PREPARING FOR VECTOR-BORNE VIRUS OUTBREAKS IN A CHANGING WORLD: A ONE HEALTH APPROACH

MAIN APPLICANT:

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The Netherlands, with its dense population of humans and livestock, international transport and travel hubs, and water-dominated landscape is particularly vulnerable to infectious disease outbreaks. We aim to understand if and how changes in climate, farming, water management and travel lead to mosquito-borne disease outbreaks, to be better prepared.

BACKGROUND AND SCOPE

Infectious disease outbreaks are increasingly common due to multiple, interacting global changes and developments in the human, animal or environment domains (Figure 1). These changes can trigger processes that disturb the fragile balance in the complex human-animal-environment ecosystem, up to the point where the conditions are created for (new) infectious disease outbreaks, in animals and/or humans. In these situations, the state of the system has reached a pathogen-specific vulnerability threshold (which we refer to as '**tipping point'**), making the system receptive to outbreaks of that pathogen if it is introduced. The Netherlands, with its dense population of humans and food animals, international transport and travel hubs (Schiphol, Rotterdam), and unique water-dominated landscape is particularly vulnerable to the occurrence of such tipping points and hence, outbreaks of (newly emerging) infectious disease.

In this project we will consider **four change scenarios** that could lead to the occurrence of such tipping points and disease emergence: (I) **changes in climate**, (II) in **water management**, (III) in **farming practices**, and (IV) **in importation risk**. Despite this expected vulnerability, emerging disease outbreaks in the Netherlands are still relatively rare. We currently study these outbreaks – when they occur – reactively, individually and within relatively isolated silos (e.g., human vs animal vs ecological health, academic research vs public health research, public vs private sector).

This ad-hoc, reactive and fragmented approach is ineffective and inefficient. Instead, the partners collaborating in this proposed project will adopt a **pro-active, integrated, multisectoral, One-Health approach** in studying emerging infectious disease outbreaks. We will develop and implement **a forward-looking integrated research agenda, measuring and modelling how projected demographic, climatological, ecological, and planological changes will impact the risk of emergence of infectious diseases in the Netherlands, and translate this understanding into effective, integrated outbreak preparedness and response actions.**

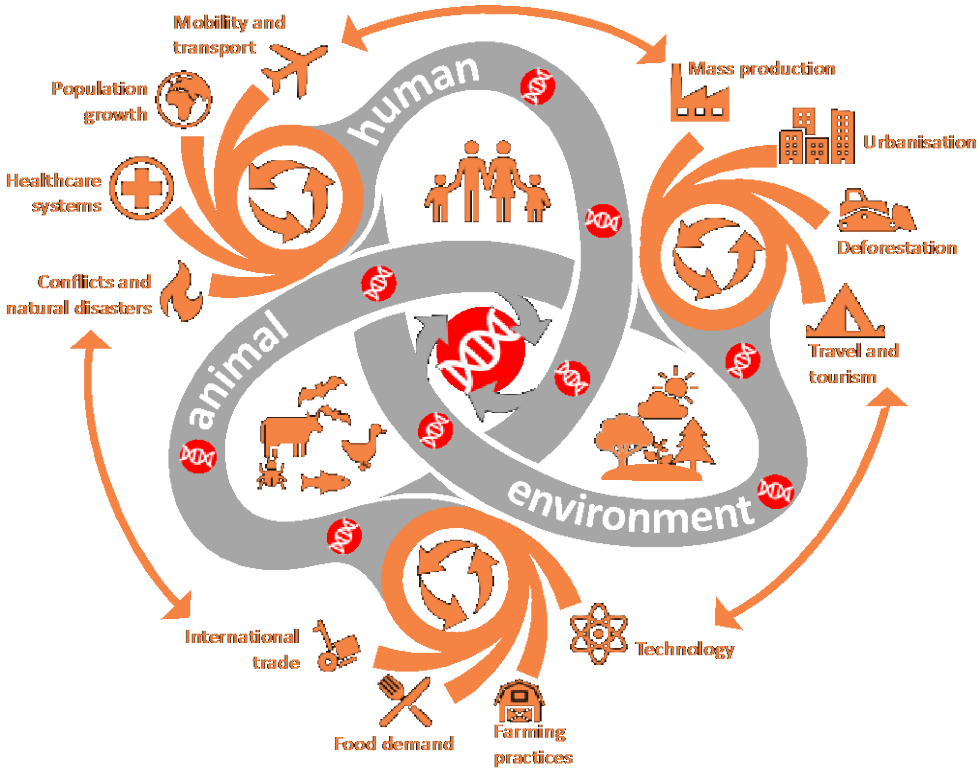

Fig. 1: Multiple global changes in the human-animal-environment ecosystem, creating tipping points for infectious diseases outbreaks.

Focus on Vector-Borne Diseases (VBD)

We will focus our research agenda on **priority VBD based on the EMZOO list** (developed by multiple stakeholders under leadership of the National Institute for Public Health and the Environment with updates based on more recent literature. These VBD are caused by viruses transmitted by common resident mosquitoes (*Culex pipiens*), or by the invasive mosquito *Aedes albopictus*, which is regularly introduced and is likely to become established in the Netherlands due to climate change (see Table 1). Recent outbreaks of VBD in livestock and wildlife, and repeated incursions of *Aedes albopictus* mosquitoes in Northern Europe highlight the importance of a preparedness research agenda for VBD for the Netherlands (including overseas territories) and the rest of Europe[Fout! Verwijzingsbron niet gevonden.,Fout! Verwijzingsbron niet gevonden.].

MOSQUITO VECTORS	STATUS	VIRUS	VIRUS FAMILY	VIRUS STATUS	IMPACT
Culex pipiens	**Resident:**				
		JEV	Flavi	Exotic	H, L, P
		WNV	Flavi	Enzootic (overseas only)	H, L, P, W
		USUV	Flavi	Enzootic (Netherlands)	W, H
		RVFV	Bunya	Exotic	L, H, W
		SINV	Toga	Enzootic	H
Aedes albopictus	**Invasive:**				
		CHIKV	Toga	Endemic? (overseas only)	H
		DENV	Flavi	Endemic (overseas only)	H
		RVFV	Bunya	Exotic	L, H, W
		YFV	Flavi	Exotic	H, W

Table 1: Vectors and viruses addressed in this proposal. 'Impact' denotes species affected by the infection. H: human, L: livestock, P: pets, W: wildlife. Virus abbreviations: JEV: Japanese encephalitis virus, WNV: West Nile virus, USUV: Usutu virus, RVFV: Rift Valley fever virus, SINV: Sindbis virus, CHIKV: chikungunya virus, DENV: dengue virus, YFV: yellow fever virus. Family abbreviations: Flavi: *Flaviviridae*, Bunya: *Bunyavirales*, Toga: *Togaviridae*.

OUR AMBITION

Our ambition is to prepare for VBD outbreaks in a rapidly changing environment. We will do this by:

- *providing pathogen specific and generic early warning indicators that measure whether our human-livestock-wildlife-ecosystem is (becoming) vulnerable for VBD outbreaks,*
- *developing novel catch all tools for outbreak detection and risk assessment,*
- *translating the knowledge into interventions based on in depth knowledge of the entire ecosystem and interactions in which such outbreaks may occur.*

WORKPLAN

The work plan is designed into four complementary, interacting pillars, with each pillar covered by research activities organized into 11 work packages (WPs), as depicted in figure 2.

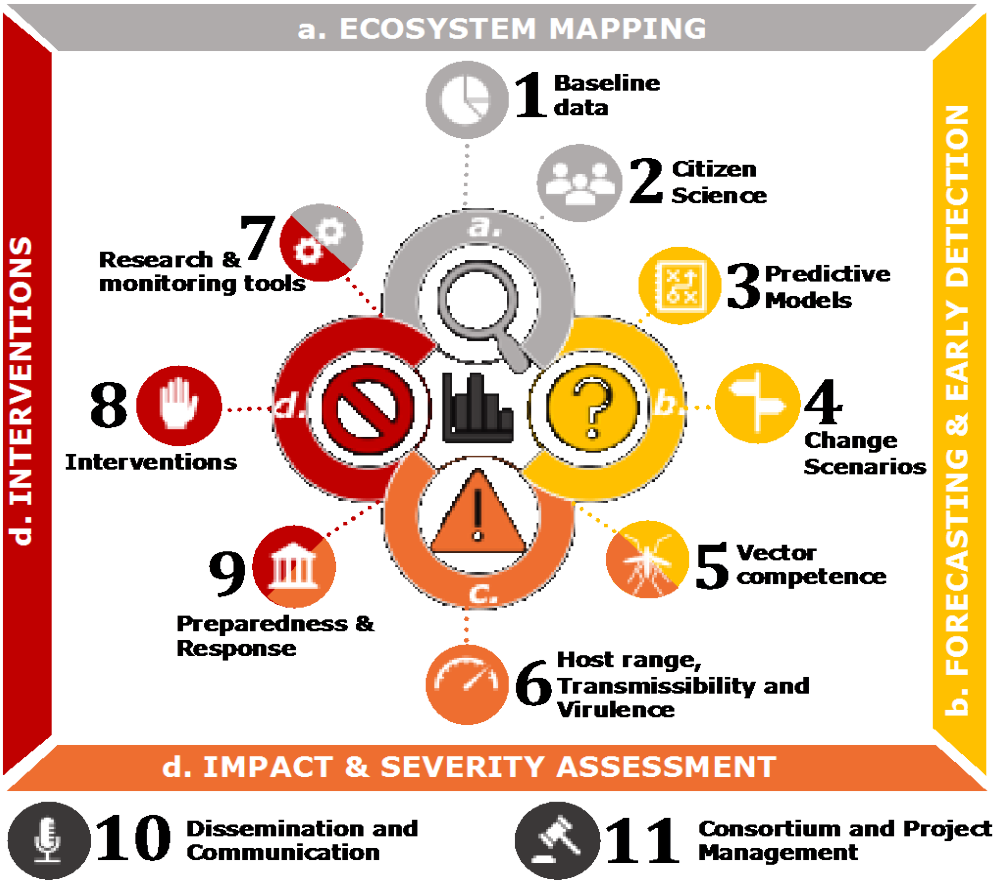

Figure 2. The eleven work packages (WPs) across the pillars of the aspired national research agenda on VBD preparedness and response.

PILLAR A: ECOSYSTEM MAPPING:

We aim to map the complex interplay between factors at high-resolution that drive VBD in the Netherlands, as a starting point for modelling the effect of changes according to the four change scenarios. We will do this by developing a deep understanding of suitability of ecosystems in the Netherlands for VBD introduction, circulation, and expansion, and – conversely- the actionable factors that determine ecosystem resilience. We will conduct a series of uniquely interconnected research studies addressing reservoir hosts, disease hosts, viruses, vectors, and their interactions, providing critical baseline data for model development. These studies will employ novel methods and tools, including the use of scalable citizen science system to overcome limitations of traditional surveillance.

WP1 and WP2 involve the collection of data and samples in VBD hosts: humans, wildlife and livestock. Data will be combined with data from the other WPs into a jointly owned data repository for visualisation and modelling. In addition to these surveys that require laboratory analyses, data collection activities are augmented through a series of innovative digital epidemiology and citizen science initiatives in WP2 for humans (travellers), mosquitoes and wild birds. The data and samples collected in WPs 1 and 2, together with data from public repositories (on e.g. climate variables, water management, travel, trade, human population density, migratory pathways, densities of domestic and wild animal hosts, densities of vectors, pollution, interactions between

these), and historic data collected by various partners and earlier studies feed into Pillar B (Forecasting and Early Detection).

Mosquitoes: In collaboration with the CMV, WUR will sample and monitor mosquito densities and blood-feeding preferences in potential hotspot zones identified through a recently completed ZonMw project. Mosquito diversity and abundance will also be assessed through next-generation-sequencing (NGS) of environmental water samples. In parallel, a mosquito identification citizen science project will be done by the general public and by high-school students , and mosquito burdens will be assessed through the "Muggenradar".
Wild birds: Wild birds, representing the most probable amplifying hosts of priority VBD, will be sampled by well-trained citizen scientists coordinated by Vogeltrekstation. Birds found dead will be autopsied, sampled and analysed. Dried blood spot samples, throat- and cloacal swabs and mosquito pools will be tested for antibodies and/or target viruses, using protein microarrays and multiplex PCRs, developed as part of this project. Spatial and temporal avian host dynamics are studied through citizen-science projects combined with detailed longitudinal studies in selected host species and in relation to virus exposure.
Travelers: eHealth modules combined with self-sampling by (returning) travellers, and risk-based testing of imported animals will be used to assess importation risk. This will be done by building on already available apps used to target travellers. The travel app "GGD reist mee" and the ZIeKA monitor (developed in response to the Zika outbreak) will be extended for targeted and prospective syndromic surveillance of travelers to detect imported infections. If symptoms compatible with an arbovirus infection are reported, the travelers will receive additional information via the app and will be asked to answer additional questions, e.g. about their exposure risk in recent days (type of accommodation, use of DEET), and whether they have sought healthcare. They will be invited to provide a blood sample via dried blood spot when they return home, which is tested for IgM/IgG and viral DNA or RNA.
Livestock: as part of a national mapping study of baseline seroprevalence to the priority viruses studied, a systematic sample of the main livestock species will be collected. Where possible, these will be derived from ongoing national surveillance programs for other diseases, that are monitored as part of statutory surveillance.
Rodents, bats, and wild herbivores: Rodents and bats are periodically sampled for other studies, and wild herbivores may be hunted or – in the case of animals used for habitat management- be subjected to periodic health checks. In the integral protocol for species sampling and testing that will be developed in WP1 (EMC), these species will be included and tested in collaboration with experts from several nature organisations with expertise in biodiversity to assess potential for wildlife sampling (WWF Netherlands; Staatsbosbeheer; Natuurmonumenten).

Expected outputs

WP1	Baseline data: Mapping of virus exposure, circulation and evolution in reservoir and disease hosts
1.	Cross consortium protocol for ecosystem mapping (6/2020)
2.	Report on effects of water quality on vector diversity and abundance (6/2022)
3.	Integrated map of antibody and virus prevalence in known reservoir and (potential) disease hosts (12/2023)
4.	Report on suitability of livestock and/or wildlife as sentinels for VBD early warning (8/2024)
WP2	**Digital eco-epidemiology and citizen science**
1.	Entomological data on density and presence of competent endemic and invasive mosquito vectors for animal and humans (09/2021)
2.	An ICT infrastructure for rapid deployment of citizen engagement during public health threats consisting of a framework for targeted surveillance of travelers (09/2021).
3.	Data on amplifying host occurrence and mortality in space and time (06/2022)
4.	Estimates of clinical syndromes compatible with the rate of introduction of VBD by travelers returning from within and outside of Europe (12/2022)

PILLAR B: FORECASTING AND EARLY DETECTION:

We will build and implement innovative models that integrate knowledge and field data from multiple sources to characterize ecosystem resilience and/or vulnerability to outbreaks. Based on these field and experimental data collected, supplemented with data relevant to model VBD life-cycles collected from public sources (e.g., KNMI, CBS, literature, data from the EDEN/EDENext EU-funded projects), we will develop a method and practical tools for early warning to quantify and predict when the critical emergence threshold will be reached for VBD. We will do this by building from advanced modelling concepts from ecology and epidemiology to develop i) model-based quantification of R_0, in ecosystems, allowing for consideration of local conditions and

temporal variation; and ii) a model-free approach to identify generic early warning indicators and ecosystem resilience parameters based on the monitoring data. USUV and the closely related WNV will be used as model pathogens, building from historic data collected. The model-based approach will be used to analyse 4 scenarios that could lead to disease emergence:

I. ***changes in climate***, using the KNMI'14 climate scenarios which underlie national adaptation and mitigation strategies as a starting point;
II. ***changes in water management***, based on climate change adaptation strategies;
III. ***changes in farming practices***, like changes in land use, use of nutrients and pesticides and population sizes;
IV. ***changes in importation risk***, such as major VBD outbreaks in tourist destinations, trends in intercontinental travel;

For each scenario, relevant data will be identified from literature, public sources, the information gathered from- and extensive interaction with the above-mentioned citizen-science projects, and when needed additional experimental studies conducted as part of the impact and severity assessment studies (see pillar c below).

WP3 (Predictive modelling) will model the complex interplay between factors that drive VBD in the Netherlands at high-resolution, by building from advanced modelling concepts from ecology and epidemiology. The model will enable us to quantify and more reliably predict when critical emergence thresholds for VBD (tipping points) will be reached. In epidemiology, most methods are aimed at understanding epidemic, endemic and control dynamics of infectious diseases, but less focussed on the emergence process. Anticipating the bifurcation from a state without, to a state with infection is critically important to public, animal and ecosystem health. We will start with USUV (which is already circulating in the Dutch ecosystems) and the closely related WNV (which is expected to arrive in the coming years) as model pathogens.

WP4 (Change Scenarios) focusses on the development of different change scenarios and scenarios for prevention and control ("what if"-comparisons), and aggregating the essential spatial statistical and empirical data to feed into an encompassing GIS, coupled with the models developed in WP3 to assess effects of these scenarios. Thereby, we aim to gain new insights into the window of opportunity that creates tipping points in these complex systems. We will analyse the four above-mentioned scenarios and examine how these local and global stressors on ecosystems, as well changes therein influence the transition from pathogen introduction to major outbreaks.

Expected outputs

WP3	Predicting outbreaks of VBD and tipping points in VBD-systems in a changing world
1.	Method to characterize R_0 in spatial, environmental, ecological and temporal heterogeneity for use in risk mapping and in assessing the potential of measures for prevention and control (8/2021).
2.	Method for uncertainty and sensitivity analysis for R_0 to aid scenario analysis and characterization of key ingredients for prediction (8/2020).
3.	Generic early warning indicators for ecosystem tipping points leading to outbreaks of VBD (8/2023).
4.	Indicators for ecosystem resilience to invasion of VBD (8/2023).
WP4	**Change scenarios**
1.	Description of scenarios (draft 6/2021, final 2/2022)
2.	Mosquitoes from experiments that can be used in other WPs (continuous between 3/2021-9/2022).
3.	Spatially explicit maps on scenarios (3/2023)
4.	Risk maps with tipping point predictions (6/2024)

PILLAR C: IMPACT AND SEVERITY ASSESSMENT:

We will establish novel models to measure potential effect of current and predicted changes in the ecosystem on ecosystem resilience and vulnerability and to develop novel tools for rapid assessment of vector competence and disease severity of emerging VBD. We aim to design and conduct a suite of experimental *in vitro* and *in vivo* studies that characterise arbovirus infections at each step of the infection cycle in reservoir hosts, disease hosts and vectors. Unique to our approach is that these studies are done in a comparative manner to allow rapid profiling of potential host range, pathogenicity, and vector competence of newly detected arboviruses that arise during the course of the project.

In Pillar C we address key knowledge gaps that are crucial to model the potential impact of an outbreak through a suite of *in vitro* and *in vivo* experiments in mosquitoes and (reservoir and disease) hosts, respectively. The work in pillar c will address a select group of critical parameters to answer key questions for risk

assessment**: 1) what vector and vertebrate species can be infected, 2) can the virus efficiently spread between vectors, animals and humans, and 3) can the virus cause (severe) disease in animals or humans?**

WP5 Vector Competence will study vector competence of *Culex pipiens* and *Aedes albopictus* mosquitoes. Although vector competence of *Culex pipiens* mosquitoes for some priority VBD has been established, these studies are usually performed using lab colonies of mosquitoes, whereas it is becoming increasingly clear that vector competence is a dynamic trait that is affected by environmental factors, including temperature, as well biotic factors such as arbovirus and mosquito genetics, and the virome and microbiome of the insect. Vector competence studies on *Aedes albopictus* have thus far mostly been studied using the Foshan strain and the Fellini strain originating from China and Italy. In WP5 we will perform vector competence studies on a colony of recently caught *Aedes albopictus* in the Netherlands and Spain. Virome and microbiome studies will be done on the mosquitoes collected and vector competence studies are performed to analyse whether the identified persistent viruses and bacteria affect transmission of the relevant VBD. Detailed histology will be performed to assess the pathogenesis of arbovirus infections in their mosquito hosts.

WP6 Host range, transmissibility and virulence will determine the susceptibility of a range of vertebrate species (in part, based on WP1 screening) to infection and evaluate their role in the transmission cycle. We will also determine whether variation within and between vector species affects arbovirus transmissibility in different vertebrate hosts (birds, mammals). As a measure of transmission risk, we will study the potential effects of each of these variables on the outcome of infection and viremia. Third, we will develop experimental models for predicting disease severity, models to determine neurotropism of arboviruses and evaluate and compare the host response of the primary target organ systems within and between animal and human hosts studied to identify key pathways that regulate innate immunity and its effect on pathogenesis in vertebrates.

Expected outputs

WP5 Virus-mosquito-ecosystem interactions
1. Novel odor-baited traps to specifically collect blood-fed mosquitoes (09/2022)
2. Feeding behavior (biting risk) of Dutch mosquitoes (09/2022)
3. Vector competence of Dutch mosquitoes, as input for prediction models of WP4 (09/2023)
4. Virome and microbiome data of Dutch mosquitoes, used for the design of intervention strategies of WP8 (08/2024)
WP6 Host range, transmissibility and virulence
1. Models to assess the vertebrate host range and reservoir potential for emerging VBD.(08/2023)
2. Knowledge of the contribution of virus, vector and host variation to transmission. (8/2024).
1. Models for assessing disease outcome (8/2024).

PILLAR D: INTERVENTIONS:

The findings from the studies in pillars a, b, and c will be used to guide development of targeted early warning systems and tools for rapid assessment of risk of emerging VBD to humans and animals, to be transferred to institutes with primary responsibility for early warning. In **WP7** we will develop innovative methods for cross-host testing across a broad range of arboviruses and arbovirus exposure to support outbreak prediction and outbreak investigations. **WP8** focusses on the development of novel interventions, **WP9** on translation of knowledge for public health action (preparedness and response) and other forms of knowledge utilisation.

A cross-cutting toolkit of advanced assays will be developed, including targeted and metagenomic NGS, protein microarrays, eDNA metabarcoding, targeted to field studies and for rapid outbreak response. To allow deployment for use in regions with limited research infrastructure, such as the Dutch Caribbean, fieldable versions of the key assays will be developed. A suite of bio-informatic tools, coupled with a data sharing and analysis platform will be developed for the entire project in collaboration with the European data infrastructure EBI/ELIXIR and the COMPARE project www.compare-europe.eu).

If an actual VBD outbreak will occur in the Netherlands during the project period, the efforts and associated resources will be realigned to target the specific disease, if agreed with the funder and in collaboration with co-financing partners with a mandate for outbreak response. Sanquin and the bloodbank of Curacao will prepare a rapid response protocol for population exposure testing during a health threat, and provide access for establishing baselines for systems serology studies.

Finally, the models developed in pillar b, and results from the ecosystem mapping exercise, scenario analyses, and experimental studies will be used to compare the potential influence of different interventions aimed at slowing, stopping or reversing conditions that (could) trigger local outbreaks. This includes insights from the experimental work on mosquito diversity in relation to land use and pollution, informing and activating citizens, influencing traveller behaviour, modulating mosquito immunity, and development of candidate vaccines. Research results that potentially lead to interventions will be identified, explored for potential suitability and discussed with relevant stakeholders for further development.

Expected outputs

WP7 Tools and approaches to support outbreak research and surveillance of VBD

1. A fieldable single assay for serodiagnosis and genomic detection of human arbovirus and eDNA-based vector prevalence (8/2023)
2. A cross-cutting toolkit of combined advanced assays targeted and feasible for rapid outbreak response on-site (8/2024).

WP8 Intervention strategies to prevent VBD outbreaks

1. Intervention strategies to reduce vector density and VBD emergence (12/2023)
2. Immune modulation strategies to render mosquito's refractory to arboviruses. (08/2024)
3. Pre-clinical data on human and veterinary VBD candidate vaccines. (06/2023)
4. Universal approach to generate safe, effective, live-attenuated vaccines for rapid response to new VBD threats. (04/2024)

WP9 Preparedness, risk assessment, and knowledge utilisation

1. Capacity building: A multidisciplinary platform for population exposure testing (12/2022)
2. A list of priority topics for preparedness and response, from a multi-stakeholder perspective (12/2022)
3. Protocol development: A multidisciplinary protocol for exposure testing (06/2023)
4. A tool for integrated risk assessment, response options and communication to professionals and the public, irrespective of the nature of the VBD (06/2023)
5. Up-to-date guidelines including vector competence, distribution, exposure assessment and control (03/2024)

KNOWLEDGE UTILISATION AND ENTREPRENEURSHIP

The research will lead to several concrete outputs (see expected outputs above). Each of these outputs is developed with specific users in mind and will require tailored knowledge utilisation and exploitation plans to support further adoption by their intended users. The communication and dissemination efforts fall under the responsibility of WP10. All data gathered as part of the project will in principle be open-access to the scientific community, as much as possible. Research results will be published in open-access journals. Where economic valorisation supports our overall purpose to improve our research preparedness and response to VBD outbreaks in the Netherlands, we will set up ad-hoc business development (BD) teams that will develop a tailored business plan, that will include a market analysis, freedom-to-operate analysis, and outline the various options for further uptake of the results based on these analyses.

Additional utilisation effort in the project is aimed at realising our societal impact on VBD preparedness and response in science, education and policy. We will hold frequent progress meetings and organise periodic consortium workshops (in collaboration with NCOH). Concerning education, the project will deliver 26 PhDs that have been trained in the One-Health, interdisciplinary, multi-stakeholder vision of our joint project. All PhD students will be co-supervised by a PI from one of the other applicants and will be seconded at least for four months in total to at least two other applicants, promoting the development of multidisciplinary scientists that are trained in a One-health environment. In close collaboration with the NCOH, we will implement a comprehensive training programme, that will combine programme-wide theoretical training, practical courses and elective courses, including vocational skills. In addition, in collaboration with Avans and Technasium and the Viruskenner programme of Erasmus MC, we will develop new practical training courses for high school students, on topics considered to be of interest.
Under coordination of the RIVM, we will translate the research results into protocols, risk assessment tools and updated guidelines for preparedness and response to VBD outbreaks. As part of the knowledge utilisation effort, three outbreak simulations will be organised, practising the updated preparedness and response tools and guidelines developed and informing the further translation into policy recommendations.

PARTNERS

The proposed project has been designed from the start as a translational, multidisciplinary, multisectoral One Health collaboration, that cross-cuts traditional silos in infectious diseases research. The consortium spans the knowledge chain from fundamental science to applied research, public health actors, governmental agencies and healthcare. In addition, it directly involves citizens and students in the project's research activities. The table below lists the partners and Principal Investigators (PIs) involved.

Erasmus University Medical Center		
Name, title(s)	*Department*	*Expertise*
Prof. Dr. Marion Koopmans	Viroscience	Viruses at the human animal interface, public health virology, preparedness research
Prof. Dr. Thijs Kuiken	Viroscience	Veterinarian, Wildlife health and disease, pathology, virology
Prof. Dr. Eric van Gorp	Viroscience	Infectious disease specialist, clinical research, outreach (Viruskenner)
Dr. Richard Molenkamp	Viroscience	Diagnostic virology, molecular virology
Dr. Barry Rockx	Viroscience	Biologist, Arbovirus pathogenesis
Dr. Byron Martina	Viroscience	Biologist, Arbovirology, Caribbean arboviruses
Dr Corine Geurts-van Kessel	Viroscience	Medical microbiologist
Utrecht University		
Prof. Dr. Hans Heesterbeek	Veterinary faculty	Mathematical biology, infection dynamics and ecosystem dynamics, VBD modelling
Prof. Dr. Andrea Gröne	Veterinary faculty	Veterinarian, Pathology, wildlife diseases
Dr. Helene Verheije	Veterinary faculty	Pathobiology, novel diagnostics
Dr. Judith van den Brand	Veterinary faculty	Veterinarian, Pathology infectious diseases
Wageningen University Research		
Prof. Dr. Marten Scheffer	Environmental sciences	Ecologist, Theory of critical transitions, modelling
Prof. Dr. Jeroen Kortekaas	Bioveterinary Research	Veterinarian, Veterinary virology, bunyaviruses
Prof. Dr. Wim van der Poel	Bioveterinary Research	Veterinarian, Veterinary virology, Zoonotic viruses
Dr. Fred de Boer	Resource Ecology Group	Disease ecology, animal ecology, modelling
Dr. Kevin Matson	Resource Ecology Group	Ecological immunology, disease ecology
Dr. Gorben Pijlman	Virology	Invertebrate virology, vector competence
Dr. Sander Koenraadt	Entomology	Entomology
Prof. Dr. Mart de Jong	Quantitative veterinary Epidemiology	Epidemiology, population biology of infectious diseases, statistical methods to quantify interventions
Dr. Aart van Amerongen	Food & Biobased Research	Rapid on-site, point-of-care diagnostics
Leiden University Medical Center		
Prof. Dr. Eric Snijder	Virology	Molecular biologist, Basic virology, antivirals, +RNA viruses
Dr. Martijn van Hemert	Virology	Molecular virologist, flaviviruses, alphaviruses, antivirals
Dr. Marjolein Kikkert	Virology	Molecular virologist, Innate immunity, flaviruses
Prof. Dr. Leo Visser	Internal diseases	Infectious disease specialist, Travel-related infections
Radboud University Medical Center		
Prof. Dr. Heiman Wertheim	Medical Microbiology	Medical microbiologist, Global health, tropical diseases, big data
Dr. Ronald van Rij	Institute for Molecular Life Sciences	Biologist, Insect viruses, Mosquito immunology

Netherlands Institute of Ecology		
Dr. Henk van der Jeugd	NIOO	Population dynamics, quantitative genetics, waterfowl biology
Avans Hogescholen		
Dr. Eefje Schrauwen	Avans	Genomics, next generation sequencing, bio-informatics
Leiden University		
Dr. Maarten Schrama	Institute for environmental sciences / Naturalis	Ecology, biodiversity in relation to land use, development of eDNA monitoring of mosquitoes
University Medical Centre Utrecht		
Prof Marc Bonten	Julius Centre	Mathematical modelling, transmission, clinical infectious diseases, clinical trials
Dr. Patricia Bruijning	UMCU	Infectious disease epidemiology, modelling
Dr Jovanka Bestebroer	UMCU	Communication and management support
Co-financiers partners		
Dr. Eline Boelee	Deltares	Water-health interlinkages, environmental disease control
Dr. Gertjan Geerling	Deltares	Ecological modelling, mapping
Prof. Dr. Jaap van Dissel	Centre for Infectious Disease Control, National Institute of Public Health (RIVM)	Public health, Director of Centre, participating with researchers from several departments
Prof Dr Aura Timen	RIVM	National coordinator disease preparedness and response
Dr. Gerard van der Schrier	Koninklijk Nederlands Meteorologisch Instituut (KNMI)	High density meteorological observational data Climate warming scenario's, high-resolution climate modelling
Prof. Dr. Ashley Duits	Red Cross Blood bank Foundation, Curacao	Blood safety, infectious diseases
Prof. Dr. Hans Zaaijer	Sanquin, Dept. Blood borne infections	Blood- borne infections, emerging infections
Dr. Ria Sluiter	Technasium Foundation	Citizen science projects in high school network
Drs. Arjan Stroo	Netherlands Centre for Monitoring of Vectors (CMV)	Entomology, vector control
(inter)national cooperation partners		
Prof dr Ruud Foppen	SOVON Dutch Centre for Field Ecology	
Drs. Ewout Fanoy	Municipal Health Service Rotterdam	
Prof. Dr. Frederic Bartumeus	CEAB-CSIC	Citizen science, data science, vector and epidemiological modelling