a vast continental and climatic gradient, all the way from our partner in South Africa all the way to Denmark, which required very close collaboration and synchronized efforts across several of the project partners.

As the project enters its final phase, efforts are being ram-

ped up to share these results and tools with all relevant stakeholders, not just via scientific publications but also through broader outreach. This will culminate in a major meeting and outreach event in

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Uganda in May 2025, hosted by the Ministry of Health in Uganda, where a comprehensive overview of the project's results will be presented to

stakeholders, including policy-makers. I look very much forward to continue the planning of this event as we enter 2025.

With that, we wish all the Consortium partners and our collaborators a very Festive Xmas season and a Happy New Year!

Anna-Sofie Stenqvist



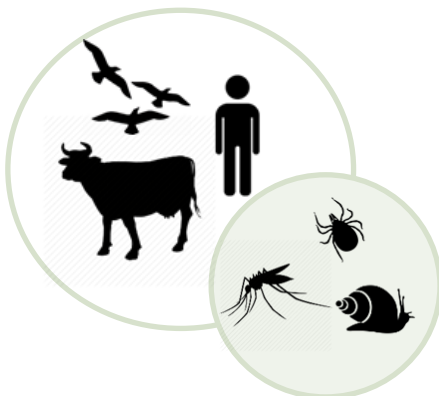
About PREPARE4VBD

Vector-borne diseases (VBDs) constitute a major challenge facing African healthcare systems and economies, but also increasingly pose a threat to Europe as spread of vectors and zoonotic VBDs is anticipated more frequently in the futu-

re. **The PREPARE4VBD project address this challenge as s a multidisciplinary consortium bringing together ten university and ministerial partners from five African and three European countries.**

PREPARE4VBD will

develop new knowledge, detection tools and surveillance systems to improve preparedness in Africa and Europe for vector-borne diseases transmitted by mosquitoes, ticks and freshwater snails to livestock and humans.



This project has received funding from the European Union's Horizon 2020 research and innovation programme under grant agreement No 101000365

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PREPARE4VBD Research Highlights

Modelling snail-borne diseases – impacts of climate change across Africa and Europe

“Prepare4VBD is contributing to greater understanding of the changing distribution of snail-borne diseases due to climate change, emphasising the need to prepare for these new realities.”

To make more informed predictions on the impact of climate change on snail-borne disease across Africa and Europe, partner UCPH has developed new models for two parasitic snail-borne diseases: schistosomiasis and fascioliasis.

The schistosomiasis models, published earlier this year in *Global Change Biology*, focus on the widespread schistosomiasis intermediate host snail *Bulinus truncatus* (Fig 1). These models show that areas in Central Africa and Southern

Europe will become more suitable for this snail in the future, while the Sahel region might become unsuitable due to increasing temperatures.

Fascioliasis risk maps for Africa have been made available on the Prepare4VBD website (Fig 2, next page). These maps show the transmission risk for the two most important species that cause fascioliasis, *Fasciola hepatica* and *Fasciola gigantica*, under current and future climatic conditions.

They show a decline for the temperature species *F. hepatica*

and a redistribution of the tropical species *F. gigantica*.

Common to both studies is that they combine multiple data sources, such as experimental data and geolocated occurrence, and multiple modelling techniques in order to make more robust and nuanced predictions.

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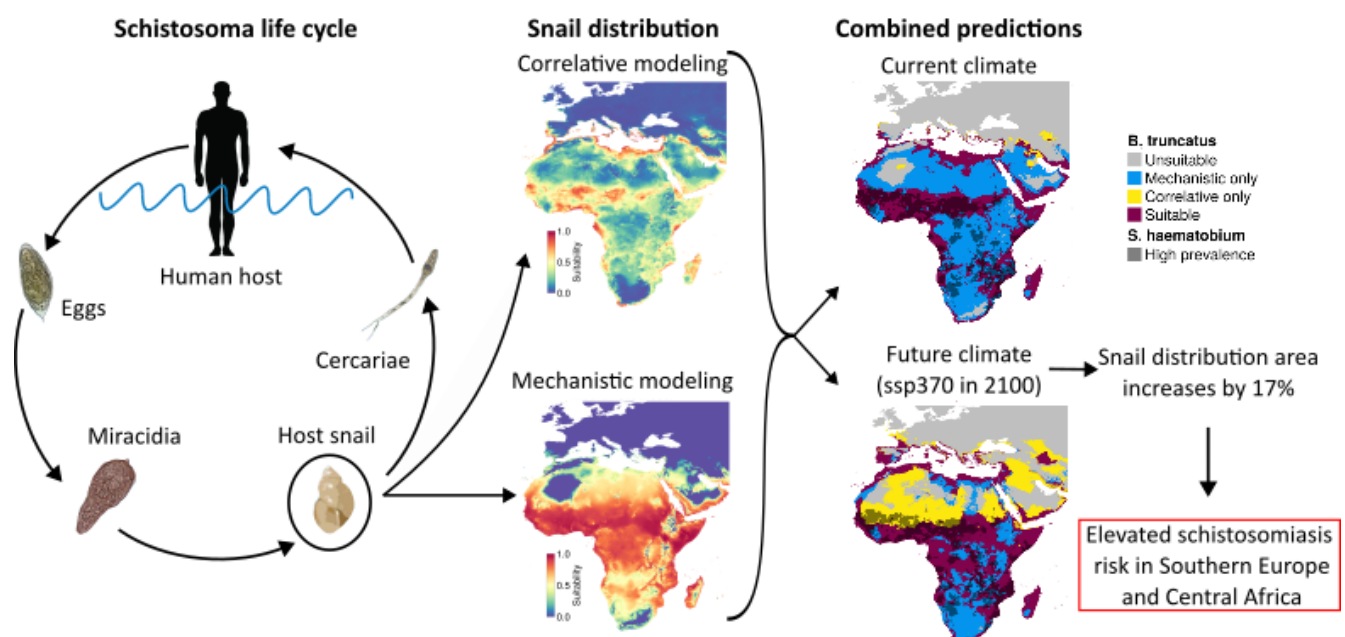


Fig 1. Example of the combined modelling approaches here shown with *Bulinus truncatus* to predict snail distribution and *Schistosoma haematobium* prevalence. Thermal suitability for *B. truncatus* predicted by the mechanistic model, habitat suitability for *B. truncatus* predicted by the correlative model and prevalence of *S. haematobium* infection, 2000–2010. (van der Deure et al., 2024)

PREPARE4VBD Research Highlights

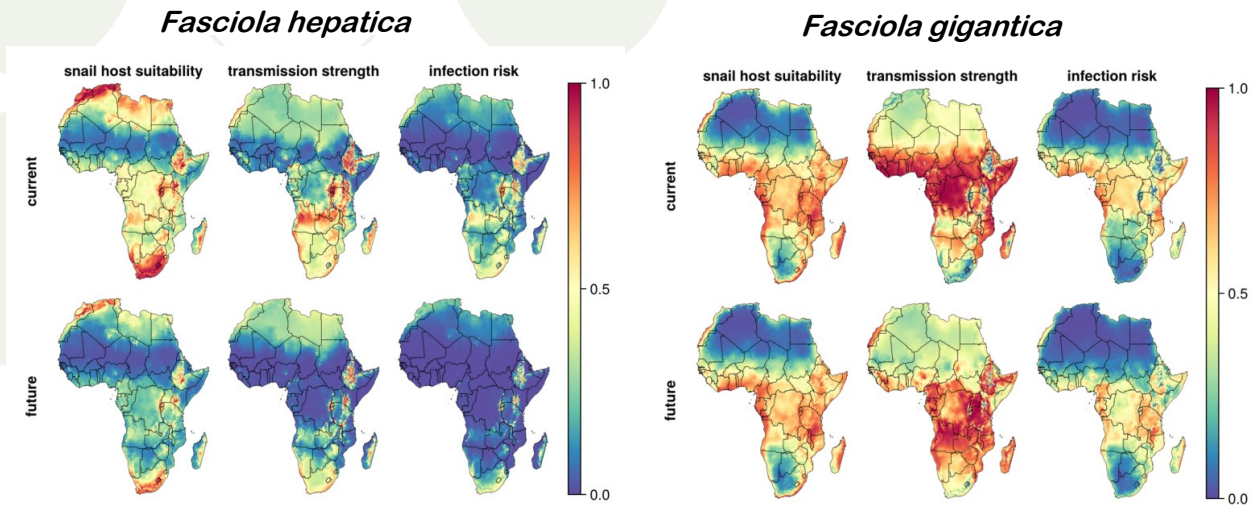


Fig 2. UCPH has developed risk maps for *Fasciola hepatica* (top) and *F. gigantica* (bottom) under current and future climatic conditions. For more information see our website (<https://prepare4vbd.eu/risk-maps/>).

... (continued)

For schistosomiasis, we use observations from a major warming experiment and a life cycle model to estimate at what temperatures populations of *B. truncatus* can survive and thrive. We also use geolocated occurrence records to fit species distribution models, which predict where a species is likely to be found based on environmental conditions in locations where a species is known to be. Each of these models have their own strengths and limitations. For instance, the species distribution models were unable to capture the thermal maximum that was observed in the laboratory. By applying both to the same species, we were able to gain a deeper understanding into the ecology of *B.*

truncatus under climate change.

For the fascioliasis, we similarly used both experimental and geolocated occurrence data. However, in this case, we use occurrence data to predict where intermediate host snails are likely to be found, while we use experimental data to predict which areas are suitable for transmission of the *Fasciola* parasites. Here we found a high degree of agreement between both models, both with regard to the spatial distribution of each *Fasciola* species and their respective hosts, and to the effects of future climate change. Here, since two models that use completely different input data and process them in different ways predict

similar outcomes, we can make these predictions with even higher confidence.

Models can be a useful tool to predict the impact of climate change on public health. However, it is important to tailor models by incorporating all the available knowledge and interpreting their outputs carefully. With the development of the models for schistosomiasis and fascioliasis discussed here, Prepare4VBD is contributing to greater understanding of the changing distribution of snail-borne diseases due to climate change, emphasising the need to prepare for these new realities.

***Fasciola gigantica* trematode infections in cattle in Uganda – species confirmed using molecular tools**

Introduction

Fascioliasis caused by two species of a trematode worm commonly referred to as liver fluke (*Fasciola hepatica* and *Fasciola gigantica*) is a neglected zoonotic disease of livestock that is widespread globally. Historically *F. hepatica* has been reported in temperate regions in Europe, Asia, Africa, the Americas and Oceania while *F. gigantica* is restricted to tropical regions of Africa and Asia. A recent review and meta-analysis for global prevalence of liver disease by Lan et al., 2024 (in Journal of Global Health) further revealed the global spread and prevalence of fasciolosis and reported a pooled seroprevalence of fasciolosis in bovine, ovine and humans to be 17%, 13% and 5% respectively. In a systematic review focusing on animal fascioliasis in eastern and southern Africa by Nambuya et al. (lead by Makerere University, Uganda), soon to be published, found high prevalences in different animal species, such as 23.4% in cattle, 23.3% in sheep, 7.9% in goats, 47.5% in mules, 23.2% in donkeys, and 12.2% in horses. Despite of this current evidence of the disease in both humans and animals, limited clinical and prevention interventions exist. Fascioliasis poses significant public health concern and economic losses by affecting several aspects of animal productivity. World-wide losses in animal productions are estimated to be over

“It is therefore imperative to undertake continuous surveillance and clearly identify the fasciola species infecting livestock and humans in different regions especially in low and middle income countries.”

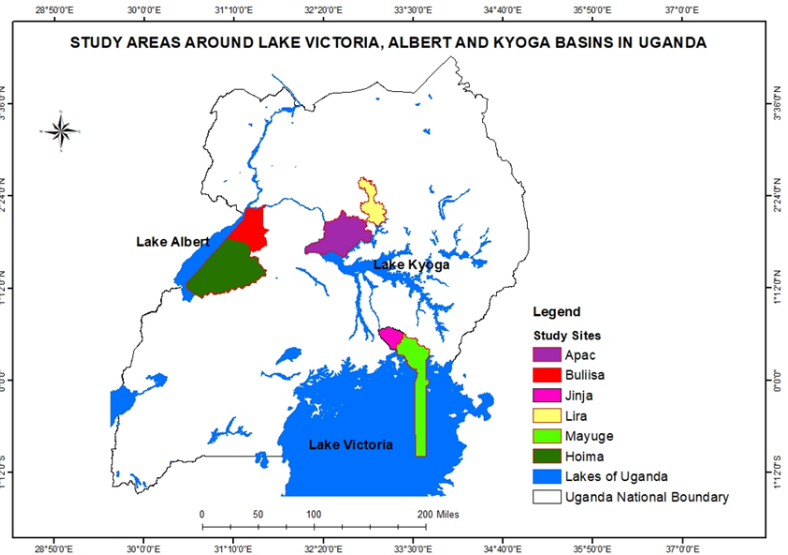


Figure 1. Map of study areas around the three lake regions in Uganda.

3.2US\$ billion dollars per year by liver fluke infection. In Uganda, annual losses to condemnation of the livers infested with *Fasciola* species have been estimated to be 10-90 thousand USD annually. As a recognised zoonotic neglected parasitic disease, World Health Organization (WHO) has estimated that about 180 million people are at risk of infection and 2.4 million people are infected with fasciolosis. This has led WHO to include the group of food-borne trematodiasis in the priority list of Neglected Tropical Diseases (NTDs) in its WHO NTD Roadmaps for 2020 and 2030. It is therefore imperative to undertake continuous surveillance and clearly identify the fasciola species infecting livestock and humans in different regions especially in low and middle income countries.

Methods

We conducted a study to determine the prevalence and genetic diversity of *Fasciola*

species in cattle slaughtered along Lake Albert, Kyoga, and Victoria basins in Uganda (Fig. 1). A cross-sectional study was conducted where adult flukes and feces were collected from slaughtered cattle in the study area. Morphological and molecular techniques were used to identify and characterise adult flukes. PCR was performed for species identification by amplifying DNA polymerase delta (*pold*) and Phosphoenolpyruvate carboxykinase (*pepck*) genes. Additionally, Cytochrome C Oxidase I (*cox I*), and NADH dehydrogenase subunit I (*nad I*) genes, and sequenced. Phylogenetic analysis was performed to determine the genetic diversity of the flukes.

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Fasciola gigantica trematode infections in cattle in Uganda – species confirmed using molecular tools

Results

The prevalence of *Fasciola* based on morphological examination was established to be 34.78% (112/322) and 14.91% (48/322) on coprological examination. Morphologically, out of 389 adult flukes identified 261/389 (67.1%), 61/389 (15.68%), and 67/389 (17.22%) were provisionally identified as *F. gigantica*, *F. hepatica*, and intermediate respectively (Fig 2). Upon PCR, all provisionally identified *Fasciola* species were confirmed to be *F. gigantica* based on pepck gene marker.



Fig 2. Morphological identification of liver flukes (above). *Fasciola gigantica* specimen (below).



Fig 3. Examining cattle liver (left). Field examination of samples (right).

Conclusion and recommendations

Our results revealed high prevalence of *Fasciola* sp infestation in the examined cattle along three lake basin areas in Uganda. We further confirmed that the *Fasciola* species that infest cattle in Uganda is *F. gigantica*. We therefore recommend intensified surveillance and proper

guidance for cattle farmers to undertake routine deworming using the recommended anthelmintics for the control of *Fasciola gigantica*. In order to improve food safety, routine meat inspection with special focus to liver as organ should be undertaken as well as public health education to avoid eating fresh potentially contaminated vegetables from hotspot areas of *fasciola* infestation.

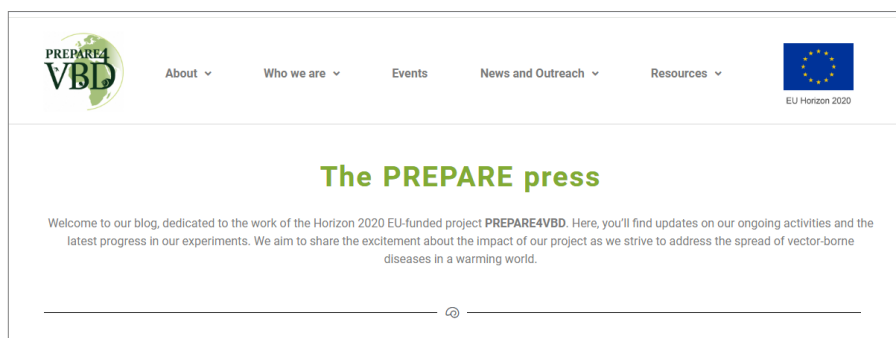
Have you seen our BLOG?

The PREPARE Press - sharing our latest research findings and activities within PREPARE4VBD

The PREPARE Press serves as the official blog for the PREPARE4VBD project. Through our blog, we bring you the latest updates on our research and experimental progress, while exploring the wider implications of our findings. We are developing the blog as a crucial tool for expanding the reach and impact of our scientific work. By sharing it on the blog, we will need to communi-

cate scientific findings in an accessible way, engaging a broader audience beyond academia, including policy-makers, industry professionals, and the public. Additionally, we hope that the blog will build awareness and inspire collaboration by showcasing the relevance and potential applications of our work.

Find our blog here:
<https://prepare4vbd.eu/blog/>



PREPARE4VBD is now on BlueSky!



Find us @prepare4vbd.bsky.social

“Science is only as strong as its ability to be shared, understood, and acted upon; discovery gains power when it reaches beyond the lab to inform and inspire the world.”

Publication Highlights

- Rua Khogali, Armanda Bastos, Dennis Getange, Joel L. Bargul, Shewit Kalayou, Nehemiah Ongeso, Joost Theo Petra Verhoeven, James Kabii, John Ngiela, Daniel Masiga, Jandouwe Villinger (2024). Exploring the microbiomes of camel ticks to infer vector competence: Insights from tissue-level symbiont-pathogen relationships. *Accepted in Scientific Reports*.
- Kuhnert P, Loosli N, Brodard I, Lindtke D, Jores J (2024). Resistance of zebu cattle (*Bos indicus*) to colonization by major ruminant hoof pathogens. *Veterinary Microbiology*, Vol 296 (110184).



News and Updates from the Project Management

Final project meeting in Uganda in May 2025

Planning of the final PREPARE4VBD project meeting to be held in Uganda, early May 2025, is a priority for the UCPH Coordinating Team and the hosting project partner VCD (Ministry of Health in Uganda). At the meeting a comprehensive overview of the project's results will be presented to stakeholders, including policymakers, so project partners in Uganda (MAK), Côte d'Ivoire (CSRS) and South Africa (UKZN) are also busy planning the outreach and stakeholder engagement activities.



Deliverables with deadline ultimo February 2025:

- **D2.4 (SwissTPH).** Maps of the geographical distribution of the disease risk, vector distribution/occurrence for the targeted diseases/vectors.
- **D3.2 (UCPH).** eDNA pipeline for detection of pathogens in environmental samples established.
- **D4.4 (UCPH).** List of Vector specific meta-barcoding primers designed and tested.
- **D7.4 (SwissTPH).** Report on simulation results of RVF transmission model to assess different intervention scenarios.
- **D8.3 (CSRS).** PREPARE4VBD MOOC on VBD surveillance - based on input (videos) from WP2-7.

Deliverables with deadline ultimo May 2025:

- **D2.5 (SwissTPH).** Table presenting disease burden estimates (zDALYs) for the partner countries in SSA.
- **D2.6 (SwissTPH).** Web-interface for surveillance data on project website.
- **D5.4 (UBERN).** scRNA-seq data analyzed and disease susceptibilities for at least one VBD predicted for one European cattle breed.
- **D7.5 (SwissTPH).** Report eport Online training module on model-based surveillance.
- **D9.4 (CSRS).** Final Stakeholder Webinar.

PREPARE4VBD
newsletter

**Newsletter editorial
board:**

Anna-Sofie Stensgaard
(asstensgaard@sund.ku.dk)

Mita Eva Sengupta
(msen@sund.ku.dk)

Jennifer Upfold
(jennifer.upfold@sund.ku.dk)



The PREPARE4VBD newsletter series are biannual and will provide updates on project progress incl. research activities and capacity building, important deadlines in the project and upcoming events.

This PREPARE4VBD newsletter can be shared with relevant or interested institutions and stakeholders.

Find the PREPARE4VBD newsletters here:

prepare4vbd.eu/newsletter





The PREPARE4VBD Consortium

PREPARE4VBD Contact information

E-mail:

info@prepare4vbd.eu

Project Coordinator:

Anna-Sofie Stensgaard, UCPH
asstensgaard@sund.ku.dk

Project Manager

Marie Nicole Sorivelle, UCPH
mariesorivelle@sund.ku.dk



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Follow the project results, news and subscribe to our newsletter on:

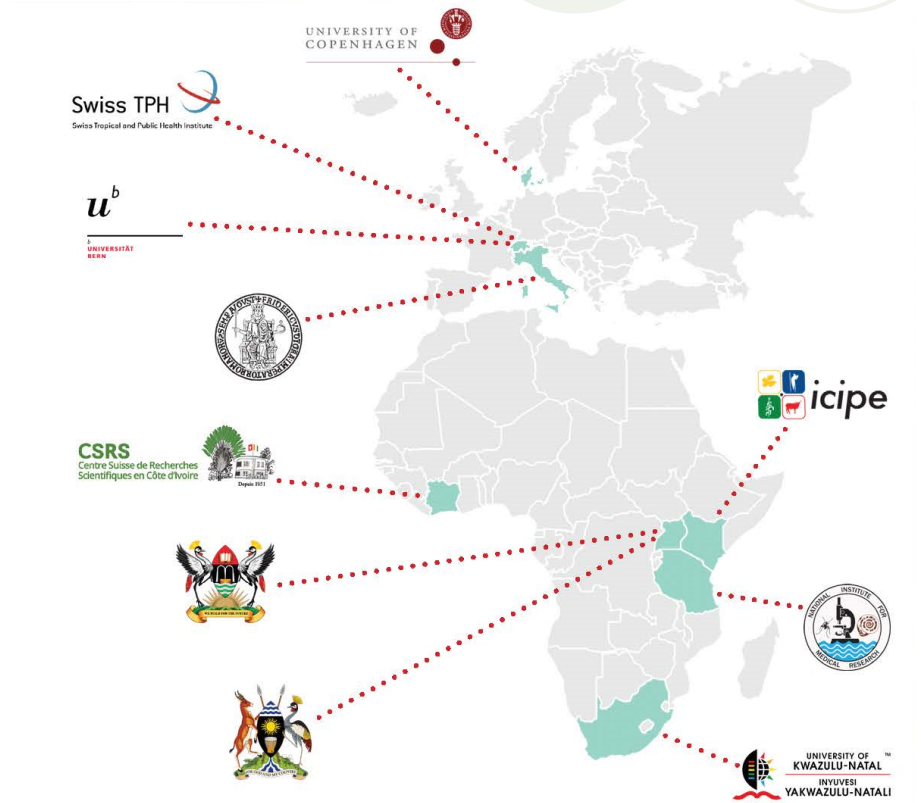
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