icrad
International coordination of research on infectious animal diseases

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Newsletter

6th Issue July 2023

EDITORIAL

Welcome to the sixth issue of the ICRAD Newsletter!

ICRAD is well on its way! This sentence is recycled from a previous newsletter and it is very satisfying to state that it is still valid.

In January 2023, a two-day mid-term meeting on the projects funded in the first ICRAD call was held in Thessaloniki in Greece. More than 40 participants attended the meeting, the majority in person together with a few on-line.

The progress of the various projects was presented and lively debated with open minds, which created a unique atmosphere for exchange of comments and ideas. Furthermore, it was obvious that the in person meeting possibility also facilitated fruitful talks during the breaks.

Generally, the participants expressed great satisfaction with the meeting, and the efforts of our Greek hosts to make the meeting such a success are highly appreciated.

Additional information about the mid-term meeting will be available on the ICRAD web-site (www.ICRAD.eu).

The 2nd ICRAD call "One Health Approach to Zoonoses Research and Innovation" has been closed. Out of 40 project proposals, ten international collaborative research projects have been nominated for funding. These interesting projects covering research on prions, bacteria and viruses, respectively, are presented in this Newsletter.

The 3rd ICRAD call 'Helminth infections and changing climate: tackling the challenges for animal health' has been launched.

The dead-line for submission of pre-proposals was June 1, 2023, and we look forward to the further progress for this call, which will be the last under ICRAD auspices.

Finally, we wish everyone a happy, sunny and joyful summer.

Per Mogensen
ICRAD project manager

Jens Nielsen
ICRAD coordinator

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2nd Call

10 Projects Succeed

List of the selected Projects

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Projects Acronyms

ScIce
LEPTIMMUNHOST
ScResGoats
POC4AIV
EPICVIR
imdiTBap
FLU-SWITCH
NanoZoo
Q-Net-Assess
AdapTB

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Projects Presentation

Acronym: SCIce

Classical Scrapie in Iceland, a model for prion diseases worldwide

Consortium:

Partner 1:
Dr. Christine Fast. Friedrich-Loeffler-Institut. Institute of Novel and Emerging Infectious. Diseases Germany (Coordinator)

Partner 2:
Dr. John Spiropoulos. Animal & Plant Health Agency (APHA). UK

Partner 3:
Prof. Dr. Gesine Luehken. Justus-Liebig University of Giessen. Institute of Animal. Breeding and Genetics. Germany

Partner 4:
Dr. Fiona Houston. University of Edinburgh. The Roslin Institute. R(D)SVS. UK

Partner 5:
Dr. Vincent BERINGUE INRAE. France

Partner 6:
Dr. Juan Carlos. Espinosa Instituto Nacional de Investigación y Tecnología Agraria y. Alimentaria-Consejo. Superior de Investigaciones. Científicas (INIA-CSIC). Centro de Investigación en Sanidad Animal (CISA). Spain

Prion diseases (i.e. BSE, Scrapie, CWD) are fatal disorders caused by the conversion of the cellular prion protein (PrPC) into an abnormal isoform (PrPSc). The diversity of prion strains in classical scrapie reveals a remarkable plasticity, resulting in different biological behaviour and even inherit the potential to cross the species barrier in relevant animal models. In this regard, it has to be kept in mind that the BSE epidemic is a sobering example of how prions can evolve to become zoonotic. Still, the mechanisms controlling prion strain evolution and the factors that determine the zoonotic potential of a prion strain are unclear.

In sheep and goats, PrPC is highly variable and TSE susceptibility in these species depends on host genotypes. Some PrP variants convert to PrPSc with difficulty, which not only has a profound impact on transmission, but is also one of the main drivers of prion strain evolution due to selective pressure. In addition, classical scrapie infected sheep shed PrPSc into the environment causing persistent environmental reservoirs facilitating re-emergence of disease, and posing significant challenges for disease control.

Iceland has a well-documented history of classical scrapie since its introduction by an infected ram in 1878, despite strenuous disease eradication efforts. The isolation of Icelandic classical scrapie, limited to one breed and originating from one scrapie case, together with its well documented history and extended archive, creates unique conditions to study evolution and persistence of prion strains over time. Moreover, the longstanding policy of depopulating and decontaminating scrapie-affected farms provides unique conditions to study the PrPSc adaptation to the environment over extended periods, which may also contribute to the development of new prion strains. Therefore in vitro and in vivo experiments will be combined to (i) study PrP gene (PRNP) sequence variation of Icelandic sheep, (ii) examine the effect of Icelandic PRNP polymorphisms on resistance to classical scrapie, (iii) characterize the alteration of prion strains in Iceland over time, including the potential evolution of zoonotic traits, and (iv) determine the effect of environmental contamination with classical scrapie prions in driving the re-emergence of the disease. The results will be combined and used for epidemiological analyses and for the development of flexible economic models for improved and cost-effective control strategies.

The evolution of prion strains has an inherent zoonotic potential and the knowledge gained in this project, using classical scrapie as a model, will be critical for controlling re-emergence of diseases and preventing the emergence of new zoonotic threats. The expected outcomes can be viewed as a blueprint for managing outbreaks of potentially zoonotic prion diseases worldwide.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: imdiTBap

Improving the diagnosis of tuberculosis in domestic ruminants through the use of new antigens and test platforms

Consortium:

Partner 1:
Dr. Javier Bezos. Complutense University of Madrid . Animal Health Department. Veterinary Faculty and VISAVET. Health Surveillance Centre. Spain (Coordinator)

Partner 2:
Dr. Martin Vordermeier Animal and Plant. Health Agency (APHA). Department of Bacteriology. United Kingdom

Partner 3:
Prof. Eamonn Gormley University College Dublin (UCD). Tuberculosis Diagnostics and Immunology Research Laboratory. Ireland

Partner 4:
Dr. Maria Beatrice. Boniotti Istituto Zooprofilattico. Sperimentale della Lombardia e dell Emilia Romagna (IZSLER). Reparto Tecnologie. Biologiche Applicate. Italy

Partner 5:
Dr. Alessandra Martucciello. Istituto Zooprofilattico. Sperimentale de Mezzogiorno (IZSM). National Reference. Centre for Hygiene and Technologies of Water. Buffalo Farming and Production (CReNBuf). Italy

Partner 6:
Dr. Mercedes Dominguez. Instituto de Salud Carlos III. Servicio de Inmunología. Spain

Partner 7:
Prof. Dr. Erman Or. Istanbul University-Cerrahpasa Internal medicine. Turkey

The impact of zoonotic tuberculosis (zTB) has been known for a long time and has resulted in the incorporation of milk pasteurization as a preventive public health measure in many countries. zTB represents a serious global threat to public health. Livestock TB control programs were originally implemented to reduce the risk posed by zoonotic transmission to humans. Diagnosis of TB in livestock is based primarily on cell-mediated immune (CMI) diagnostic tests (intradermal test/IT and interferon-gamma release assay/IGRA) using PPDs (purified protein derivatives from Mycobacterium bovis and M. avium) that are sub-optimal in terms of diagnostic sensitivity and specificity. Therefore, there is a need to continue working on the development and improvement of diagnostic techniques, not only CMI based tests but also humoral antibody-based tests, that have shown good performance in some species. Bovine PPD consists of a largely undefined mix of proteins, lipids and carbohydrates obtained from cultures of M. bovis AN5. Since some of the immune-reactive antigens are also present in non-pathogenic environmental mycobacteria (NTM), this can lead to a reduction in test specificity. Ongoing research into specific antigens has been recommended in order to improve diagnostic performance. Over the past two decades, specific M. bovis antigens and host biomarkers of infection (cytokines) have been identified, paving the way for the development of defined antigen-based assay and TB diagnostic platforms. In this project we intend to close knowledge gaps in field performance of prototype antigen formulations (DSTF, P22) and develop novel diagnostic platforms. This will contribute to TB eradication in domestic ruminants and represent an important step towards reaching the global goal of human TB eradication set for the year 2050 (End TB strategy, WHO).

The scientific quality of the project is supported by the extensive experience and scientific reputation of the consortium composed of:
1. VISAVET Health Surveillance Center (EU-RL for Bovine Tuberculosis). Universidad Complutense de Madrid (UCM). Spain (Coordinator).
2. Servicio de Inmunología (SI) del Instituto de Salud Carlos III (ISCIII). Spain.
3. Animal and Plant Health Agency (APHA). Department of Bacteriology. United Kingdom.
4. University College Dublin (UCD). Tuberculosis Diagnostics and Immunology Research Laboratory. Ireland.
5. Istituto Zooprofilattico Sperimentale Della Lombardia e dell´Elimia Romagna (IZSLER). Reparto Tecnologie Biologiche Applicate. Italy.
6. Istituto Zooprofilattico Sperimentale de Mezzogiorno (IZSM). Centre for Hygiene and
Technologies of Water Buffalo Farming and Production (CReNBuf). Italy.
7. Istanbul University Cerrahpasa (IUC). Internal Medicine Unit. Turkey.

The project is divided in four WP with different activities that can be summarized in:
WP1. Validation of DSTF and P22 antigens in cattle, goats and buffalo under different epidemiological situations using IT, IGRA and multicytokine platform (MCP).
WP2. Supply of DSTF and development of a MCP.
WP3. Production of P22 protein complex, validation of P22 ELISA and development of a novel antigen capture ELISA for TB diagnosis in domestic ruminants.
WP4. Critical assessment of the performance of IT and IGRA using DSTF and P22 and novel diagnostic platforms developed in this project.

The results generated will be evaluated in order to define their utility to accelerate TB control and eradication policies.

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Acronym: EPICVIR

Emerging porcine influenza and coronaviruses

Consortium:

Partner 1:
Prof. Dr. Kristien Van Reeth. Ghent University, Faculty of Veterinary Medicine Department of Translational Physiology, Infectiology and Public Health (DI04). Belgium (Coordinator)

Partner 2:
Prof. C.A.M. (Xander) de Haan. Utrecht University (UtrechtU). Department of Biomolecular Health Sciences. Netherlands

Partner 3:
Dr. Maria Montoya. Centro de Investigaciones Biológicas Margarita Salas. Molecular Biomedicine. Spain

Partner 4:
Dr. Elma Tchilian Pirbright Institute Host responses. United Kingdom

Partner 5:
Prof. Mario Castro Ponce. Universidad Pontificia Comillas. Institute for Research in Technology. Spain

Partner 6:
Dr. Martin Lopez Garcia. University of Leeds. Applied Mathematics. United Kingdom

Influenza and coronaviruses have caused some of the deadliest pandemics in humans, and swine are key viral reservoirs. Influenza viruses of type A (swIAV) and porcine respiratory coronavirus (PRCV) are enzootic in swine and target epithelial cells of the airways. Still, they differ in pathogenicity and immune control. Cattle are the natural host of influenza D virus (IDV), but it is now an emerging virus in swine (swIDV), and its pathogenesis remains underexplored. SwIAV has enormous and still increasing genetic diversity, with many "reassortant" genotypes circulating simultaneously, and is a proven zoonotic and pandemic threat. The pandemic potential of PRCV and swIDV is uncertain.

We shall compare the transmission, pathogenesis, and host tropism of 6 different swIAV genotypes, swIDV and PRCV, to address 4 questions:

1) What are the transmission dynamics of swIVs and PRCV between swine and from swine to ferrets, which are used as a model for humans?

2) What key early events and immune mediators govern the outcome of swIV and PRCV exposure and may tip the balance to mild or severe disease?

3) What is the zoonotic potential of swIV and PRCV? Do some of the novel H1 swIAV genotypes pose a higher risk than the well-known swIAV? How efficiently do swIDV and PRCV replicate in human airways? Which viral traits may contribute to host switching?

4) Can an integrated mathematical model of viral replication, transmission, pathogenesis and immune control identify key events in the virus-host interaction to inform control strategies?

We will perform *in vivo* studies (Q 1, 2) in the swine and ferret host, and in vitro studies (Q 3) in differentiated airway cultures of swine, humans, and ferrets, with maximal similarity to the in vivo situation. Finally, we will use novel mathematical models to provide quantitative information from the integrated data (Q 4).

Our results will help predict the zoonotic potential, transmission, and pathogenicity of existing and emerging swIVs and PRCVs.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: AdapTB

Defining the Molecular Determinants of Mycobacterial Adaptation and host:pathogen Interaction to inform bTB control

Consortium:

Partner 1:
Dr. Sharon Kendall. The Royal Veterinary College PPS. UK (Coordinator)

Partner 2:
Prof. Stephen Gordon. University College Dublin. School of Veterinary. Medicine. Ireland

Partner 3:
Dr. Nathalie Winter. INRAE-ISP. Animal Health. France

Partner 4:
Dr. Mickaël Riou. INRAE- PFIE. Animal Heath. France

Partner 5:
Dr. Irene Nobeli. Birkbeck, University of London. Biological Sciences. United Kingdom

Partner 6:
Dr. Fabiana Bigi. National Institute of Agricultural Technology (INTA). Institute of Biotechnology. Argentina

Bovine tuberculosis (bTB) is a threat to the agricultural industry, biodiversity, animal health and human health. It is caused by bacteria belonging to a complex of genetically similar lineages known as the *Mycobacterium tuberculosis* complex (MTBC). The canonical animal- adapted species, *Mycobacterium bovis* (Mb), is the main agent of bTB in partnered countries and is a multi-host pathogen capable of infecting cattle, wild-life reservoirs and humans. Eradication programmes in the partner countries have failed to eradicate bTB resulting in an increased financial, zoonotic and ecosystem risk. There is a heterogeneity in the hosts' immune response to infection with Mb and this directly influences the risk of transmission from infected cattle. In the best-case scenario, the pathogen is cleared by the host innate immune system. Failure to control infection results in bacterial replication, pathology and onward transmission. In AdapTB we will identify the underlying mechanisms by which Mb interacts with the host to avoid immune clearance, drives pathology and transmits.

The AdapTB consortium consists of a multi-disciplinary team of scientists with expertise in molecular mycobacteriology, immunology, *ex vivo* and *in vivo* models of bTB and bioinformatics. Our aim is to better understand how Mb interacts with the innate and adaptive arms of host immunity to influence disease progression and transmission. We will use whole genome transposon mutagenesis to determine the bacterial effectors of dissemination and survival in the face of innate and adaptive immunity. We will use targeted bacterial mutants to further dissect the host response in *ex vivo* and *in vivo* models measuring parameters such as cytokine response, cellular migration, granuloma formation and dissemination.

The AdapTB consortium is made up of 6 partners across 4 countries: The Royal Veterinary College and Birkbeck, UK (Dr Sharon Kendall and Dr Irilenia Nobeli); University College Dublin, Ireland (Professor Stephen Gordon); Institut national de recherche pour l'agriculture, l'alimentation et l'environnement – INRAE, France (Dr Nathalie Winter and Dr Mickael Riou) and Instituto Nacional de Tecnologia Agropecuaria – INTA, Argentina (Dr Fabiana Bigi).

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: LEPTIMMUNHOST

Comparative host and species-specific immune responses of macrophages infected with zoonotic Leptospira *interrogans*

Consortium:

Partner 1:
Dr. Catherine WERTS. Institut Pasteur Paris. France (Co-ordinator)

Partner 2:
Dr. Karina Cynthia Caimi. National Institute of Agropecuarian Technology. Institute of Agrobiotechnology and Molecular Biology. Argentina

Partner 3:
Prof. Dr. Dirk Werling. Royal Veterinary College. Pathobiology and Population Sciences. United Kingdom

Partner 4:
Dr. Česlovas Venclovas. Vilnius University. Life Sciences Center, Institute of Biotechnology. Lithuania.

Partner 5:
Prof. Dr. David Goodlett. University of Victoria. Department of Biochemistry and Microbiology. Canada

The "One Health" concept recognizes that human, animal, and environment health are closely interrelated. *Leptospira interrogans* are the causative bacterial agent of leptospirosis, an emerging zoonotic disease affecting humans and animals, worldwide. Pathogenic leptospires present in the environment can infect a broad range of hosts and the disease may appear as an acute, even fatal infection in accidental hosts, such as humans or livestock, or progress into a chronic, mainly asymptomatic infection in its natural hosts, such as mice and rats. In cattle, leptospirosis is responsible for high economic losses due to reduction in both, dairy and beef industry, and to high abortion rates. To improve on this, it is imperative to understand the innate immune responses elicited in different hosts, as this is key to understand the diverse disease outcomes seen in the different hosts. Many immunological experiments conducted in mice have allowed the understanding of some aspects of the immune responses during leptospirosis. However, our recent work has shown clear differences in the response seen in other mammalian hosts such as human and cattle. In this proposal we aim to apply a comparative analysis of the innate immune responses elicited by macrophages from divergent hosts such as bovines, pigs, mice, hamsters, and humans upon infection with various zoonotic *Leptospira* strains that were responsible for distinct outcomes of disease. The goal of this project will be to understand differential and specific immunological processes and pathways. More specifically, we aim to compare some Toll-like receptors recognition of membrane components of leptospires, using structural, biochemical, genomic, immunological, high content screening confocal microscopy and computational modelling approaches. This project should help to better understand the innate immune mechanisms driving host specificities of leptospirosis, and accordingly tailor host directed intervention strategies.

Key words: *Leptospira,* TLR, innate immunity, macrophages, cattle

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Acronym: NanoZoo

Protein nanoparticle vaccine platform for rapid response against zoonotic viruses in poultry and swine

Consortium:

Partner 1:
Dr. Gorben Pijlman. Wageningen University. Laboratory of Virology. the Netherlands (Coordinator)

Partner 2:
Prof. Dr. Linda King. Oxford Brookes University. Department of Biological and Medical. Sciences. United Kingdom

Partner 3:
Prof. Dr. Robert Possee
Oxford Expression Technologies. United Kingdom

Partner 4:
Dr. Morten Nielsen. University of Copenhagen. Dept. of Immunology and Microbiology. Denmark

Partner 5:
Prof. Dr. Andreas. Suhrbier. QIMR Berghofer Medical. Research Institute. Inflammation Biology Group. Australia

Partner 6:
Dr. Marielle van Hulten. MSD Animal Health. Poultry R&D. Netherlands

Partner 7:
Dr. Wian De Jongh. AdaptVac. Denmark

Novel vaccine platforms are urgently needed to produce efficacious, safe, low cost, and rapidly adaptable ('plug-and-play') vaccines to face the threat of zoonotic viral diseases in livestock. Protein nanoparticle vaccines, e.g. the highly successful porcine circovirus and the human papillomavirus vaccines, are generally considered an optimal vaccine format because of their high efficacy and intrinsic safety. Built on our success with clinical testing of a nanoparticle vaccine against covid-19 (H2020 Prevent-nCoV, clinical trial COUGH-1), the aim of the NanoZoo project is to apply our unique protein nanoparticle vaccine platform for rapid response against zoonotic viruses in poultry and swine. This technology involves expression of viral antigens in insect cells combined with antigen presentation on protein nanoparticles to induce a superior immune response. In the NanoZoo project, this approach will be applied for developing novel vaccines against two important zoonotic viral diseases in poultry (Avian influenza virus and Newcastle disease virus) and two emerging vector-borne zoonotic viral diseases in swine (Japanese encephalitis virus and Getah virus). Viral glycoproteins, or immunodominant subunits thereof, will be expressed in insect cells using the robust baculovirus expression system to ensure correct folding and glycosylation of the antigen. The viral antigens will then be coupled onto self-adjuvanting protein nanoparticles to be evaluated in vaccination studies (with/without adjuvants) in relevant animal models (chicken and mice). The baculovirus expression system will be engineered as a very fast 'plug-and-play' platform to go in a single step from a synthetic gene to viral antigen production, which will outcompete novel mRNA vaccine platform technologies in terms of speed, volume and cost. The project brings together academic and industry experts in viral antigen expression, nanoparticle vaccines and animal health.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: Q-Net-Assess

Improved molecular surveillance and assessment of host adaptation and virulence of *Coxiella burnetii* in Europe.

Consortium:

Partner 1:
Dr. Tom McNeilly. Moredun Research Institute. Disease Control. United Kingdom (Coordinator)

Partner 2:
Dr. Katja Mertens-Scholz. Friedrich-Loeffler Institut. Institute of Bacterial Infections and Zoonoses. Germany

Partner 3:
Dr. Marcella Mori. Sciensano. Infectious diseases in animals. Belgium

Partner 4:
Dr. René van den Brom. Royal GD. Department of small ruminant, equine and companion animal health. Netherlands

Partner 5:
Dr. Ana Hurtado. NEIKER - Basque Institute for Agricultural Research and Development. Animal Health Department. Spain

Partner 6:
Dr. Rousset Elodie. ANSES, Laboratory of Sophia Antipolis. Animal Q fever Unit. France

Partner 7:
Dr. Xavier Bailly. INRAE, France National Research Institute for Agriculture, Food and Environment. Clermont Auvergne Rhone Alpes. France

Q fever is an important zoonotic pathogen caused by the bacterium *Coxiella burnetii*. Clinical signs in humans range from more common flu- like symptoms to persistent and potentially fatal infections. Ruminant livestock, and sheep and goats in particular, are the primary source of human infections, although *C. burnetii* can infect a wide range of other animals including wildlife and ticks. In ruminants, *C. burnetii* can cause abortion, stillbirth and weak offspring, mainly in sheep and goats, although most infections are asymptomatic. Thus, host range and outcome of infection is highly variable. Currently, our understanding of how *C. burnetii* genotype contributes to this variation is limited.

The main methods currently used for *C. burnetii* genotyping generate only limited genomic information and are difficult to standardise between laboratories. Whole genome sequencing (WGS) has revolutionised molecular epidemiology and surveillance of many zoonotic pathogens as it provides comprehensive genetic information and is easily standardised. However, to date only relatively few *C. burnetii* strains have been sequenced, largely due to difficulties in isolating the bacteria from field samples.

We have assembled a consortium with unique expertise in *C. burnetii* surveillance and genomics to allow collation of *C. burnetii* positive samples from a wide range of hosts (livestock, wildlife, and humans) with accurate clinical data. *C. burnetii* will be isolated from these samples using optimised isolation methods. Isolated strains, plus available archived strains, will be submitted for WGS to generate a comprehensive database of annotated *C. burnetii* genomes, which will include phenotypic data from the field and *in-vitro* cellular assays. WGS data will be analysed using novel bioinformatics approaches to identify molecular determinants of *C. burnetii* host range and virulence. Finally, project outputs will be synthesised into a recommended framework for future molecular surveillance of *C. burnetii.*

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: ScResGoats

Classical scrapie in genetically resistant goats: questioning current concepts and policies

Consortium:

Partner 1:
Dr. John Spiropoulos. Animal & Plant Health Agency. United Kingdom (Coordinator)

Partner 2:
Dr. Evridiki Boukouvala. Hellenic Agricultural Organization-DIMITRA, Veterinary Research Institute. Infectious and Parasitic Diseases. Greece

Partner 3:
Dr. Giuseppe Ru. Istituto Zooprofilattico Sperimentale del Piemonte. Liguria e Valle d'Aosta. Struttura Complessa Epidemiologia e Analisi del. Rischio. Italy

Partner 4:
Dr. Natalia Fernández-Borges. Instituto Nacional de Investigación y Tecnología. Agraria y Alimentaria (INIA-CSIC). Centro de Investigación en Sanidad Animal (CISA). Department of pathology, immunology and control of infectious diseases. BMCP Prion Group. Spain

Transmissible spongiform encephalopathies (TSE) or prion diseases are incurable, fatal, neurodegenerative diseases affecting animals and humans. The causative agent of these diseases are prions, which are pathogenic proteins (PrP) derived by conformational changes in the tertiary structure of a naturally occurring protein (PrP). Animal TSE have come to prominence due to the classical bovine spongiform encephalopathy (C-BSE) epidemic. Despite intense research efforts the origin of C-BSE is still speculated. However, it is well documented that affected animals consumed C-BSE contaminated feed, as a result of changes to rendering practices, and that C-BSE is zoonotic. Classical scrapie (C-scrapie) is a naturally occurring TSE affecting sheep and goats and its existence is known for centuries. This has allowed host-pathogen interactions to evolve resulting in the emergence of multiple strains and development of resistance to the disease depending on the sequence of PrP . The later was used to design extensive breeding programmes for genetic resistance that helped minimise or eliminate C-scrapie from sheep in many countries.

Similar genetic resistance breeding programmes to TSE in goats seem to be less successful mainly because the identification of polymorphisms conferring strong resistance is not as straightforward as it is in sheep. In addition, the prevalence of resistance associated polymorphisms in many goat populations is low, and their distribution is heterogeneous and non-universal. However, certain polymorphisms have been identified that may confer resistance if present in homozygous or heterozygous state. Despite this, in Greece, C-scrapie cases have been detected in goats with resistant PrP genotypes and certain herds appear to be more affected than others. These observations raise the following policy and scientific issues which need to be addressed: (a) are these cases attributed to a specific strain(s) that can propagate in animals otherwise genetically resistant to C-scrapie? (b) what are the biological properties of the novel strain(s) and especially their zoonotic potential? (c) are there other polymorphisms that can counterbalance the protection conferred by the polymorphisms which are associated with genetic resistance? (d) could sheep which share pastures or premises with affected goats act as a reservoir of these strains? To address the above questions, animals of interest will be identified, the full length of their PrP sequence will be determined, and the biochemical and biological properties of the strain(s) isolated from those animals will be determined, including their zoonotic potential. Finally, the epidemiology of these cases will be studied.

The results of the project will increase the scientific knowledge about host pathogen interactions, strain evolution, acquisition of zoonotic potential and will provide policy makers with additional control strategies for contrasting prion diseases.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Acronym: POC4AIV

Preventing zoonoses by screening Avian Influenza Virus (AIV) in wildlife birds and poultry using a novel rapid point of care system

Consortium:

Partner 1:
Prof. Anders Wolff. Danish Technical University. Bioengineering. Denmark (Coordinator)

Partner 2:
Dr. Valentina Panzarin. Istituto Zooprofilattico Sperimentale delle Venezie. Division of Comparative Biomedical Sciences. (DSBIO). Italy

Partner 3:
Prof. Dr. Grzegorz Woźniakowski. Nicolaus Copernicus University in Toruń. Department of Diagnosis and Clinical Sciences. Poland

Partner 4:
Dr. Žanete Šteingolde. Institute for Food Safety, Animal Health and the Environment "BIOR". Latvia

Partner 5:
Prof. Arvo Viltrop. Estonian University of Life Sciences. Institute of Veterinary Medicine and Animal Sciences. Estonia

Partner 6:
Dr. Aslıgül Kurt. IVBIO Technology Inc. Turkey

Partner 7:
Dr. Beatrice GRASLAND. French Agency for Food, Environmental and Occupational Health & Safety (ANSES). Laboratory of Ploufragan-Plouzané-Niort. France

Partner 8:
Dr. Anders Petersen. DNA Diagnostic A/S. Denmark

POC4AIV is a cross-sectoral research project with the aim to prevent zoonotic AIV by early diagnosis at the animal-human-environment interface.

A fluorescence-based point of care instrument (fPOC) will be developed for the rapid detection of AIV in poultry, wild birds and their environment. The core technology patented by the coordinator (DTU) was developed as a proof of concept for the detection of SARS-CoV-2, in H2020 CORONADX.

The fPOC for AIV detection is an advanced version of VETPOD, a diagnostic tool validated within the H2020 VIVALDI. To detect the target, fPOC will be equipped with a fluorescence-based optical system that guarantees higher sensitivity and results in 15-30 min. In addition, a new sample preparation method based on magnetic beads will be developed to enhance overall performance.

The fPOC will be validated according to the WOAH standards for AIV detection. An implementation study for fPOC deployment will be carried out to provide additional data on its performance in the field. In details, its suitability for surveillance, AIV confirmation and tracing will be evaluated with respect to diverse levels of disease prevalence.

The use of fPOC will also be evaluated as part of well-established diagnostic workflows, as an upstream screening method for subsequent identification of potentially zoonotic viruses by rRT-PCR and NGS.

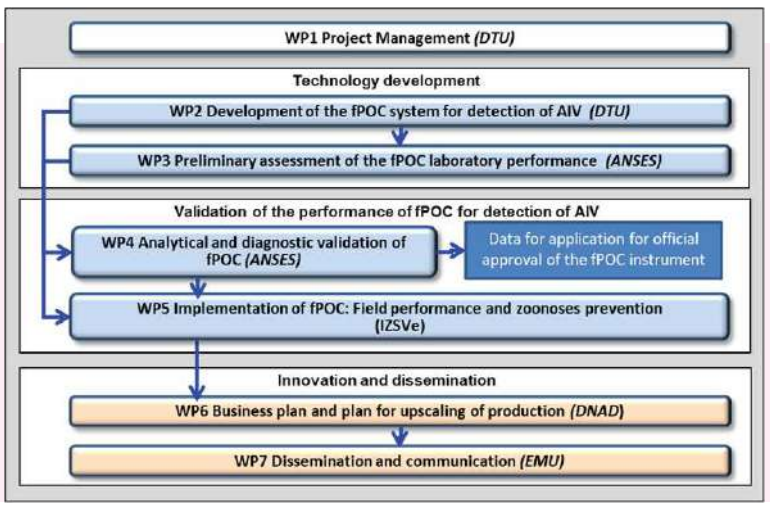
Finally, the possibility to use fPOC to detect AIV in different species/sample types will be explored using saliva specimens from experimentally challenged animals and artificially spiked samples. This will pave the way for wider use of fPOC in AIV susceptible mammals (e.g. swine, mink, and human).

The industrial partners will apply for WOAH official approval to use fPOC for AIV screening in wild birds and poultry and will develop roadmaps for industrial production and commercialization of fPOC in the EU and Turkey.

The objectives of POC4AIV are:
1. Development and manufacturing of a prototype point of care systems for AIV detection.
Key performance indicators: 6 prototype fPOC systems and 500 cartridges (for 5000 samples) to be distributed to partners for validation and implementation.
Addressed in WP2

2. Validation of fPOC system for laboratory and field use.
Key performance indicators: Assessment of fPOC performance and preparation of the validation dossier. Expected DSe above 90%. Expected DSp above 98%.
Addressed in: WP3, WP4 and WP5

3. Preparation for commercialisation: application for official approval and marketing.
Key performance indicators: WOAH application for the use of fPOC for on-site detection of AIV and plans for scaling-up fPOC production.
Addressed in WP6.



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Acronym: FLU-SWITCH

Identification of factors driving the emergence and spread of avian influenza viruses with zoonotic potential

Consortium:

Partner 1:
Dr. Romain Volmer. INRAE - Ecole nationale veterinaire de Toulouse. UMR 1225 IHAP. France (Coordinator)

Partner 2:
Dr. El-Sayed Mohammed. Abdel-Whab. Friedrich-Loeffler-Institut. Institute of Molecular. Virology and Cell Biology. Germany

Partner 3:
Dr. Robert de Vries. Utrecht Institute for Pharmaceutical Science. Chemical Biology & Drug Discovery. Netherlands

Partner 4:
Dr. Isabella Monne. Istituto Zooprofilattico. Sperimentale delle Venezie. Division of Comparative Biomedical Sciences (DSBIO). Italy

Partner 5:
Prof. Paul Digard. The University of Edinburgh. The Roslin Institute. United Kingdom

Partner 6:
Dr. Ashley Banyard. Animal and Plant Health Agency. Virology. United Kingdom

Partner 7:
Dr. Pawel Sikorski. University of Warsaw. Centre of New Technologies. Poland

Partner 8:
Dr. Zeynep Ahsen. KOÇER. Izmir Biomedicine and Genome Center. Technological Research Program/Emerging Viral Diseases Laboratory. Turkey

Avian influenza viruses (AIV) represent a major zoonotic threat. The antigenic diversity of AIV and the likely absence of pre-existing immunity in the human population means they have pandemic potential. It is thus crucial to identify AIV strains that have high potential for cross-species transmission and to understand their routes for adaptation to humans.

The FLU-SWITCH project addresses the zoonotic potential associated with the switch of H5 and H7 low pathogenic avian influenza viruses (LPAIV) to highly pathogenic avian influenza viruses (HPAIV). Evolution of the typical LPAIV monobasic HA cleavage site (CS) to a multibasic CS is critical to produce an HPAIV. While this step is not the major determinant of AIV adaptation to humans, H5 and H7 strains have caused the majority of zoonotic AIV infections in recent decades and the LPAIV to HPAIV switch is an important facet of this, both for the likelihood of human contact and potential pathogenesis. In addition the global spread of H5N1 HPAIV and the rising number of mammalian infections caused by this virus further justify the need to better understand the zoonotic potential of HPAIV.

FLU-SWITCH will investigate whether specific mutations in the viral genome associated with the LPAIV to HPAIV switch can promote cross-species transmission and increase the risk of zoonosis. The contribution of host factors to HPAIV emergence will also be investigated to determine how the host species influences LPAIV evolution. As the risk of AIV adaptation to humans is dependent on virus prevalence and geographic distribution, we will analyse the factors modulating HPAIV spread in Europe. Finally, we will analyse the consequences of vaccine-induced pre-existing immunity on the evolution of AIV. We will integrate these parameters to develop a risk assessment tool for the zoonotic potential of AIV.

FLU-SWITCH will generate knowledge on the mechanisms of emergence of AIV with zoonotic potential. Identifying virological markers, host species or environmental factors contributing to their emergence and spread could ultimately be used to eliminate AIV of concerns at source, for the benefit of animal and public health.

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Open Research Europe

O.R.E.: the European Commission's Diamond Open Access Publishing Platform

Open Research Europe launched in March 2021 and is designed for publishing the outputs of Horizon-funded research. This includes multiple funding initiatives, as follows:

-Horizon 2020 and Horizon Europe

-European Research Council

-Marie Skłodowska-Curie Actions

-COST Actions

-Euratom

-ERA-NET Cofunds

The platform is broad scope, meaning that it is designed for publishing research from any academic discipline, as the European Commission funds research across all disciplines. The broad scope of the platform means that it is particularly well-suited to interdisciplinary research. We have now published over 400 articles and continue to see growing interest in submission and publication.

Our platform is designed to support fast publication and open peer review, enabling ideas and research to be shared quicky and assessed in a collaborative and iterative manner. We also use a Diamond Open Access publishing model, which means that eligible research outputs are published open access at no cost to the researcher. All article processing charges are covered centrally by the European Commission

Benefits for Research

There are lots of reasons why you might want to consider publishing articles with Open Research Europe. Our rapid open access publication enables others to build upon new ideas right away, wherever and whoever they are. Our focus on open research or open science principles, such as data sharing, transparency and attribution, removes obstacles to collaborative research. The model also shifts the way research and researchers are evaluated by supporting research assessment based on the intrinsic value of the research rather than the venue of publication.

We offer a broad range of different article types that are designed to facilitate sharing non-traditional research outputs that commonly would not be accepted by more traditional publishing venues, such as Data Notes, Method Articles and Software Tool Articles. These types of articles are designed to help you share your ideas earlier in the research process, allowing you to receive peer review feedback which should ultimately improve the outcomes of your research. All of our article types are indexed in Scopus and PubMed, along with many other indexers.

Further information and contact

There is a huge amount of available on our website, linked above, but our team is also happy to receive questions about publishing via email. Please contact us at publishing@open-research-europe.ec.europa.eu.

icrad
International coordination of research on infectious animal diseases

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Midterm Meeting

10-11 January 2023

Thessaloniki, Greece

This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 862605

Midterm Meeting

Publicity

Antimicrobial Activity

hiips://www.ertnews.gr/roi-idiseon/apeili-gia-ti-dimo-sia-ygeia-se-pagkosmio-epipedo-i-anthektikotita-ton-mikrovio n-sta-antiviotika/

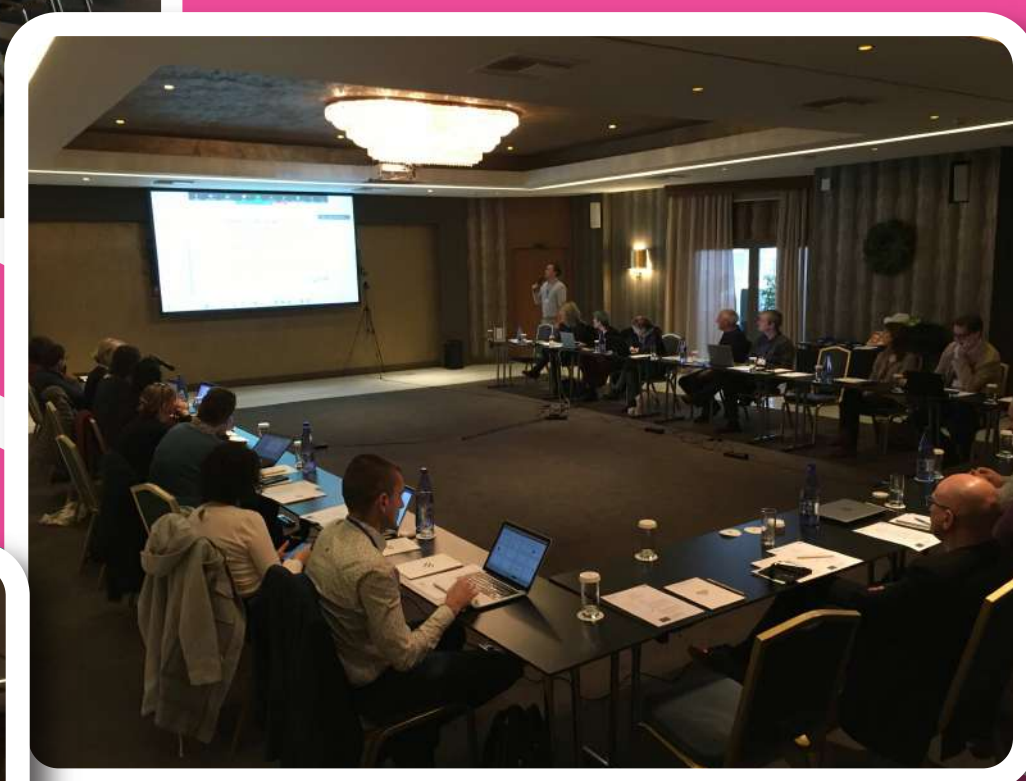
Measures of Surveillance and Control of the African Swine Feaver

hiips://www.youtube.com/watch?v=uBxKbyGu3Ow

Science Training Seminars - Science and Fake News

hiips://www.youtube.com/watch?v=Q9CUayuHmgw


Sandra. Bionna.



Initial Online Meeting of the 2nd Call Projects 8 June 2023

icrad
International coordination of research on infectious animal diseases

An online meeting was organized to disseminate information about ICRAD 2nd call projects at 8 June 2023.

AGENDA

10:30 – 10:40	Registration-Connection
10:40 – 10:45	Welcome and Introduction (**Jens Nielsen, ICRAD Coordinator)**
10:45 – 11:00	Overview of ICRAD (**Nikki Mackie-UKRI BBSRC)**
11:00 – 11:45	Presentation of 4 projects LEPTIMMUNHOST 11:00-11:15, **Dr. Catherine Werts** ImdiTBap 11:15-11:11.30, **Dr. Javier Bezos** NanoZoo 11:30-11.45, **Dr. Gorben P. Pijlman** Flu-Switch 11:45-12:00, **Dr. Romain Volmer**
12:00 – 12:15	Break
12.15– 14:00	Presentation of 6 projects Q-Net-Assess 12:15-12:30, **Dr. Tom McNeilly** SclCe 12:30-12:45, **Dr. Christine Fast** EPICVIR 12:45-13:00, **Dr. Kristine Van Reeth** ScResGoats 13:00-13:15, **Dr. Jhon Spiropoulos** AdaptTb 13:15-13:30, **Dr. Sharon Kendall** POC4AIV 13:30-13:45, Prof. Anders Wolff
13:45 -14:15	Presentation of ORE (**Dr Ruth Fleet, Open Research Europe, EU)**
14:15-14:30	General Discussion- End of the meeting

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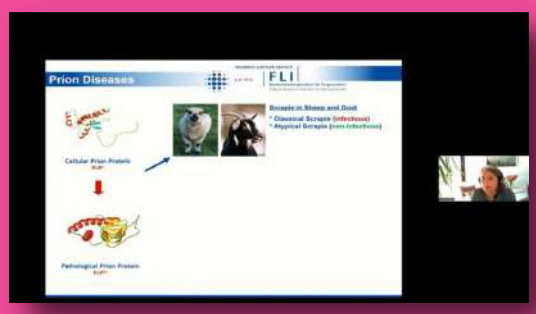
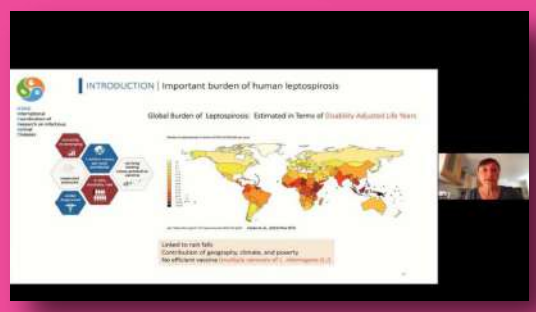
ICRAD Aims
Improve the ability to control and prevent emerging and endemic diseases
Increase preparedness and ability to respond to emerging and endemic livestock threats
Contribute to the reduction of antimicrobial and antiparasitic use in livestock and to minimising the development of resistance for the benefit of animal and public health
Contribute to animal welfare by better prevention of diseases and renewed animal management and farming systems
Contribute to food security and competitive and sustainable livestock systems
icrad


Prion Diseases
FLI
Cellular Prion Protein
Pathological Prion Protein


INTRODUCTION | Important burden of human leptospirosis
Global Burden of Leptospirosis: Estimated in Terms of Disability Adjusted Life Years


Background
Swine influenza A virus (swIAV)
• H1N1, various HA lineages and reassortants
• Zoonotic and pandemic potential!!!
Swine influenza D virus (swIDV)
• Swine as spill-over host, emerging
• Zoonotic potential?
Porcine Respiratory Coronavirus (PRCV)
• Alpha-coronavirus, enzootic
• Zoonotic potential?


imdTBap
Work Packages
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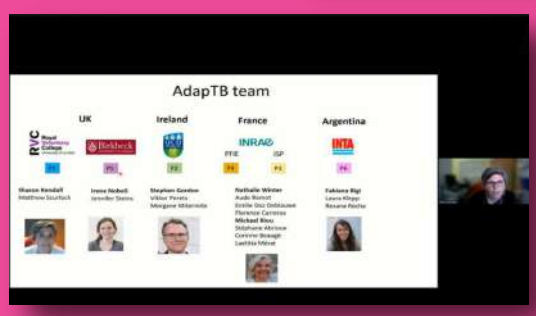
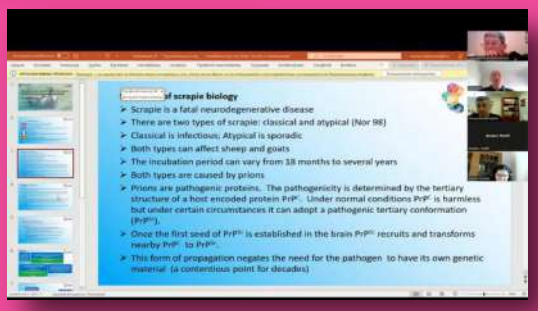
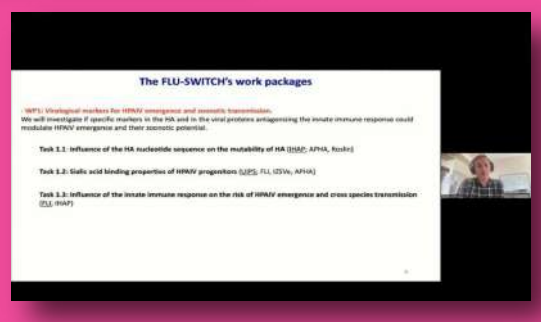
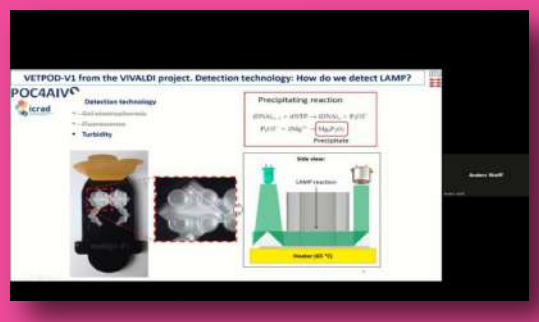
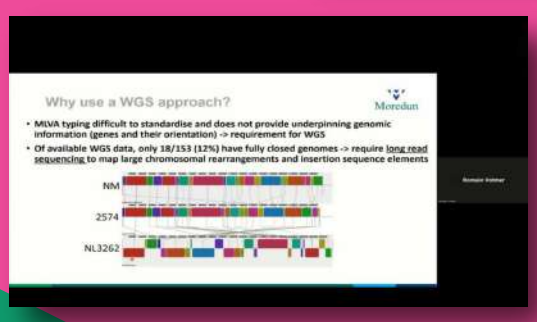

AdapTB team
UK
Ireland
France
Argentina

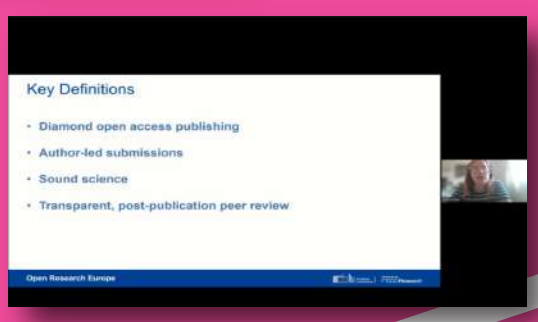

ABNCoV2 Phase 1
First-in-human trial completed - suggests strong antibody response and favorable safety profile


of scrapie biology
Scrapie is a fatal neurodegenerative disease
There are two types of scrapie: classical and atypical (Nor 98)
Classical is infectious; Atypical is sporadic
Both types can affect sheep and goats
The incubation period can vary from 18 months to several years
Both types are caused by prions
Prions are pathogenic proteins. The pathogenicity is determined by the tertiary structure of a host encoded protein PrP. Under normal conditions PrP is harmless but under certain circumstances it can adopt a pathogenic tertiary conformation (PrP).
Once the first seed of PrP is established in the brain PrP recruits and transforms nearby PrP to PrP.
This form of propagation negates the need for the pathogen to have its own genetic material (a contentious point for decades)


The FLU-SWITCH's work packages
Task 1.1: Influence of the HA nucleotide sequence on the mutability of HA (IHAP, APHA, Roslin)
Task 1.2: Sialic acid binding properties of HPAIV progenitors (UPS; FLI, IZSVe, APHA)
Task 1.3: Influence of the innate immune response on the risk of HPAIV emergence and cross species transmission (FLI, IHAP)


VETPOD-V1 from the VIVALDI project. Detection technology: How do we detect LAMP?
POC4AIV
icrad
Detection technology
Turbidity
Precipitating reaction
Precipitate
Side view
LAMP reaction


Why use a WGS approach?
Moredun
MLVA typing difficult to standardise and does not provide underpinning genomic information (genes and their orientation) -> requirement for WGS
Of available WGS data, only 18/153 (12%) have fully closed genomes -> require long read sequencing to map large chromosomal rearrangements and insertion sequence elements
NM
2574
NL3262


Key Definitions
Diamond open access publishing
Author-led submissions
Sound science
Transparent, post-publication peer review
Open Research Europe

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