# ERRAZE@WUR: Early Recognition and Rapid Action in Zoonotic Emergencies

ERRAZE@WUR is an ambitious One Health research and investment programme at Wageningen University & Research. It aims to deliver new scientific knowledge and practical tools to help prevent future pandemics and mitigate their impact when they do occur.

Within ERRAZE@WUR, WUR scientists apply their knowledge of agri-food systems, the Global One Health approach, ecology, animal health, virology and epidemiology, societal impact, systems transformations and many more fields of expertise, to making the world safer from zoonoses.

wur.eu/erraze
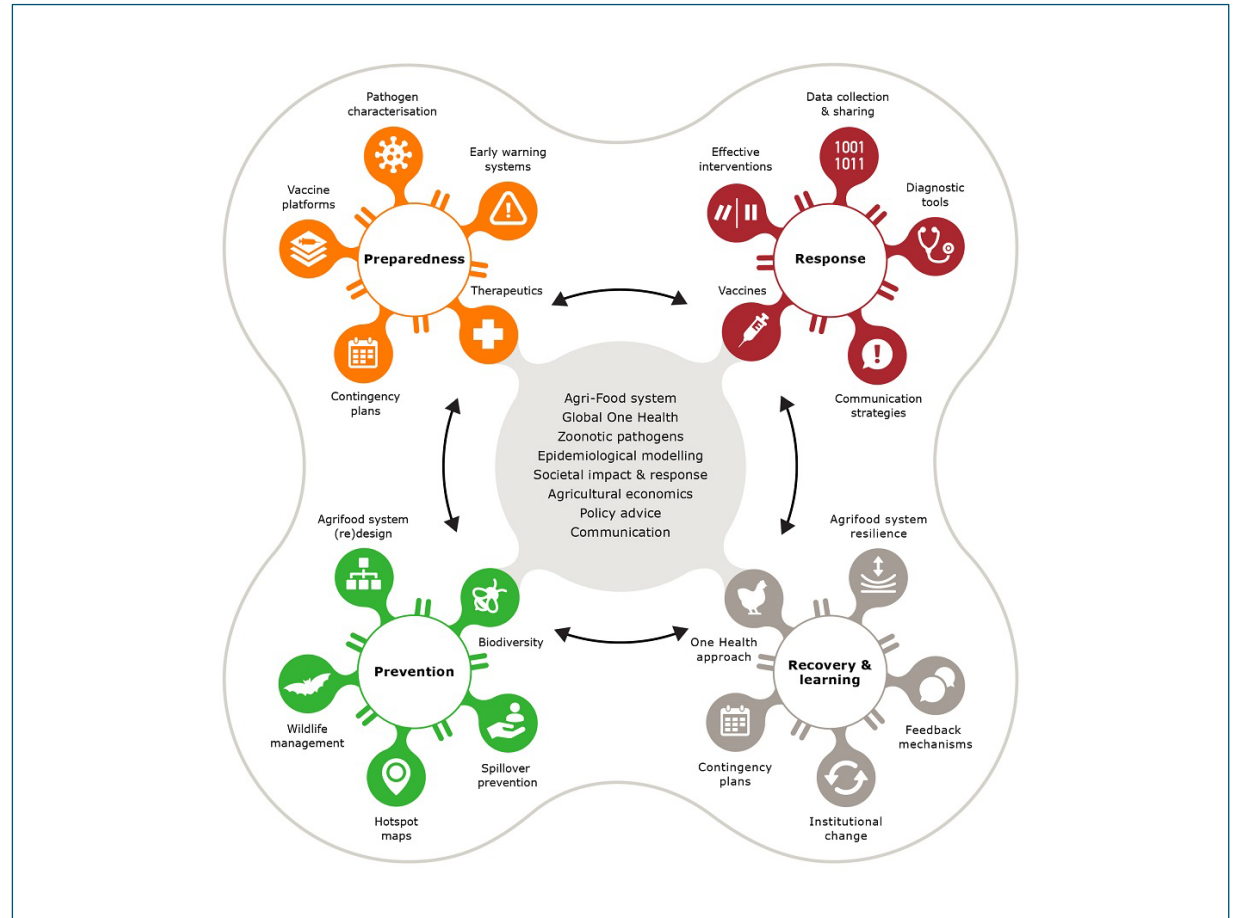
Preface

ERRAZE@WUR

With enjoyment we herein present the projects that have been funded with ERRAZE grants. Most projects are ongoing, and some have been finalised. Further output from the projects will be included as it becomes available.

One Health collaborations

All projects have involvement from researchers of at least two science groups of Wageningen University & Research. Many projects dovetail with partnering ERRAZE projects; in this document it has proven impossible to visualise all these interconnections. In addition, teams have been able to leverage funding from additional funding sources. We want to acknowledge the support from the Dutch Ministries of Health, Welfare and Sport, and Agriculture, Nature and Food Quality, in particular.

Find out more

For more information on the projects, click the links in the project descriptions, reach out to the project leads, or contact Joukje Siebenga, programme manager of ERRAZE.

Content – Projects are organised by investment area

Facilities and equipment

Diagnostics, detection and characterisation pipeline

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Scenario studies, and systems approaches; towards transformations and change

Host – pathogen interactions

Effective vaccines

Capacity building and knowledge exchange

Facilities and equipment

We invest in continuous improvements to WUR's ability to fulfil its role in mitigating and preventing future outbreaks of zoonotic disease, by upgrading our facilities and equipment. This helps us in our role as a research provider, and in continuing to deliver scalable and reliable diagnostic services to our internal and external stakeholders.

These investments enable for example the purchase of lab equipment, the implementation and validation of techniques new to our labs but not novel to science, and the digitisation and automation of laboratory processes.

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Automation and digitisation in diagnostic capabilities; crisis response

WUR capacity for rapid and large-scale testing during zoonotic emergencies and outbreaks of notifiable animal diseases have been strengthened by automation and digitisation.

The pre-analysis steps and many of the analyses are being automated. The aim is for all generated data to be immediately digitised and stored. That way, the investments enable streamlining of the logistics of sample streams, and increase the capacity, quality and accuracy of analyses.

Facilities and equipment

Project lead   Heather Graham
Year   2021-2023
More information   website article

Home

Develop and implement a FAIR data infrastructure

FAIR (Findable, Accessible, Interoperable, Reusable) data management is the norm for research. Here we will implement a fit for purpose, and easy-to-comply-with data infrastructure that enables efficient data management, automated access, and use of multiple data sources to perform real-time data-driven analysis and monitoring of emergent pathogens and epidemics.

This WP will be executed in close alignment with WP1 and WP2, ensuring that data generated by automated processes for diagnostics and detection of novel pathogens comply with FAIR principles, both within WUR and for researchers or end-users outside WUR, and with input from Wageningen Data Competence Centre. To this end, Yoda, a share-collaborate environment for research data, is being used. Yoda is the user-friendly interface on top of the iRODS architecture and language. Yoda enables you and your research partners to securely deposit, share, publish, and preserve (large amounts of) research data during all stages of a research project.

Facilities and equipment

Investment area	Facilities and equipment
Project lead	Dirkjan Schokker
Year	2021-2025

Home

Diagnostics, detection and characterisation pipeline

We invest in the development of new methods and approaches to be able to detect and characterise new and (re-) emerging pathogens.

In order to prevent such pathogens from spreading and turning into a new pandemic, it is critical that One Health professionals can implement measures to limit or stop spread as early as possible.

So we need to know where to look, what to look for and how often to look to be effective and draw reliable conclusions about safety, or to ring the alarm.

We also need to have the (diagnostic) tools that detect the right infectious agents, and we need to be able to interpret whether a pathogen has the potential to be dangerous to animals, humans, the environment or all of them.

Updating existing methods for (novel) pathogen detection, identification and characterisation

To develop surveillance and early warning systems for emerging zoonoses, WUR aims to expand its knowledge and research capacity on the pathogen – animal (/ human) interface. This will involve the purchase of state-of-the-art equipment to improve methods for pathogen (signature) detection and characterisation, and the possibility to scale-up, miniaturise and standardise rapid response infrastructure. The proposed investments include the strengthening and strategic alignment of e.g., PCR and sequencing capabilities across science groups and locations. In addition, we propose to establish a cell bank of respiratory tract organoids of different host species, including livestock (cattle, goat, pig), experimental animal species (ferret, hamster, rabbit), pets (dogs, cats) and humans (as reference tissue). Culture conditions will be established, optimised and protocols will be developed and validated to prepare organoid-derived respiratory epithelial cell cultures grown at air-liquid interface on transwell filters.

Diagnostics, detection and characterisation pipeline

| **Project lead** | Wim van der Poel |
| **Year** | 2021-2023 |

Home

Novel diagnostic reagents and therapeutics for zoonoses; A non-immune library of llama single-domain antibodies

Antibodies have great utility in zoonotic emergencies. They can be used both as therapeutic agents and as reagents in diagnostics. Previously, WUR relied on the immunisation of experimental animals for the generation of recombinant llama antibodies, which involves a relatively lengthy process.

With both the wish to reduce the reliance on animal experimentation and the need for ready and fast access to antibodies in mind, we wanted to create a non-immune llama antibody library for direct isolation of recombinant llama antibodies against any novel emerging zoonotic agent, that eliminates the future need for animal experiments. Such a library has applicability beyond the scope of ERRAZE@WUR, relevant for WUR and third parties. With funding from ERRAZE, we generated a large (4.4 billion clones) naive phage display library in two successive steps using blood samples from 47 non-immunized animals (11 camels, 23 llamas and 13 alpacas).

The first-generation library of 23 animals has been tested by isolation of antibodies against twelve model antigens. Antibodies could be isolated for all targets, although some further refinements are still being undertaken. This library is now ready for rapid isolation of novel antibodies in case of a novel pandemic.

Diagnostics, detection and characterisation pipeline

Project lead   Michiel Harmsen
Year   2021-2023
More information project and showcase

Home

Sampling methods; How and what to sample

The ultimate goal of this project is to set up an early warning system for emerging zoonotic pathogens and parasites in wildlife, agricultural and urban areas by trapping blood-sucking insects. At several selected field locations, blood-fed mosquitoes and *Culicoide*s biting midges were captured. These blood-fed insects were sent to our collaborators at WBVR and WENR for DNA and RNA analyses. The remaining mosquitoes (not blood fed) were sent to collaborators at ErasmusMC for West Nile virus and Usutu virus detection.

A scientific publication will outline the feasibility of our proof-of-principle concept. Further improvements in the catching efficiency of blood-fed mosquitoes are being undertaken. This is being done in the 3 wetland and 3 farm locations where we previously caught the highest number of blood-fed mosquitoes as well as the largest biodiversity of mosquito species. We will extend the sampling period duration and optimise the trapping approach. Traps with fermenting molasses and synthetic blend of the bioactive compounds of fermenting molasses seem most effective.

During the new catching season, we will use combinations of odour-baited trapping and eDNA sampling methods to assess blood-feeding patterns and mosquito-host interactions. In addition, we are examining with customs and NVWA the process of sampling of bushmeat samples arriving at Schiphol airport, to set up a process of routine monitoring of (zoonotic) pathogens in such samples.

Diagnostics, detection and characterisation pipeline

Project lead   Ralph Buij
Year   2021-2025
More information Showcase and article

Home

Metagenome data and analysis tools

For the early recognition and subsequent characterisation of new and emerging pathogens, innovative molecular tools and bioinformatics approaches will be implemented. Diverse pathogen sequences and communities from different matrices obtained from reservoirs, hosts and environments need to be characterized and evaluated to ensure the early recognition of pathogens that potentially pose a pandemic risk. The project focuses on practical tools for nucleic acids extraction, enrichment strategies and sequencing methodologies from real-life samples.

A library is being constructed, using metagenomic data. The project also uses bioinformatics to evaluate and analyse outcomes of all sorts of pathogen sequences and communities from different matrices of reservoirs and hosts. Rapid phylodynamics will be performed using classical phylogenetics and Bayesian models as appropriate. Ultimately, it will be attempted to predict phenotypic properties of emerging mutations using the library and new knowledge of metadata and machine learning.

Diagnostics, detection and characterisation pipeline

Project lead   Wim van der Poel
Year   2021-2025
More information   Showcase

Home

Fast scalable diagnostics

To prevent newly emerging zoonotic viruses from spreading widely and quickly, early detection plays an important role. For effective early detection, diagnostic tools are needed that have multiple characteristics. Using our knowledge of pathogen families that are considered to have a high likelihood of emergence, we develop and refine fast (on-site) detection tools ('targeted'). We consider which types rapid tests can be developed and can they be performed on-site, and for which types of samples. And we assess to what extent they provide a greater chance of detection than an 'untargeted' screening method.

To answer these questions, we apply two approaches. First, we aim to detect antibodies against viruses in blood from animals (birds and mammals); that means we're investigating whether zoonotic viruses are circulating in the animal population. This is done by developing easy to use rapid tests for on-site application and an expandable Luminex multiplex assay for detailed analyses in a laboratory.

Subsequently we develop a multiplex LAMP test for the specific on-site detection of identified novel pathogens or a combination of LAMP with CRISPR-Cas detection.

Diagnostics, detection and characterisation pipeline

**Project lead**   Peter Bonants
Year   2021-2025

Home

Using airway organoids to characterize infection kinetics

Respiratory viruses are amongst the leading global zoonotic threats to human health. Primary or stem cell-based human airway epithelial cells are increasingly used as model systems for virus characterisation, as they reflect the structure of the airways more faithfully than immortalized cell lines. We have previously established a biobank of multispecies mammalian airway organoids for air-liquid interface studies. These include livestock (cattle, goat, pig), experimental animal species (ferret, hamster, rabbit), pets (dog, cat) and humans (as reference tissue). Here, we have used these mammalian airway organoids to establish infection models with viruses belonging to families that harbour zoonotic viruses with pandemic potential, including influenza viruses, coronaviruses and paramyxoviruses. Primary read-out parameters were virus replication and dissemination (growth curves, assessment of phenotype of infected cells). These were be assessed using a combination of antibody staining, real-time RT-PCR assays and in situ RNA hybridization.

By comparing the tropism of these viruses for airway organoids of different host species, including those of humans, we aimed to validate these models as predictors of zoonotic and pandemic potential of newly emerging viruses. These studies will be continued in follow-up projects funded from other sources.
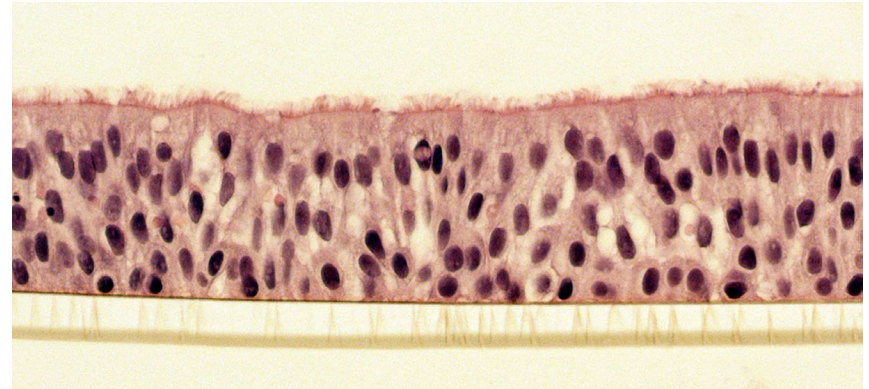
Diagnostics, detection and characterisation pipeline

Project lead	Rik de Swart
Year	2021-2023
More information	Showcase

Home

Mosquitoes as auxiliary troops in disease monitoring

We aim to develop fieldable assays that monitor pathogen circulation by using mosquitoes as 'flying syringes' and screening their blood meals. Diagnostic tests based on LAMP-PCR will be validated to identify pathogen, mosquito and host species, from the blood in the mosquitoes. The test, we envision, requires limited resources and will be highly valuable for disease surveillance in resource-poor settings.

Diagnostics, detection and characterisation pipeline

Project lead   Sander Koenraadt

Year   2022-2023

Home

Data and modelling to shape interventions

Widely available data and knowledge has the potential to help decision makers reach conclusions about what interventions might be best suited to limit or stop the spread of infectious diseases. For this the data needs to be parsed so that potential scenarios can be analysed and comprehensively assessed.

Through several approaches we address the collection of data (both traditional data and nontraditional data – such as web-derived information), and the analysis of that data.

We aim to create a framework that helps break the silos separating epidemiological modelling, and socio-economic modelling. This way, ideally, decision makers of the future will have a better way to weigh all the options at hand.

Home

Development of effective early warning and surveillance systems for detection of emerging epidemic pathogens

The risk assessment modelling is used to underpin the development of risk-based warning and surveillance systems for early detection of emerging pathogens. For the development of these models, avian influenza has been selected as model disease, since the viruses causing this disease spread globally, and they affect wild and domestic birds and, sporadically, mammals and humans. The methods and data structure informing our risk assessment models are generic, but they can be made pathogen specific by including pathogen specific risk factors.

A thorough identification of drivers and risk factors for the occurrence and spread of infections was made (e.g., host populations, production systems, weather, socioeconomic factors). Subsequently a comprehensive overview of data sources for the identified drivers/risk factors and procedures for data retrieval, processing and integration was developed. This data is then used to combine knowledge based (mechanistic) models with machine learning modelling techniques.

One Health, environmental and socio-economic factors are considered to assess and predict presence, distribution and or emergence of zoonotic pathogens at global and local (the Netherlands) levels. The models assess risks at different levels: in wildlife, domestic animals and at the level of the spill-over at the animal-human interface.

Data and modelling to shape interventions

|	
Project lead	Jose Gonzales
Year	2021-2025
More information	Showcase and publication

Home

Developing quick-response models for multi-host outbreaks

Mathematical models can provide key insights in the potential for a new disease to spread. These models summarize the real-world spread of a disease into a few mathematical rules that aim to capture the most relevant mechanisms. When these models match reality well enough, they help us predict how an outbreak might develop next, and what we can do to stop it or slow it down.

We do not know which disease will come next, but many diseases have common traits, like how they spread or which animals they infect. Within ERRAZE, we are building a modelling framework that can be quickly adapted to different diseases, especially those that affect people, wildlife, and farm animals. We have now finalized the prototype of the model, and are expanding its capabilities, such that it can accommodate modeling the spread of diseases like rift valley fever, bluetongue disease and swine influenza.
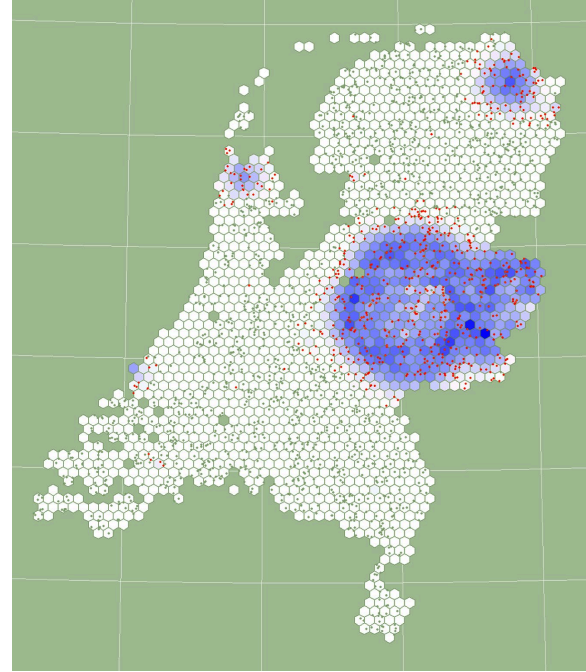
Data and modelling to shape interventions

Project lead   Quirine ten Bosch
Year   2022-2024
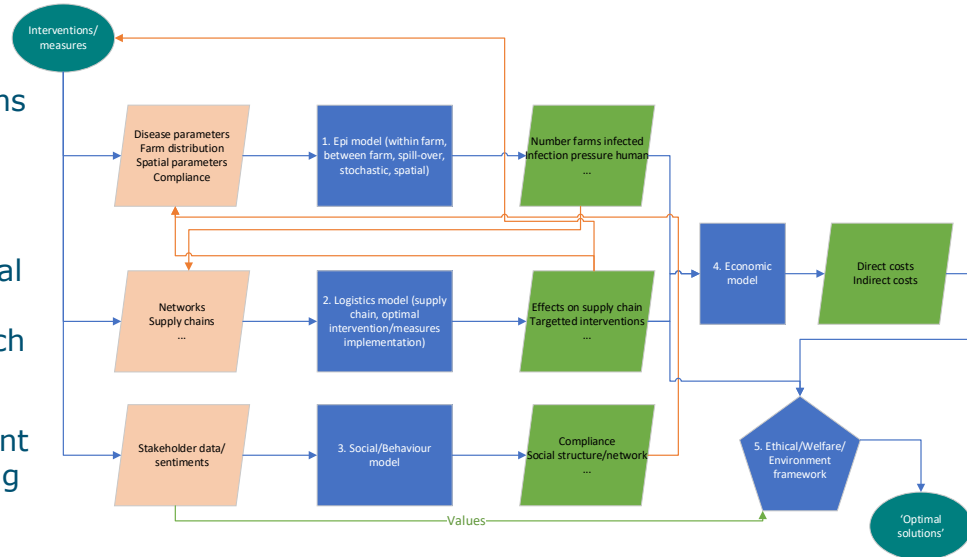**More information** showcase

Home

Combining epidemiological and socio-economic insights to optimise the outcomes of control strategies

Interventions targeted at outbreak preparedness and response are evaluated with computer models to produce 'the best' solution. However, these evaluations often only consider the epidemiology, followed by economic evaluations. In preparedness and response human action is vital.

Thus, behaviour or more specifically compliance is vital in these strategies. Similarly, other perspectives can limit or enhance the effectiveness of interventions such as logistics, welfare or ethical concerns.

In approaching the planning of interventions to prevent or contain outbreaks in a holistic way, by incorporating behaviour, epidemiology, economy, and logistics, we are working on developing models incorporated in a framework to help decision makers prepare for zoonotic outbreaks of infectious diseases.

Diagram elements:
- Interventions/ measures
- Disease parameters / Farm distribution / Spatial parameters / Compliance
- 1. Epi model (within farm, between farm, spill-over, stochastic, spatial)
- Number farms infected / Infection pressure human …
- Networks / Supply chains …
- 2. Logistics model (supply chain, optimal intervention/measures implementation)
- Effects on supply chain / Targeted interventions …
- Stakeholder data/ sentiments
- 3. Social/Behaviour model
- Compliance / Social structure/network …
- 4. Economic model
- Direct costs / Indirect costs
- 5. Ethical/Welfare/ Environment framework
- 'Optimal solutions'
- Values

Data and modelling to shape interventions

Project lead	Michel Counotte
Year	2021-2025
More information	showcase

Home

Targeting indoor social spaces for SARS-CoV-2 control: Intersecting models with behavioural and epidemiological data towards informed decision making

Where we spend our time and interact with other people determines the ability for respiratory pathogens to spread through populations. This notion lies at the basis of many control measures. In the context of the SARS-CoV-2 pandemic, these include lockdowns, curfews, teleworking, and (partial) closures of public sectors. While shown to be effective in reducing the overall transmission, it is hard to predict and quantify the impact of such intervention measures. Given the substantial economic and societal impacts of these measures, this lack of knowledge impedes the judicious use of these measures. Here, we combine behavioral and epidemiological data into a new model framework to investigate how changes in our time expenditure can curb epidemics.

Data and modelling to shape interventions

Project lead   Quirine ten Bosch

Year   2022-2024

Home

Studying the impacts of COVID-19 mitigation policies on mental health:
A microsimulation modelling approach

The COVID-19 pandemic has highlighted the importance of tailored preparedness plans to cope with potential disease outbreaks. During the pandemic, a major challenge for policymakers was finding the balance between containing the disease and supporting mental health and well-being. Although COVID-19 lockdowns and accompanying restrictions mitigated the spread of the virus, many countries witnessed significant increasing rate of depression during these periods. It is not clear the extent to which different lockdown scenarios impacted depression rates, and whether these effects might be felt in the future.

To that end, a microsimulation model, COMMA (COvid Mental-health Model with Agents), was developed to simulate behaviors of individuals under different lockdown scenarios, both actual and hypothetical, and of varying duration, sequence and severity. COMMA helps to understand how the prevalence of depression changed in each scenario.

Data and modelling to shape interventions

Project lead	Kristina Thompson
Year	2022-2023
More information	COMMA open source Model

Poster, poster, abstract, webinar.

Home

Scenario studies, and systems approaches; towards transformations and change
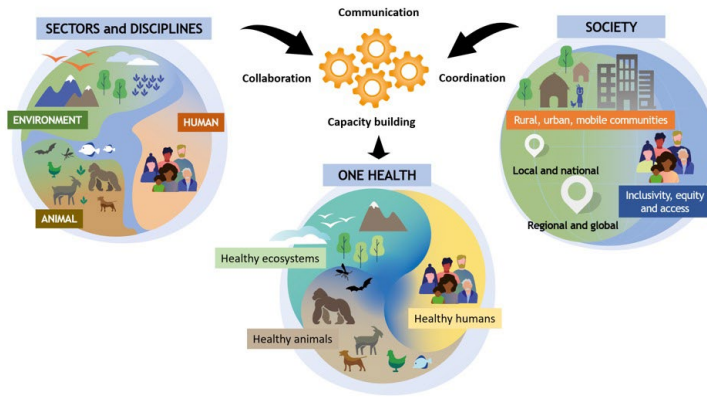
One Health is an integrated, unifying approach that aims to sustainably balance and optimize the health of humans, animals, plants and ecosystems. It recognizes the health of humans, domestic and wild animals, plants and the wider environment (including ecosystems) are closely linked and interdependent.

The approach mobilizes multiple sectors, disciplines and communities at varying levels of society to work together to foster well-being and tackle threats to health and ecosystems, while addressing the collective need for clean water, energy and air, safe and nutritious food, taking action on climate change, and contributing to sustainable development.

Wageningen is well known for its ability to collaborate across disciplines to accomplish real change to systems. For successful Global One Health outcomes it is imperative that a systems approach is applied.

Here we aim to use the new knowledge developed a range of areas of expertise (virology, epidemiology, ecology, detection surveillance and diagnostics, socio-economic human factors that shape and drive zoonosis risks, etc) to develop frameworks and approaches to achieving real, effective and durable change to accomplish safer and more resilient food systems, in balance with resilient and thriving ecosystems.

*Left: definition by One Health High Level Expert Panel, 2021

Home

Scenario study: Preparedness for the transmission of pandemic viruses in the food chain

Governments and the food industry make major efforts to ensure food safety throughout the global supply chain and support food availability. Experiences with Coronavirus disease 2019 (COVID-19) have re-emphasized the need for preparedness in many sectors, including the food sector. This position paper analyzes the potential introduction and transmission of pandemic viruses via the food chain and hypothesizes which new food safety issues could arise. Two scenarios, a gastrointestinal virus and a respiratory virus, were explored.

Overall, if a pandemic virus associated with the food chain was to occur, our preparedness is currently lacking given our potentially limited knowledge of introduction and transmission pathways, as well as access to methods to detect the viral presence and infectivity and model the transmission of the pathogens, even though the economic and societal impact of such a scenario is likely extensive.

Narrowing the knowledge gaps on introduction and transmission, and improvement of analytical feasibility is required to benefit our preparedness against the emergence and spread of future foodborne pandemic pathogens.

Scenario studies, and systems approaches

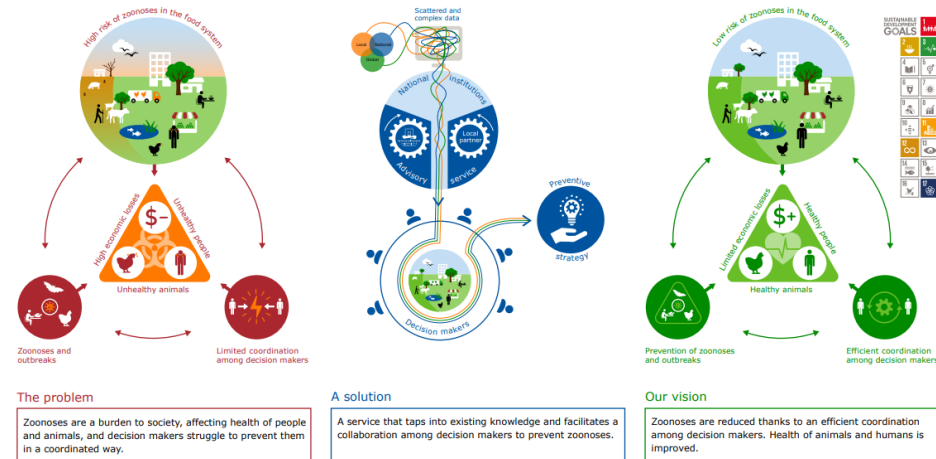|	
Project lead	Jen Banach
Year	2021-2023
More information	Scientific article

Home

ZoNoH - Putting One Health into action: Preventing zoonoses in Kenya by fostering collaboration in the food system

In Kenya, zoonosis prevalence remains extremely high – and not only threatens human and animal life, but also poses a significant socio-economic burden. The ZoNoH project aims to strengthen the capacity of two Kenyan County One Health Units (COHU) so they can better manage zoonoses in their food system, hence contributing to the prevention of the pandemics of tomorrow.

The initiative will involve capacity building for One Health and Food Systems operationalisation, and tap into existing data (at global, national, and local levels) to assess the health and socio-economic impacts of zoonoses on local food systems. These approaches will ultimately lead to the co-creation of contextualised zoonoses prevention strategies for the two COHUs. Moreover, the ultimate goal is to deliver a service that is scalable and that might be applied in further geographies.

To realise ZoNoH, WUR has partnered with Transdisciplinary Consultants Limited (TCL), a Kenyan organisation specialised in One Health operationalisation projects.

The problem
Zoonoses are a burden to society, affecting health of people and animals, and decision makers struggle to prevent them in a coordinated way.

A solution
A service that taps into existing knowledge and facilitates a collaboration among decision makers to prevent zoonoses.

Our vision
Zoonoses are reduced thanks to an efficient coordination among decision makers. Health of animals and humans is improved.

Scenario studies, and systems approaches

Project lead   Annabelle Daburon
Year   2022-2025
More information   Project website

Home

Understanding effects of biodiversity on disease risks:
Exploring synergies between animal and plant systems in an international workshop series

Unprecedented biodiversity loss influences disease risks in humans, animals, and plants. However, research fields related to diseases in these different groups operate relatively independently. In our boundary-crossing workshop series we work towards novel integrative conceptual frameworks that advance current understanding about biodiversity-disease relationships for different infectious agents in different ecosystems.

Scenario studies, and systems approaches

Project lead   Liesje Mommer

Year   2022-2023

Home

Mapping zoonoses risks resulting from man made changes

Nature and green environments are essential for people's health and well-being. A healthy and livable environment for humans is only possible a healthy nature that is in balance, with good water and soil quality. This should take into account possible risks due to zoonoses, because this risk simply follows from living with (and in the vicinity of) nature and other animal species. The need to consider the risks of (zoonotic) pathogens is therefore evident in the area-based approach, but not yet embedded. With more space being created for greenery and water in Dutch cities, promoting biodiversity and can thereby lead to a change in zoonotic risk. Increased risk can be due to more frequent and intensive contact between wild fauna and humans. On the other hand, a good 'design' can also contribute to a reduced risk, if a robust and resilient system is designed, e.g., with the presence of natural predators to prevent pests and an excess of potential carriers of pathogens (vectors). The research in this project serves to create a basis for a weighting framework for decision making around such changes in relation to zoonoses risks.

Scenario studies, and systems approaches

Project lead Marion Kluivers

Year 2024-2026

Home

Integrating social sciences in preventing and controlling zoonotic disease epidemics – a literature review

Human behaviour is key when controlling disease outbreaks but an overview of how to positively modify it during zoonotic disease epidemics is lacking. This project reviews the integration of social sciences when responding to, and preventing, zoonotic disease epidemics in order to optimise human behaviour to lower the societal burden of these diseases.

Scenario studies, and systems approaches

Project lead   Bart van den Borne

Year   2023-2024

Home

Wildlife Meat Trade and Zoonosis Emergence (WILDMEATZE): a threat to the integrity of the global food supply chain and human health

The project aims to establish an international scientific team that will investigate the extent of illegal bushmeat trade and its threat to international food systems due to the emergence of foodborne zoonotic and antimicrobial resistant pathogens. The activities will increase our understanding of the threat and help to build a resilient future food system. This project is executed in close collaboration with the Sampling methods; How and what to sample project to set up an early warning system for emerging zoonotic pathogens and parasites in wildlife, agricultural and urban areas.

Scenario studies, and systems approaches

Project lead   Sara Erasmus

Year   2022-2023

Home

Can biodiversity conservation and participatory surveillance together reduce zoonotic disease risks?

Biodiversity loss and emerging infectious diseases are two global crises that are both related to human disturbance of natural systems. Evidence is accumulating that biodiversity loss disrupts complex ecological interactions that can trigger pathogen spillover from wildlife reservoir hosts to livestock and humans. Biodiversity conservation has therefore been promoted as an effective measure to control infectious diseases with a wildlife origin. However, very few studies exist that have tested this strategy.

In this project, we test the effectiveness of biodiversity conservation in reducing zoonotic disease risk along an anthropogenic disturbance gradient. However, pathogen spillover risk from wild and domestic animals and people is not only a biological phenomenon and a social phenomenon. Effective strategies need to actively engage with communities working and living with animals, to create effective surveillance and intervention methods with and for these communities.

To date such community-centered approaches, focusing on people's practices and strategies have been missing. In the project, we also test the effectiveness of participatory surveillance by local communities in reducing zoonotic disease risk.

Scenario studies, and systems approaches

Project lead   Frank van Langevelde &
                    Helen Esser

Year   2023-2027

Home

Developing a One Health policy screening tool

From a democratic public policy perspective, One Health is aimed at weighing trade-offs of the values, interests, issues and partial solutions of interdependent components of a complex adaptive ecosystem. At a global scale One Health-relevant policies are associated with several policy problems. 1. Global commons are sub-optimally governed by fragmented authorities in separate policy sectors. 2. The broad One Health spectrum is in practice narrowed down to short term pathogen control. 3. Amendments to policy proposals may overlook minority interests and un(der)represented values, such as animal health, long term ecosystem balance or preventable disproportionality of impact among vulnerable groups, regions or countries.

The One Health approach is an attempt to operationalise the precautionary principle during policy preparations identifying and proposing actions to prevent harm and promote resilience across components of the planetary biosphere. The One Health policy screening tool, developed in this project, provides an overview as input to the political designation of priorities. The tool informs a consideration of a government's weighing of One Health aspects, as well as to assess the policy proposal's integrative capacity for One Health.

Scenario studies, and systems approaches

The tool supports the identification of potential policy impacts or lacking consideration of a range of One Health core aspects, and a rapid appraisal of the current integrative capacity of the implementation infrastructure. It consists of a turntable model, a policy indicator index, an overview of open access databases, and a checklist for policy proposal screening that enables deliberative decision-making.
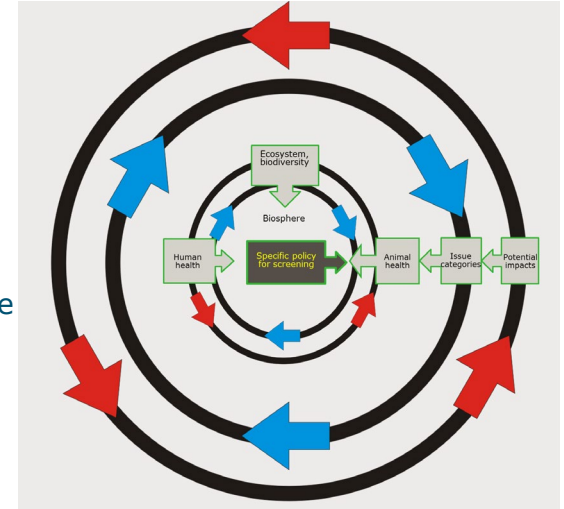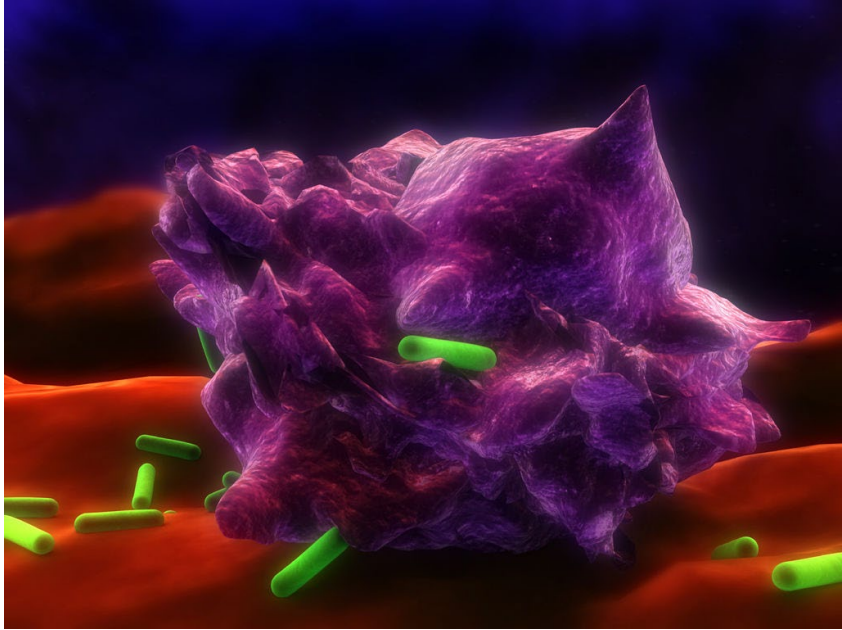

Project lead   Marleen Bekker

Year   2023

More information   Abstract
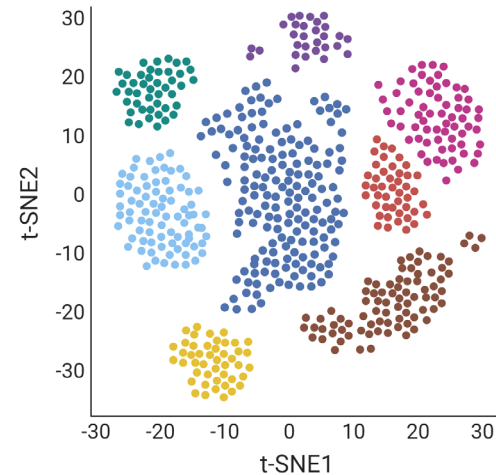
Home

Host – pathogen interactions

In several projects we aim to increase our understanding of host – pathogen interactions. This will help us find new ways to deliver treatments, develop vaccines or vaccination strategies, or devise other ways to prevent harm from zoonotic infections in animals or humans.

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Dissecting the host response during Rift Valley Fever Virus infection: a single-cell transcriptomics approach

Rift Valley Fever is an arthropod-borne viral zoonosis mostly affecting animals but can also affect humans. Despite the threat that Rift Valley Fever virus (RVFV) poses to animal and public health and the absence of approved therapeutics and vaccines for human use, several fundamental aspects of the RVFV infection cycle remain poorly understood.

In this project, we will use single-cell RNA sequencing technology to gain a better understanding of the fundamental biology of RVFV. A comprehensive understanding of pathogens of public health concern is crucial for pandemic prevention and better preparedness. By studying the responses that hosts employ to counteract viral infections, we aim to uncover several molecular pathways markedly affected during virus infection and contribute to the body of knowledge required to develop effective medical countermeasures in the event of an outbreak.

Single cell transcriptomics RVFV infected liver cells
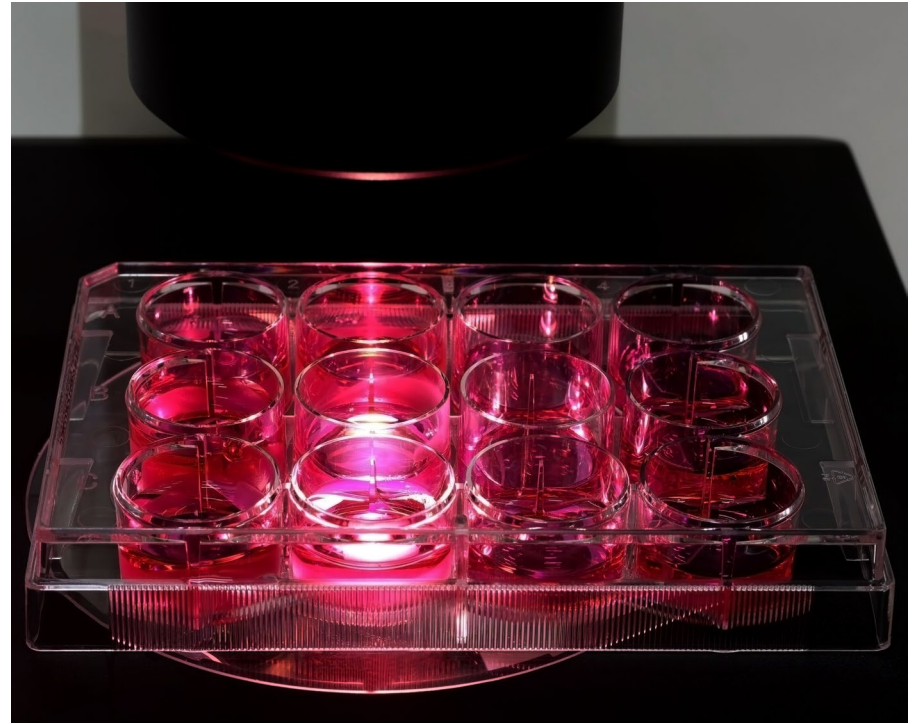
Host – pathogen interactions

Project lead   Erick Bermudez Mendez

Year   2022-2023

Home

Ex vivo models to detect mammalian adaptations in avian influenza viruses

Due to the large host range of avian influenza viruses, it is challenging to characterize changes in host range due to mutations. *Ex vivo* models could be a useful tool for rapid risk assessment of HPAI (highly pathogenic avian influenza)viruses and annotation of mammalian virulence factors. In this project primary cell lines of porcine, human, chicken and duck origin are set up to investigate host drift and zoonotic capacity of emerging HPAI viruses.

Host – pathogen interactions

Project lead   Luca Bordes

Year   2022-2023

Home

Effective vaccines

WUR has knowledge that underpins the full development cycle of novel vaccines.
From understanding the vaccine target sites, via the process engineering skills to produce and purify the vaccines, to modelling the best approach to implement vaccination strategies.

ERRAZE funds a number of projects to support the further strengthening of the crosshatch of collaborations across different disciplines that contribute towards new, safe and effective vaccines, for animals, humans and plants.

West Nile Virus vaccination-mosquito challenge model

The aim of this study is to vaccinate laboratory mice with West Nile Virus (WNV) live-attenuated vaccines (LAV) and compare their protective efficacy against WNV challenge via mosquito bite and the gold standard intraperitoneal injection.

The specific objectives are to:

1. immunize mice with WNV LAVs and study the induction of neutralizing antibodies, and

2. challenge the mice with wildtype WNV using mosquito bite or intraperitoneal injection and determine the vaccine efficacy.

Effective vaccines

Project lead   Gorben Pijlman

Year   2022-2023

In vitro study to compare the immunogenicity of a Japanese Encephalitis Virus vaccine based on three different vaccine platforms

Japanese Encephalitis Virus (JEV) is a mosquito-transmitted virus that can cause severe encephalitis in humans and reproductive and neonatal losses in swine. The envelope glycoprotein E of JEV will be used as a model antigen to evaluate the immunogenicity of three different vaccine platforms. These platforms include: 1. Virus-Like Particles (VLPs) displaying the JEV-E protein produced in a Baculovirus expression system; 2. mRNA vaccines encoding JEV-E; and 3. Freeze dried microalgae that produced JEV-E.

These three vaccine platforms will be assessed in vitro for their potential to activate naïve antigen-specific T cells. This will be done by examining the uptake and expression of the JEV-E antigen by antigen presenting cells (i.e., human, porcine and murine Dendritic Cells (DCs)), its presentation on major histocompatibility complex I (MHC-I) molecules, the activation of antigen-presenting cells, and the production of cytokines.

The study will reveal the potential of the different vaccine platforms to induce CD8+ restricted cytotoxic T cells, to activate DCs, and their ability to modulate T cell responses (e.g., promote Th1, Th2, Th17 or Tregs).

This project will contribute to the development of effective and safe vaccines for humans and production animals (One Health approach) that can be rapidly deployed in response to new outbreaks.
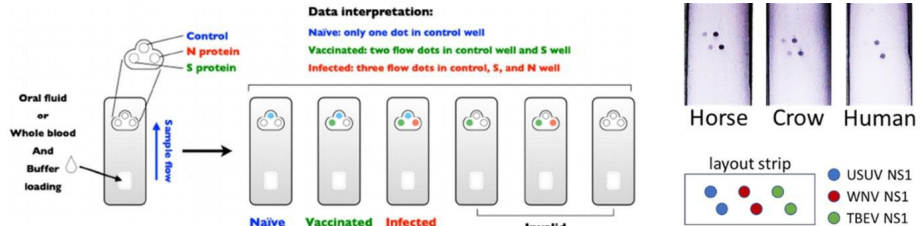

Effective vaccines

Project lead   Edwin Tijhaar

Year   2023-2024

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Species-independent lateral flow test to differentiate vaccinated from infected animals (DIVA)

The emergence of animal diseases frequently goes along with travel and trade restrictions. Vaccination is considered one of the most powerful tools to reduce disease burden, though an active vaccination policy by itself is not sufficient to fully restore international travel and trade. Ideally, vaccinated animals to be transported are subjected to a quick and reliable test able to Differentiate Infected from Vaccinated Animals (DIVA). For a large set of vaccines, the DIVA immune response can be detected by specific ELISA assays, yet these tests need to be performed in a laboratory setting, thereby preventing quick availability of test outcomes. With recent innovations in lateral flow test (LFT) development and applications, alternatives to ELISA have become available that can be performed on-site and with results obtained within minutes. Here we propose to develop a DIVA LFT for the emerging Rift Valley Fever virus in relation with a live-attenuated vaccine, and provide proof of principle. RVFV is a pathogen emerging in Africa in ruminants and humans and has a risk of being introduced in naive regions.

Expanding on promising results with a single analyte LFT, a multi-analyte test setup will be implemented in this project that includes a DIVA marker, which is only recognised by sera derived from infected animals and not by sera obtained from vaccinated animals. This research will not only boost Arbovirus vaccine programmes in general but will also open new avenues for multi-analyte lateral flow testing in other disciplines.


Effective vaccines

Project lead   Aart van Amerongen

Year   2023-2024

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ViVA: enabling Viral Vector technology in microAlgae for biopharmaceutical production

The seed project enabled the first steps towards obtaining a viral vector that will enable vaccine and protein therapeutic production in a safe and sustainable photosynthetic platform: microalgae. Microalgae can support post-translational modifications required for protein therapeutics folding and functionality, are edible, and, unlike mammalian and insect cells, do not contain viruses/prions that can also infect humans. The successful production of the majority of the required plasmids for DNA delivery and guide-RNAs, will be followed up in a continuation of the project with funding from NWO.

Project lead   Sarah D'Adamo
Year   2022-2023

Effective vaccines

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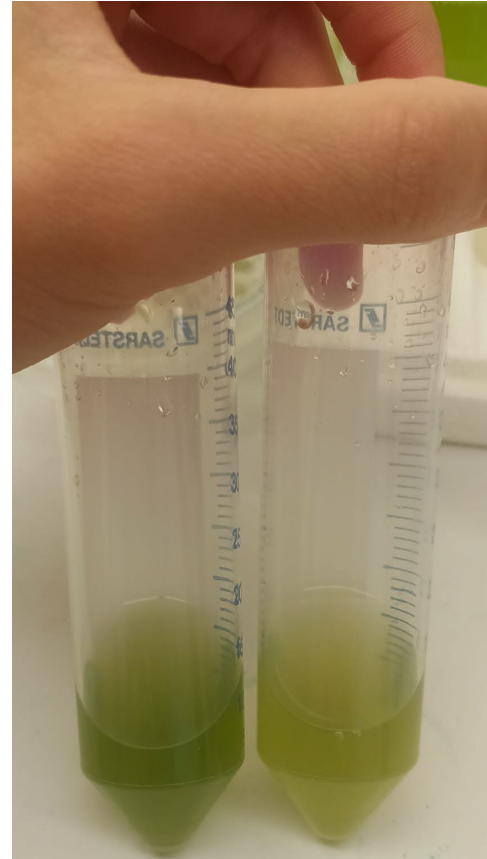
Exploring the mechanism of biased hypermutation in recombinant Newcastle Disease Virus expressing vaccine antigens

In this project we work towards the development of improved protocols for production of NDV-vectored vaccines. The NDV vector was used as a platform for a potential SARS-CoV-2 vaccine, when we detected the process of biased hypermutation in the insert region of the vector.

We will explore the mechanism by which foreign genes inserted into the live-attenuated Newcastle Disease Virus vector become a target of the cellular enzyme ADAR1, resulting in biased hypermutation and reduced vaccine effectiveness.

We aim to develop novel vaccine design- and production protocols that reduce or eliminate the emergence of biased hypermutation.

We will use identify RNA motifs that promote biased hypermutation, by comparing results of ADAR1 binding assays with observed levels of biased hypermutation in NDV genomes. The results can help improve the development of stable, safe and effective NDV-based vaccines.

Adenosine deaminase acting on RNA-1 (ADAR1): (A)denosine → (I)nosine RNA = (T)hymine → (C)ytosine cDNA
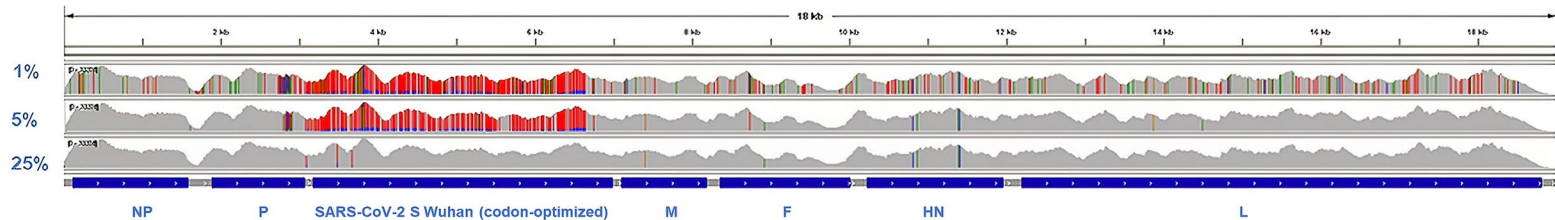
Effective vaccines

Project lead   Rik de Swart

Year   2023-2024

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Capacity building and knowledge exchange

Within ERRAZE we prioritise capacity building and exchange in various ways. First and foremost, transfer of knowledge and experience between different researchers in an integral part of all projects.
We organise symposia where people from within WUR and our external and even international partners come to share ideas.

In the One Health Talks and Drinks monthly seminars staff from across WUR come to learn, connect and discuss One Health topics.

And in several dedicated projects we specifically fund knowledge exchange - in two directions - between global young researchers and WUR staff.

Grassroots Resilience and Pandemic Preparedness in Africa (GRAPPA)

This project is working on a research platform for integration of approaches and empirical evidence from the Social Sciences, Ecology and Epidemiology

The exchange and sharing of knowledge and insights around existing PhD-level research activities in Africa will solidify increased knowledge about local capacity in Africa for prevention and rapid response to health threats and effective ways to support communities in achieving health resilience through local surveillance and community health system interventions.

Capacity building and knowledge exchange

Project lead   Harro Maat
Year   2022-2023

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Co-hosting the World Food Forum Global One Health Special Prize; capacity building and exchange

In collaboration with the World Food Forum* ERRAZE sponsors the Transformative Research Challenge Global One Health. With the prize, we stimulate young researchers across the world to take on a One Health challenge in their region, to help create safer and more resilient food systems. The teams of researchers are provided mentorship by experienced One Health researchers, and the 10 best submissions are granted a monetary prize to bring their idea into practice. Throughout the process of bringing their projects to practice, the cohort will be offered further training and a community of practice for the exchange of knowledge and experiences.

* World Food Forum (WFF) is an independent, youth-led global network of partners facilitated by the Food and Agriculture Organization of the United Nations (FAO). It aims to spark a global movement that empowers young people everywhere to actively shape agrifood systems to help achieve the Sustainable Development Goals (SDGs) and a better food future for all.

Capacity building and knowledge exchange

Project lead   Joukje Siebenga

Year   2023

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Global One Health symposium, April 2024

On 23-25 April 2024, Wageningen University & Research (WUR), the Global One Health Research Partnership (GOH-RP) and the Dutch National Institute for Public Health and the Environment (RIVM) will convene the international symposium "Paradigm shifts for Global One Health".

We welcome researchers, decision makers and One Health practitioners to join us for this action oriented meeting. The first two days will comprise of plenary talks and discussions, offering many opportunities for interaction and for participants to present ongoing research. On April 25th, the spotlight will be on One Health PhD students, and there is time for workshops to facilitate future collaborations.

Event registration opens in January 2024.

Paradigm shifts for Global One Health
Greater resilience requires transformations and integration

23-25 April 2024, Wageningen, The Netherlands

Capacity building and knowledge exchange

Event website

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