



**D0.3.2: Report on the
COVRIN kick-off meeting,
31st March 2021
JIP COVRIN WP0**

Responsible Partner: UoS (23)

Contributing partners: All partners



GENERAL INFORMATION

European Joint Programme full title	Promoting One Health in Europe through joint actions on foodborne zoonoses, antimicrobial resistance and emerging microbiological hazards
European Joint Programme acronym	One Health EJP
Funding	This project has received funding from the European Union's Horizon 2020 research and innovation programme under Grant Agreement No 773830.
Grant Agreement	Grant agreement n° 773830
Start Date	01/01/2018
Duration	60 Months

DOCUMENT MANAGEMENT

Title OHEJP deliverable	D0.3.2: Report on the COVRIN kick-off meeting, 31st March 2021		
WP and task	WP0-T3.2		
Leader	Daniel Horton (UoS, 23)		
Other contributors	Wim van der Poel (WBVR, 31); WP leaders; Carlijn Bogaardt (UoS, 23)		
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Dissemination <i>Author's suggestion to inform the following possible interested parties.</i>	OHEJP WP 1 <input type="checkbox"/> OHEJP WP 2 <input type="checkbox"/> OHEJP WP 3 <input type="checkbox"/> OHEJP WP 4 <input checked="" type="checkbox"/> OHEJP WP 5 <input type="checkbox"/> OHEJP WP 6 <input type="checkbox"/> OHEJP WP 7 <input type="checkbox"/> Project Management Team <input checked="" type="checkbox"/> Communication Team <input type="checkbox"/> Scientific Steering Board <input type="checkbox"/> National Stakeholders/Program Owners Committee <input type="checkbox"/> EFSA <input type="checkbox"/> ECDC <input type="checkbox"/> EEA <input type="checkbox"/> EMA <input type="checkbox"/> FAO <input type="checkbox"/> WHO <input type="checkbox"/> OIE <input type="checkbox"/> Other international stakeholder(s): Social Media: Other recipient(s):		



D0.3.2: REPORT ON THE COVRIN KICK-OFF MEETING, 31ST MARCH 2021

Introduction

COVRIN aims to integrate research by One Health EJP partner institutes on the topics of SARS-CoV-2 emergence, risk assessment and preparedness. The project has two main operational objectives: (i) to identify drivers for the emergence and spread of SARS-CoV-2, and (ii) to generate data and build models for risk assessment of SARS-CoV-2. To achieve these objectives, integrative research activities are focused on four topics: (i) research on detection of SARS-CoV-2 in animal species and the environment; (ii) research on SARS-CoV2 molecular and biological characterization; (iii) SARS-CoV-2 surveillance and risk assessment, focussed on the animal human interface; and (iv) coronavirus preparedness. The overall aim of the COVRIN project is to generate and share data of these integrative research activities, in order to increase the preparedness for future coronavirus outbreaks.

The kick-off meeting for COVRIN was held on 31st March 2021. This Deliverable consists of the minutes of this meeting, and the slide decks of the presentations given by the project coordinator and work package leaders. E-mail addresses have been removed for privacy reasons.

Meeting minutes (circulated to COVRIN participants in April 2021)

Welcome and introduction to COVRIN (Wim van der Poel, WBVR)

Work package overview presentations (WP leaders)

See attached slides

Actions arising

- **All:** Consider and provide information (inc. contact person) to COVRIN coordinators on other EU funded activities. (e.g PREZODE) that overlap or align with COVRIN (to contribute to imminent scoping exercise T0.3).
- **Project coordinators:** circulate annex requesting ethical information
- **WP leaders:** complete animal ethics information by return when circulated
- **All:** complete and return any outstanding Y5 budget templates
- **All:** Partners involved in other OHEJP projects relevant to COVRIN: e.g TELE-VIR (Pipeline for NGS to variant dashboard-WP2), Orion and Matrix (surveillance, WP3), should contact relevant COVRIN WP leaders to initiate communication links are in place.
- **All:** If partners already have any tools that could be of use in a WP, contact WP leader directly and consider presenting at ASM satellite meeting (<https://onehealthjep.eu/asm-satellite-workshop-2021/>)
- Add the following to the COVRIN OHEJP website (when available): (1) contact details of everyone involved in COVRIN (**coordinators/WP leaders**); (2) presentation slides (**coordinators**)
- **All:** check whether your institute is correctly stated as partner under the relevant WPs/tasks
- **WP leaders:** Organise WP specific launch meetings



To note

- Project length: A 9 month extension to EJP has been requested (still under consideration). If approved, then COVRIN will still end in Dec 22 but final deliverables can be submitted in 23 (as per the current Gantt chart). If the extension is not approved, then all deliverables will be required to be submitted before end Dec 22 and the Gantt chart will be updated accordingly. **Risk of this for delivery of deliverables is noted.**
- ANSES and OHEJP TELE-VIR project both have NGS based mutation detection pipelines in development that are relevant for WP2
- OHEJP projects MATRIX and ORION are integrative projects including surveillance and are of relevance for WP3
- STAR-IDAZs group are organising a workshop of pandemic prevention initiatives
- Budget for Y5 requires finalisation
- There is a Nidovirus meeting in June is a good opportunity for presentation of results and networking: <https://fems-microbiology.org/opportunities/nido2020-xvth-internationalnidovirus-symposium/>



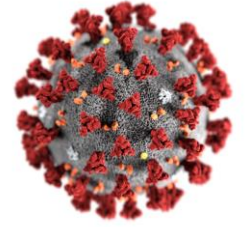
COVRIN

Joint Integrative Project 1

Wim van der Poel, WBVR
Daniel Horton, UoS
(PLs COVRIN)

2019-nCoV Wuhan, China, Covid-19 Pandemic

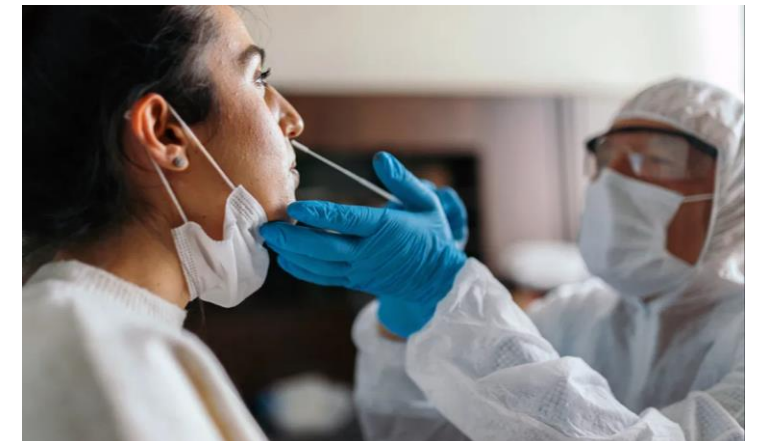
Main clinical manifestations



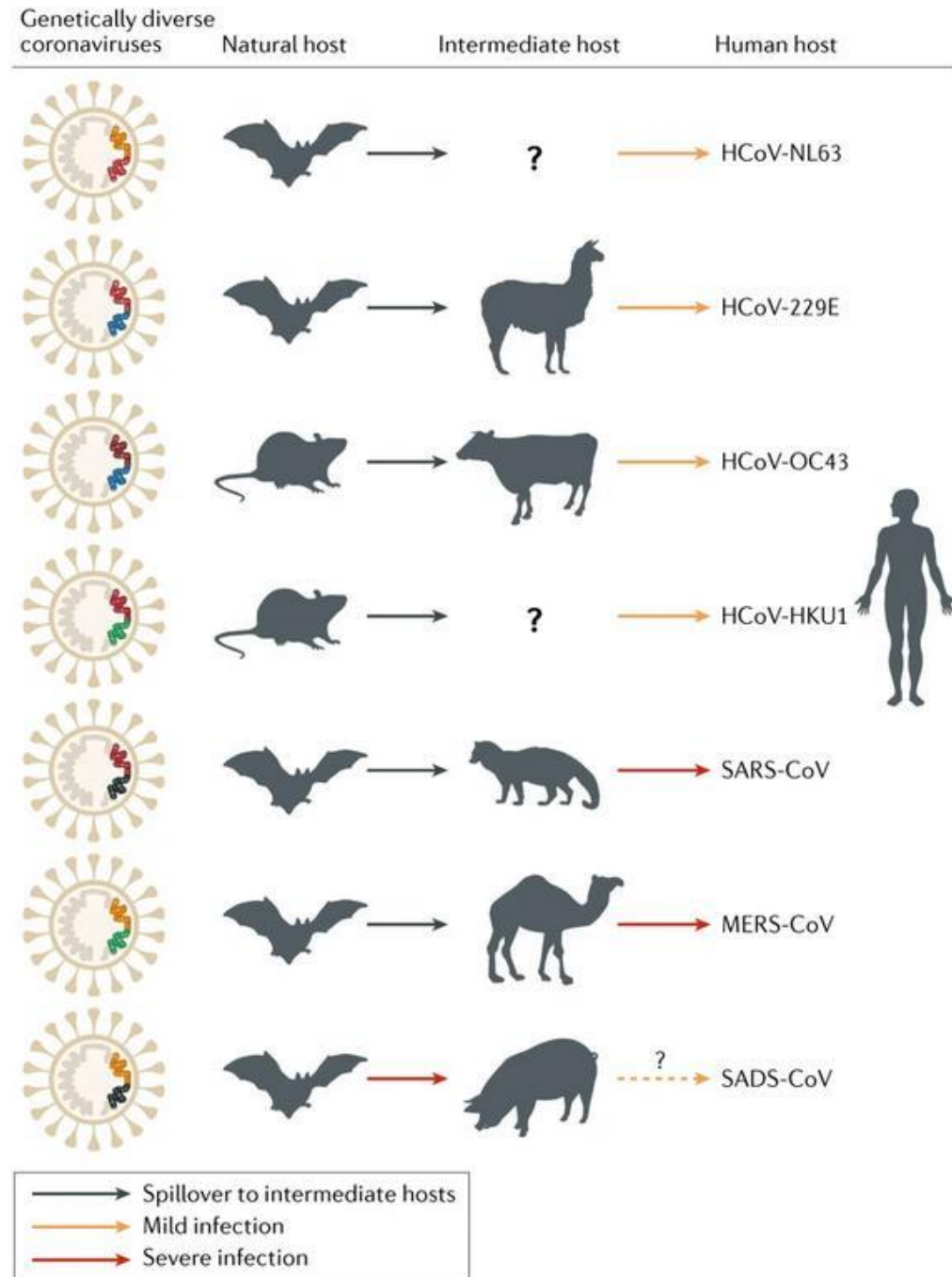
- fever (83%)
- Cough (82%)
- Shortness of breath (31%)
- Muscle ache (11)
- Confusion (9%)
- Headache (8%)
- Sore throat (5%)
- Rhinorrhoea (4%)














Chen et al., The Lancet, 2020



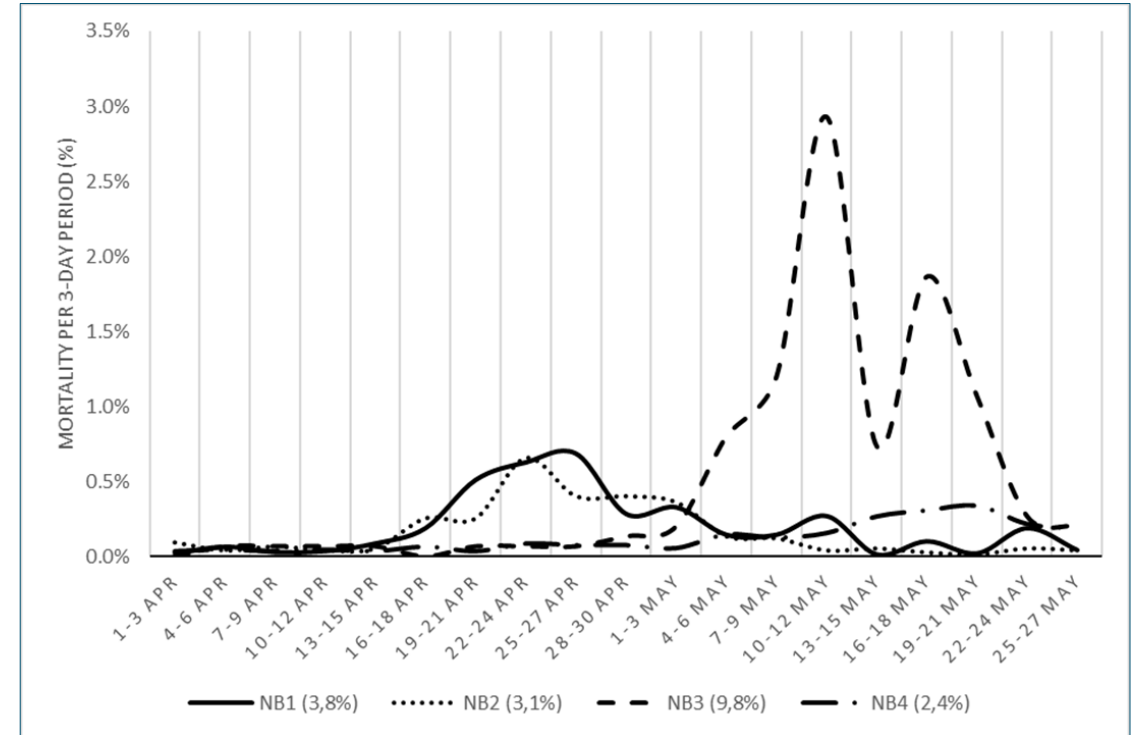
Coronavirus hosts

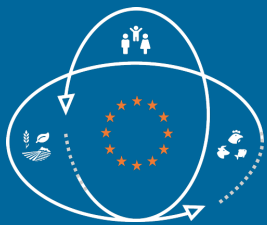


SARS-CoV2 susceptibility animals

Animal species	Clinical signs	Virus replication	Excretion infectious virus	
Non human primates	✓	✓	✓	
Cats 	✓	✓	✓	
Ferrets, Mink	✓	✓	✓	
Raccoon dogs 		✓	✓	
Hamsters	✓	✓	✓	
Fruit bats 		✓	✓	
Cattle		(✓)		
Swine 		(✓)		
Rabbits		✓	✓	
Dogs 		✓		
Chicken				

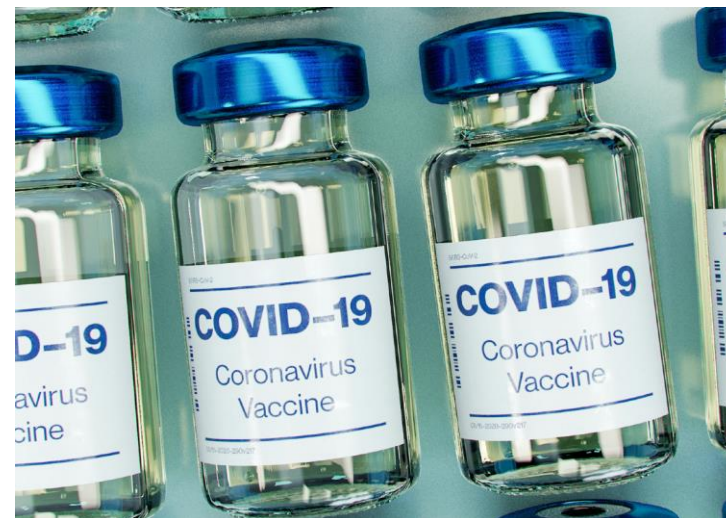
SARS-CoV2 in farmed mink





Covid-19 pandemic current developments

- New diagnostics
- New variants
- New hosts
- New vaccines
- Environmental contamination
- Other





COVRIN

SARS-CoV2 Research Integration & Preparedness

- Drivers for Emergence and Spread, and Risk Assessment of SARS-CoV2
- Responsible Partners:
 - Wageningen Bioveterinary Research (WBVR)
 - University of Surrey (UoS)
- Contributing partners:
 - ANSES (P1), Ages (P2), Sciensano (P4), VRI (P8), Bfr (P9), FLI (P10), INIA (P16), UCM (P17), INRAe (P19), APHA, (P21), UoS (P23), ISS (P27), IZSAM (P28), IZSLER (P29), RIVM (P30), WBVR (P31), NVI (P33), PIWET (P34), INIAV (P35), INSA(36), SVA (P41).



COVRIN Integrative Research project

Strategic goals

- Develop common COVID-19 protocols that support OHEJP collaborations
- Develop common infrastructure for COVID-19 research
- Integrate COVRIN deliverables into the work processes of OHEJP partners
- Reduce overlaps of COVID-19 research within OHEJP
- Develop a common OHEJP structure on Coronavirus preparedness



COVRIN

Operational Objectives

Two main integrative research objectives:

1. To identify drivers for the emergence and spread of SARS-CoV2
2. To generate data and build models for risk assessment of SARS-CoV2



COVRIN organisation

- Coordinators: Daniel Horton (UoS); Wim van der Poel (WBVR)
- 1 March 2021 – 31 December 2022
- Budget 2M euro
- Joint Integrative project, WP4 EJP
- WP-, Task-, Subtask Leaders
- Webpage, OH EJP website

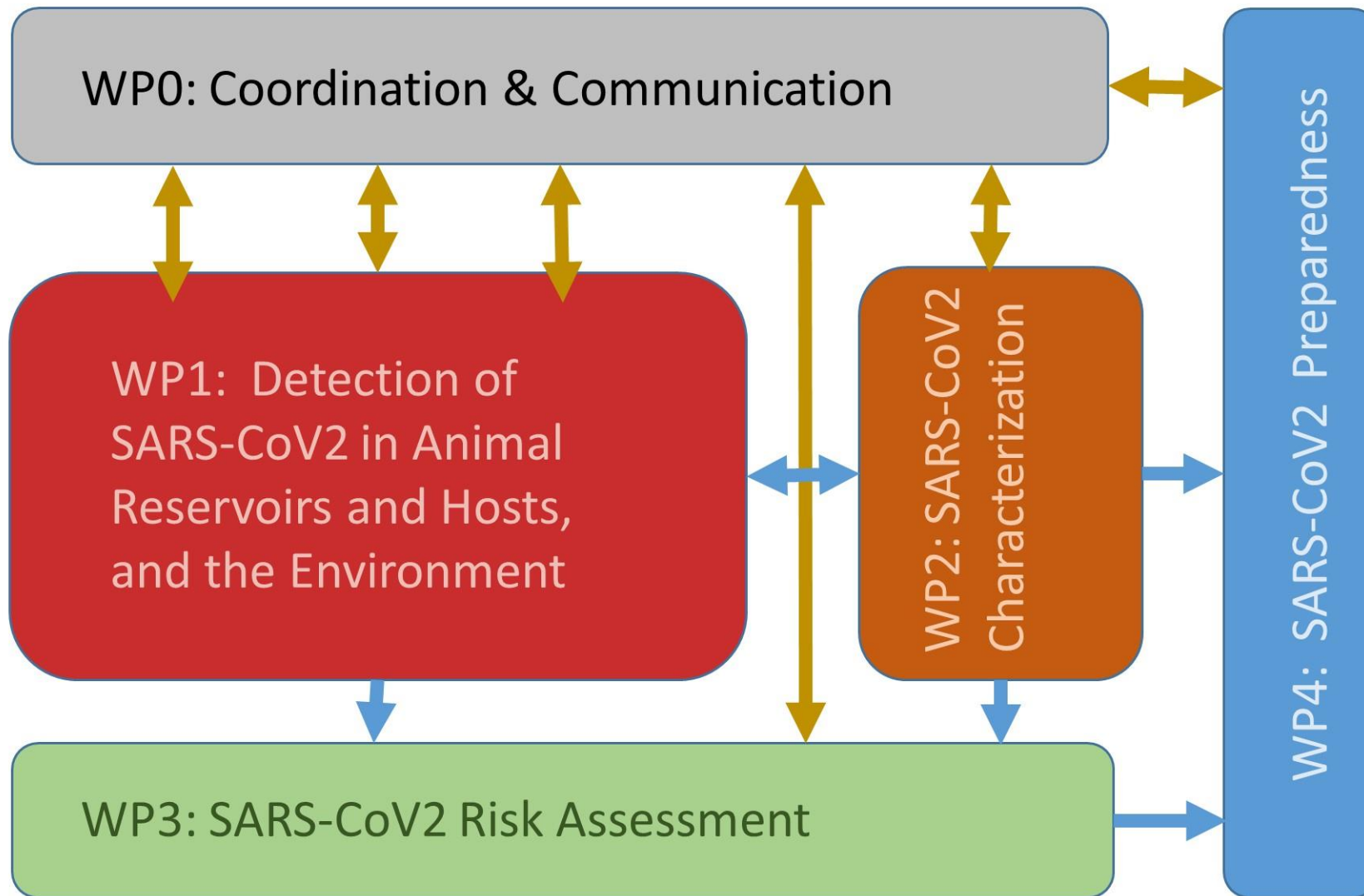


COVRIN workpackages

- WP0: Coordination and communication
- WP1: Detection of SARS-CoV2 in animal reservoirs and hosts, and the environment
- WP2: SARS-CoV2 characterization
- WP3: Risk assessment and surveillance
- WP4: Coronavirus preparedness

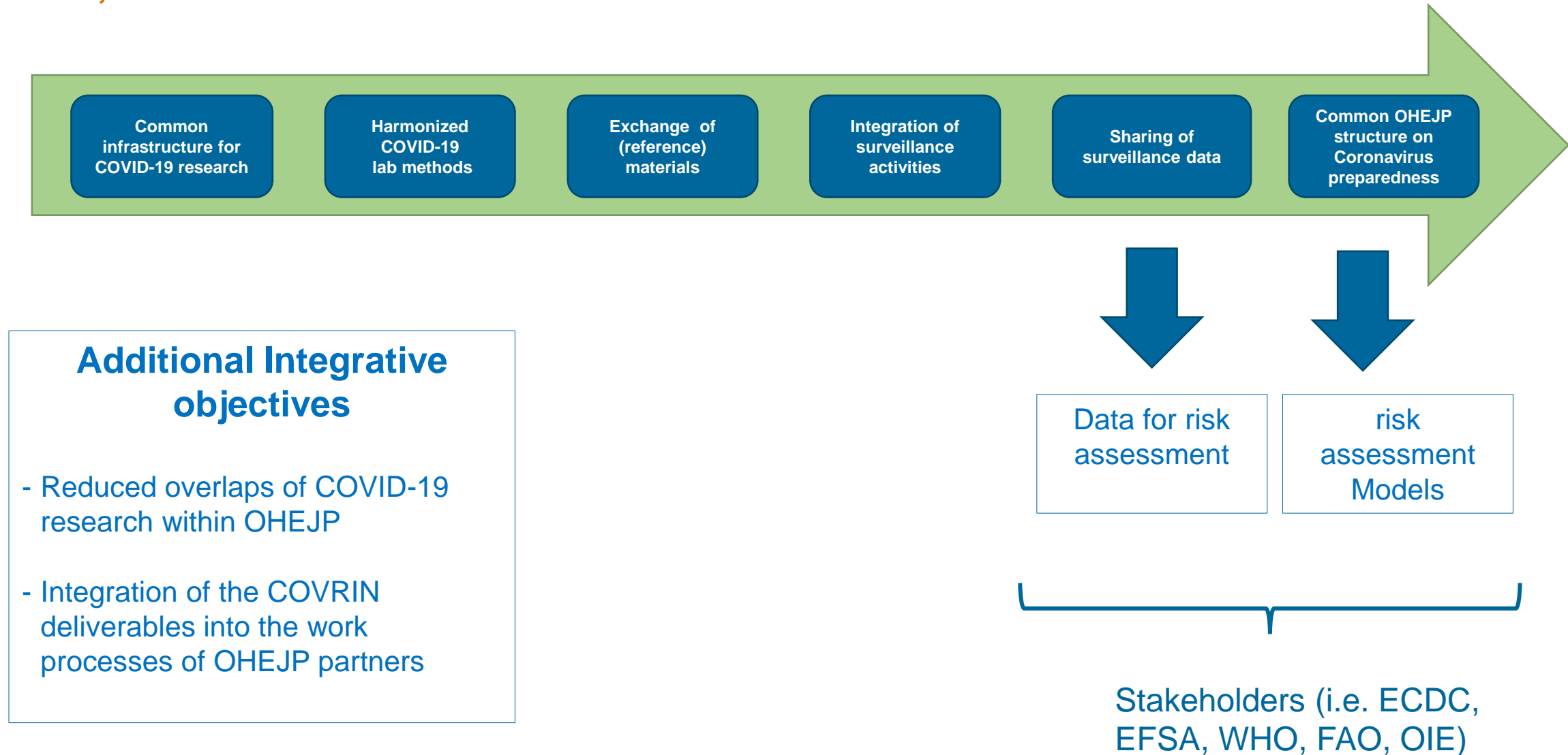


SARS-CoV2 Research Integration & Preparedness COVRIN 2.0



Strategic focus of COVRIN integrative topics

PREVENT, DETECT AND RESPOND





WP0 Coordination and communication

- T0.1: Internal project organisation:
- T0.2: Communication and reporting
- T0.3: Meetings and stakeholder connection



WP0 Coordination and communication

- T0.1: Internal project organisation:
 - Management of information flows; Meetings organisation,
 - Organisation of data sharing.
 - -> DMP leader: Lotte Houwens (WBVR);
 - -> Regular meetings of WP-leaders (incl. deputies)
 - -> WP leaders to organise WP meetings
- T0.2: Communication and reporting
 - Periodical reports; internal and external communication
 - -> Connection with EJP Com-team
 - -> Webpage contact point



WPO Coordination and communication

- T0.3: **Meetings** and stakeholder connection
 - Task Leader: Dan Horton (UoS)
 - Contributors (all):
ANSES (P1), Ages (P2), Sciensano (P4), VRI (P8), Bfr (P9), FLI (P10), INIA (P16), UCM (P17), INRAe (P19), APHA, (P21), UoS (P23), ISS (P27), IZSAM (P28), IZSLER (P29), RIVM (P30), WBVR (P31), NVI (P33), PIWET (P34), INIAV (P35), SVA (P41).
- KO March 2021, online
- Mid-term meeting (Jan-Feb 2022 tbc) – Online/hybrid
- Final meeting December 2022- In person, location TBC



WP0 Coordination and communication

- T0.3: Meetings and **stakeholder connection**
 - *Rapid reporting of relevant results is aligned with PREVENT-DETECT-RESPOND.*
 - *Results or information arising from activities co-funded by COVRIN, which may affect the risk posed by SARS-CoV-2 will be reported to REA by email or telephone by the COVRIN leadership group (Project leader, deputy leader, WP leaders) as soon as they are informed.*
 - *At this stage, national authorities are also informed.*
 - *The potential results or information to be communicated rapidly may include but is not exclusive to: new detections of SARS-CoV-2, genome or antibodies, detections in a new geographical area or an increase in detections in livestock, wildlife or environmental samples.*
- Contact points from stakeholders ECDC, EMA, EFSA will be invited to meetings
- Close liaison with OHEJP WP5 (Science to Policy) team also important
- These activities are in addition to the existing OHEJP dissemination activities



WP0 Coordination and communication

- T0.3: Meetings and stakeholder connection
 - 0.3.1 Scoping exercise to avoid overlap with other EU funded COVID-19 activities
 - Literature and survey based exercise, due M45

Thank you for your
attention!



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COVRIN

Joint Integrative Project
Kick Off Meeting 31st March 2021

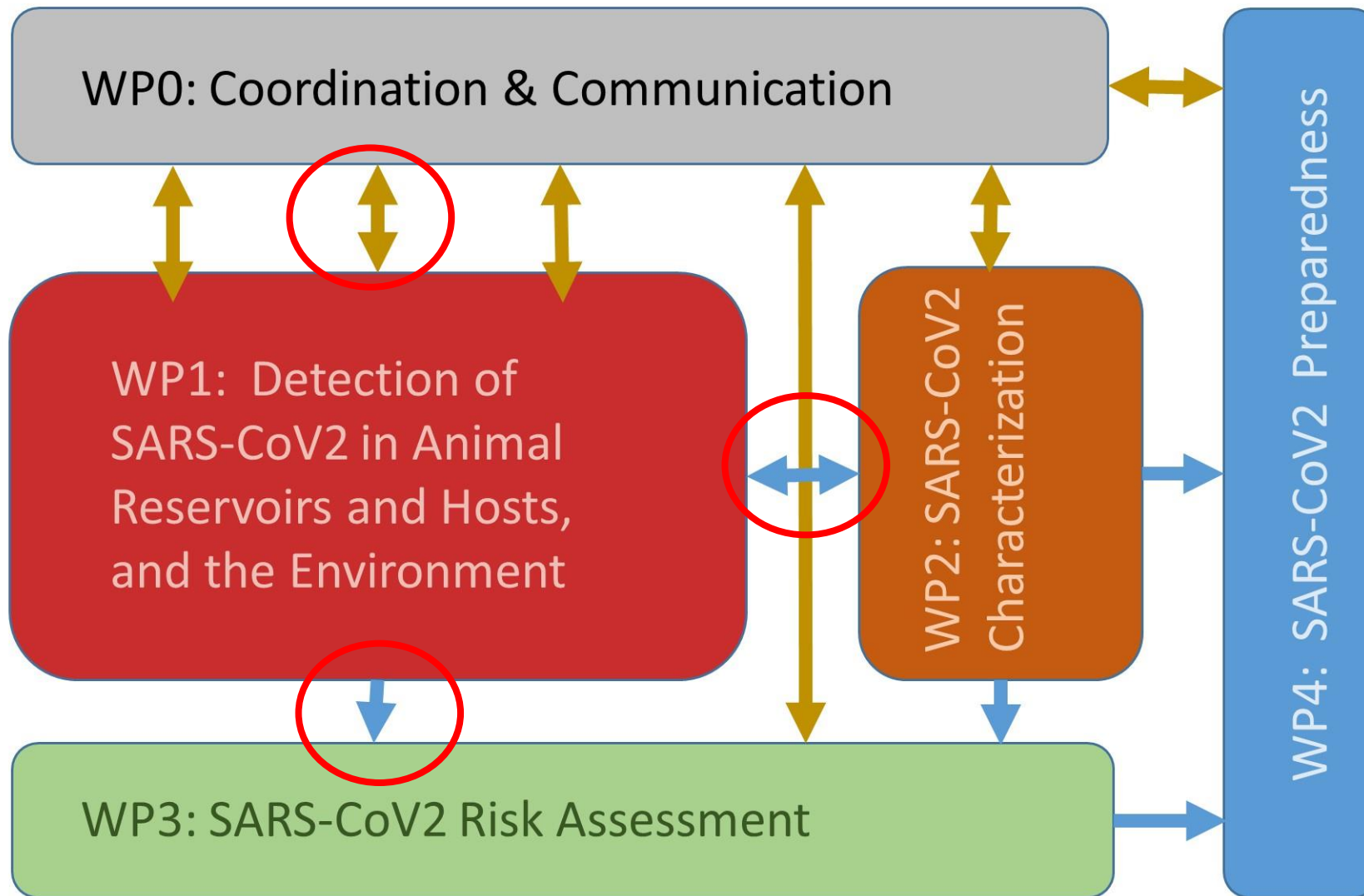


WP1

*Daniel Horton, UoS
Deputy Project Leader
WP1 leader*



SARS-CoV2 Research Integration & Preparedness COVRIN 2.0





WP1 Detection of SARS-CoV2 in animal reservoirs and hosts, and the environment

Leaders: Dan Horton (UoS), Martin Groschup (FLI)

- T1.1: SARS-CoV2 genome detection in livestock, wildlife, pets and environmental samples
- T1.2: Optimization and harmonization of immunological SARS-CoV2 antigen and antibody detection methods in domestic and wildlife animals.
- T1.3: Definition of bioavailability of virus in fomites, water, and the environment



WP1 Detection of SARS-CoV2 in animal reservoirs and hosts, and the environment

T1.1: SARS-CoV2 genome detection in livestock, wildlife, pets and environmental samples

- Task leader: Mikael Leijon (SVA)

Contributors: ANSES (P1), Ages (P2), Sciensano (P4), FLI (P10), UCM (P17), APHA (P21), UoS (P23), ISS (P27), IZSAM (P28), IZSLER (P29), RIVM (P30), WBVR (P31), NVI (P33), INIAV (P35), SVA (P41)

- ST1.1.1 Report on available data from SARS-CoV-2 virus genome testing in companion animals and livestock – (Lorraine McElhinney, APHA)
- ST1.1.2 Report on available data from SARS-CoV-2 virus genome testing in wildlife, (Elodie Monchatre-Leroy, ANSES)
- ST1.1.3 Report on available data from SARS-CoV-2 genome detection in environmental samples (Sandra Martin-Latil, ANSES)



WP1 Detection of SARS-CoV2 in animal reservoirs and hosts, and the environment

T1.2: Optimization and harmonization of immunological SARS-CoV2 antigen and antibody detection methods in domestic and wildlife animals. Task Leader: Martin Groschup, FLI

Contributors: ANSES (P1) VRI (P8) APHA (P21) UoS (P23) ISS (P27) IZSAM (P28) IZSLER (P29) RIVM (P30) WBVR (P31) NVI (P33) PIWET (P34) INIAV (P35)

- ST1.2.1 Evaluation of antigen detection methods in clinical samples from animals (Markus Keller , FLI)
- ST1.2.2 Evaluation of methods for antibody detection animals (Ana Moreno Martin, IZSLER)



WP1 Detection of SARS-CoV2 in animal reservoirs and hosts, and the environment

T1.3: Definition of bioavailability of virus in fomites, water, and the environment (Ana Maria de Roda Husman, RIVM,)

Contributors: ANSES (P1) VRI (P8) FLI (P10) APHA (P21) WBVR (P31)

- ST1.3 Report on the bioavailability of virus on fomites, water and the environment (Benoit Gassilloud ANSES)

COVRIN - CoronaVirus Research Integration

WP2 - SARS-CoV2 characterisation



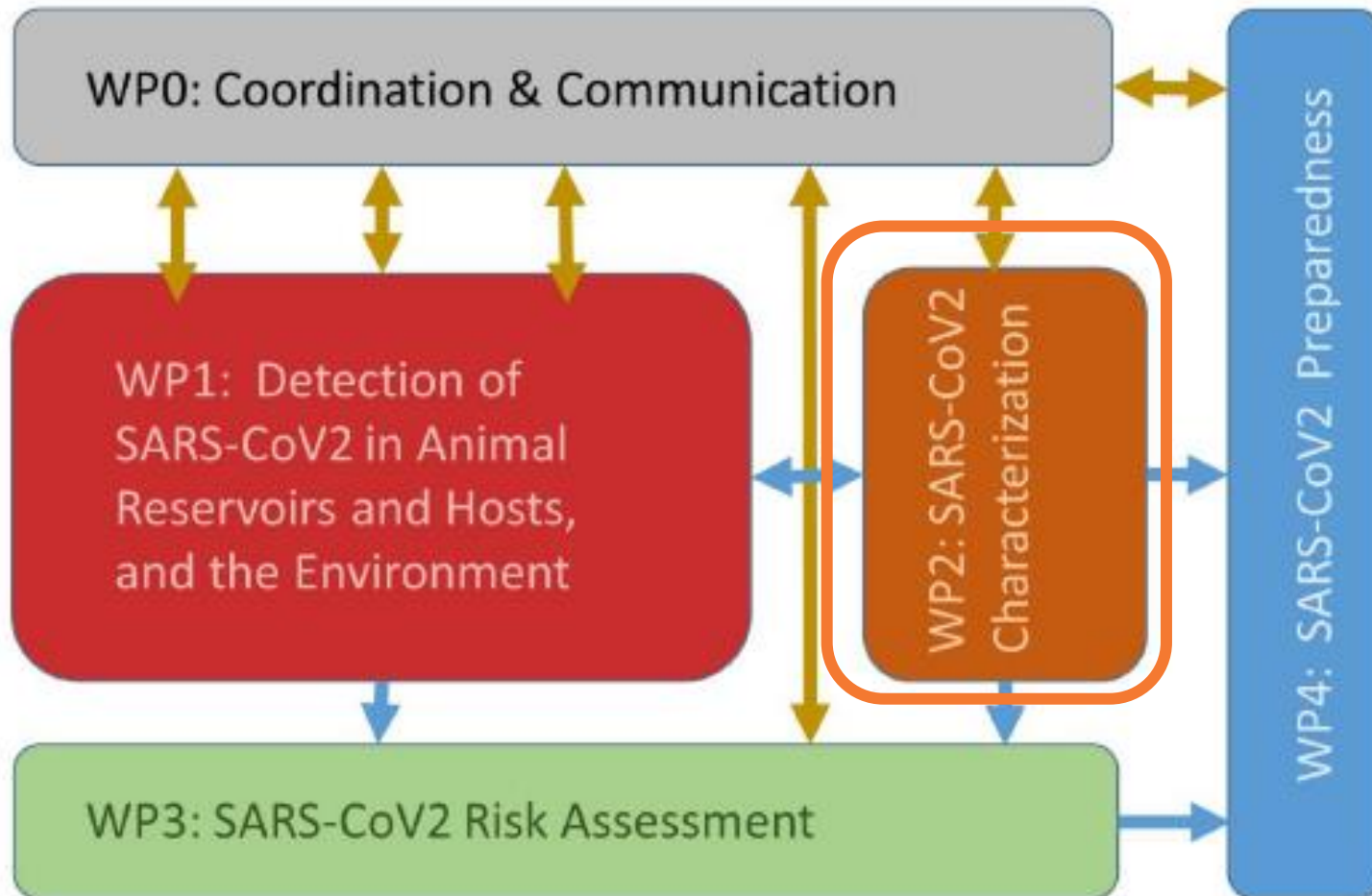
Sharon Brookes – APHA P21

31 March, 2021



WP2: SARS-CoV2 characterisation

SARS-CoV2 Research Integration & Preparedness COVRIN 2.0



- Develop common COVID-19 protocols that support OHEJP collaborations
- Develop common infrastructure for COVID-19 research
- Integrate COVRIN deliverables into the work processes of OHEJP partners
- Reduce overlaps of COVID-19 research within OHEJP
- Develop a common OHEJP structure on Coronavirus preparedness



WP2 Objectives: SARS-CoV2 characterisation

Two main overall operational objectives of COVRIN

- To identify drivers for the emergence and spread of SARS-CoV2
- To generate data and build models for risk assessment of SARS-CoV2

To characterize SARS-CoV-2 variants - mapping of evolutionary changes of SARS-CoV-2 viruses isolated within and across human and different animal species.

To characterise SARS-CoV-2 mutations and recombination events, particularly during adaptation to alternative hosts.

Virus characterization is a key capability that will complement virus surveillance and risk assessment of zoonotic and reverse zoonotic transmission, potential immune evasion and reinfection, and to determine impacts for vaccine development (S-gene) or antiviral medication (RdRp).



WP2 - SARS-CoV2 Characterisation

Sharon Brookes, APHA (P21)

Alessio Lorusso, IZSAM (P28)

• T2.1 Genome analyses

- ST2.1.1 Protocol repository
- ST2.1.2 Harmonisation sampling and methods NGS
- ST2.1.3 Phylogenetic analyses

• T2.2 In vitro and in vivo characterization of SARS-CoV2

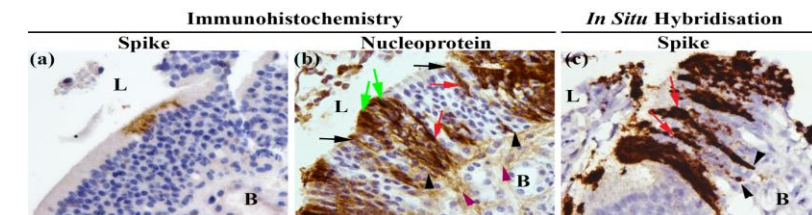
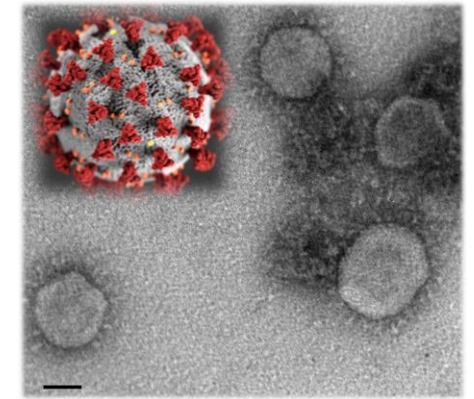
- ST2.2.1 Cell culturing
- ST2.2.2 Antigenicity studies
- ST2.2.3 Complex cultures

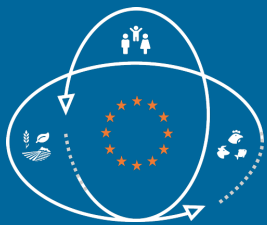
• T2.3 Development and optimization of animal models

- ST2.3.1 Animal models protocols
- ST2.3.2 Pathology toolbox
- ST2.3.4 Establishment of virus-host interaction parameters

• T2.4 Analyses of virus traits related to zoonotic transmission

- ST2.4.1 Variant analyses species jumps
- ST2.4.2 Identification of antigenic site modifications
- ST2.4.3 In vivo studies virus variants





WP2 Tasks / Subtasks and Leads

Add persons from each Partner Institute for delivery

T2.1 Genome analyses

Vitor Borges (INSA)

ST2.1.1 Protocol repository

Maud Contrant (ANSES)

ST2.1.2 Harmonisation sampling and methods NGS

Maud Contrant (ANSES)

ST2.1.3 Phylogenetic analyses

Alessio Lorusso (IZSAM)

T2.2 In vitro and in vivo characterization of SARS-CoV2

Anita Solhaug (NVI)

ST2.2.1 Cell culturing

Anita Solhaug (NVI)

ST2.2.2 antigenicity studies

Daniel Horton (UoS)

ST2.2.3 Complex culture

Stefan Finke (FLI)

T2.3 Development and optimization of animal models

Sharon Brookes (APHA)

ST2.3.1 Animal models protocols

Elodie Monchatre Leroy (ANSES)

ST2.3.2 Pathology toolbox

Fabian Lean (APHA)

ST2.3.4 Establishment of virus-host interaction parameters

Maria Dahle (NVI)

T2.4 Analyses of virus traits related to zoonotic transmission

Barbara Holzer (Ages)

ST2.4.1 Variant analyses species jumps

Paul Brown (ANSES)

ST2.4.2 Identification of antigenic site modifications

Unni Grimholt (NVI)

ST2.4.3 In vivo studies virus variants

Joe James (APHA)

(P21) APHA – Tony Fooks, Falko Steinbach
Lorraine McElhinney, Joe James, Alex Byrne



Task 2.1 - Genome analyses

Lead: INSA (P36) (Vitor Borges)

Participants: ANSES (P1), FLI (P10), APHA (P21), ISS (27), IZSAM (P28), IZSLER (P29), WBVR (P31), NVI (P33), PIWET (P34), INIAV (P35), SVA (P41)

Whole genome sequences by NGS (various methods) of SARS-CoV-2 strains from humans and animals.

a) Methodologies exchange and harmonisation

Archival samples of wild and domestic animals will be used for CoV RNA detection and NGS.

b) Sample type (clinical – field or experimental / isolate) and extraction protocols plus validation,

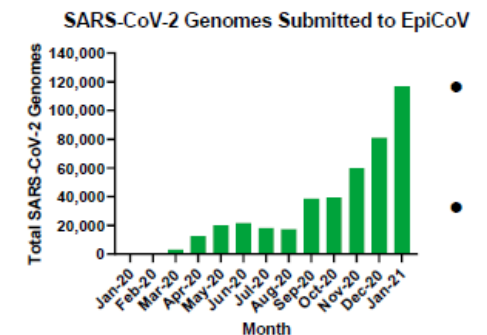
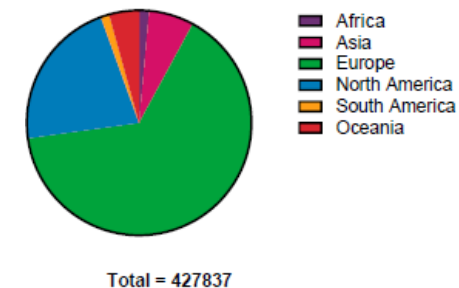
Phylogenetic analysis and investigation for potential virulence traits will be performed.

c) Nucleic acid comparisons – both consensus and minor variant analyses.

d) Phylogenetic relationships among human and animal strains.

e) Amino acid analyses – receptor binding sites, antigenic sites etc

Selected strains may be also used for downstream biological characterization (T2.2 & 2.3).



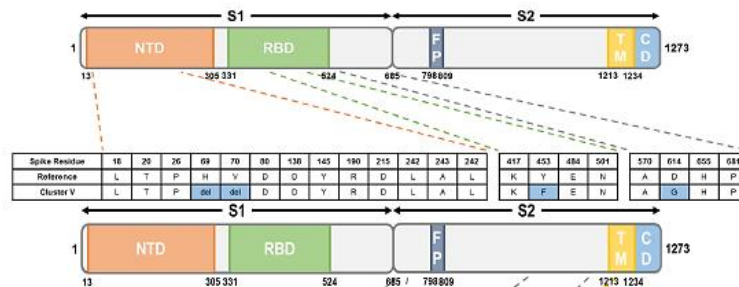
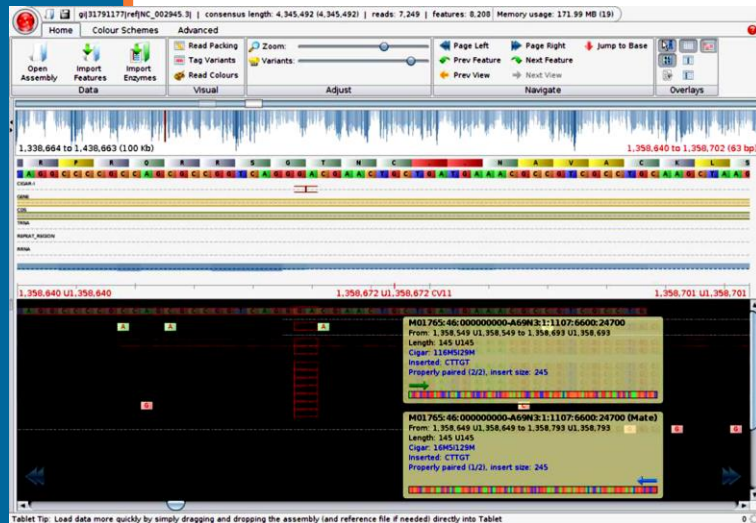
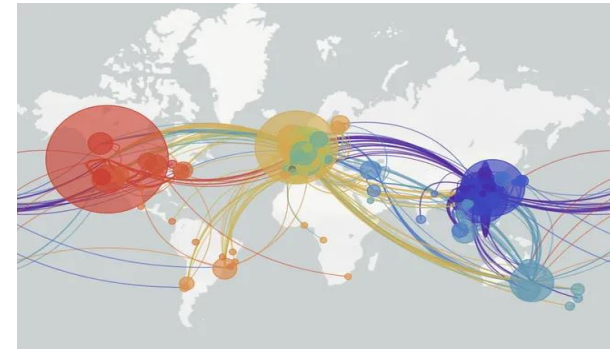
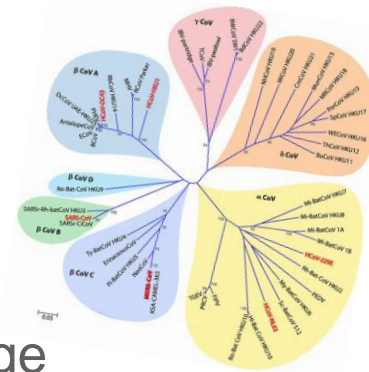


Task 2.1 Deliverables

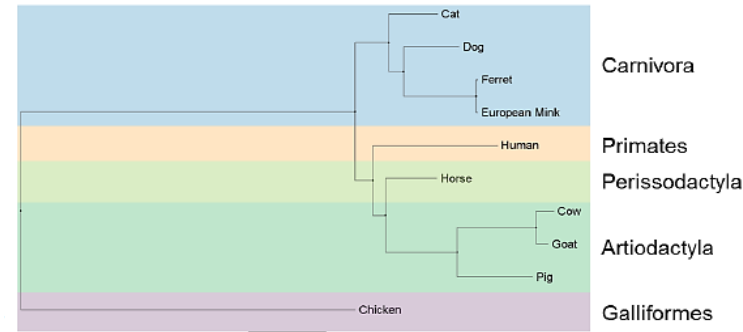
D2.1.1 Report on the established website protocol repository.

D2.1.2 Report on the comparisons of variants and reference sample exchange

D2.1.3 Report on the development of an algorithm for novel virus assessment.



Spike Residue	692	701	716	982	1027	1118	1229
Reference	I	A	T	S	T	D	M
Cluster V	V	A	T	S	T	D	I



ACE2	19	24	27	28	30	31	34	36	37	38	41	42	45	79	82	83	326	329	330	363	364	365	367	383
Human	S	Q	T	F	D	K	H	E	E	D	Y	Q	L	L	M	Y	Q	E	N	K	G	D	R	R
Mink	S	L	T	F	E	K	Y	E	E	E	Y	Q	L	N	T	Y	E	Q	N	K	R	D	R	R
Ferret	S	L	T	F	E	K	Y	E	E	E	Y	Q	L	N	T	Y	E	Q	N	K	R	D	R	R
Dog	S	L	T	F	E	K	Y	E	E	E	Y	Q	L	L	T	Y	Q	E	N	K	G	D	R	R
Cat	S	L	T	F	E	K	H	E	E	E	Y	Q	L	L	T	Y	Q	E	N	K	G	D	R	R
Cow	S	Q	T	F	E	K	H	E	E	D	Y	Q	L	N	T	Y	Q	D	N	K	G	D	R	R
Goat	S	Q	T	F	E	K	H	E	E	D	Y	Q	L	N	T	Y	Q	N	N	K	G	D	R	R
Pig	S	L	T	F	E	K	L	E	E	D	Y	Q	L	L	T	Y	Q	N	N	K	G	D	R	R
Chicken	D	-	T	F	A	E	V	R	E	D	Y	E	L	S	R	F	E	T	N	K	R	D	R	R
Horse	S	L	T	F	E	K	S	E	E	E	H	Q	L	L	T	Y	Q	E	N	K	G	D	R	R

Alex Byrne, APHA



Task 2.2 In vitro and ex vivo biological characterisation

Lead: NVI (P33) (Anita Solhaug)

Participants: FLI (P10), APHA (P21), IZSAM (P28), WBVR (P31)

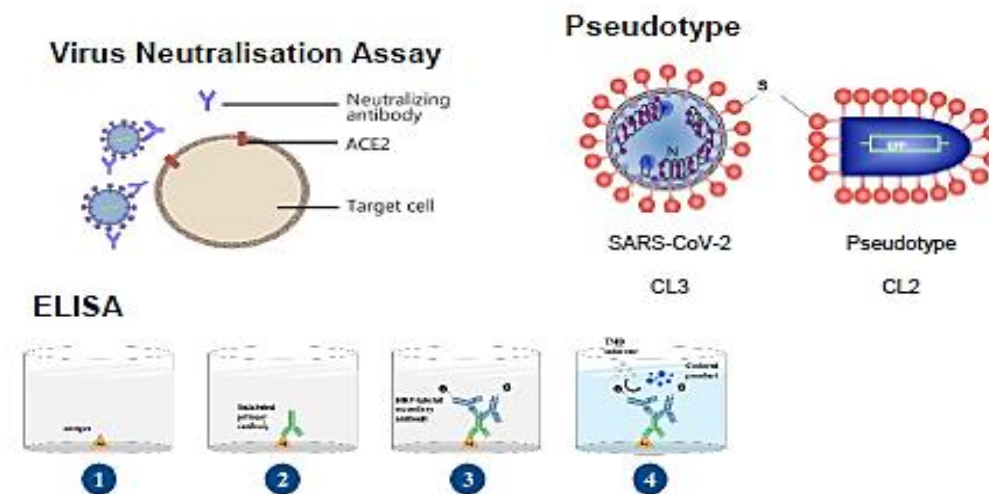
Assessment of in vitro systems for characterization of SARS-CoV-2 strains.

Including live virus (infectious) recovery sensitivity and species specificity.

- a) Cell lines of species origin,
- b) Virus Neutralisation Assays optimisation – wild type and pseudotypes

Ex vivo explants and air-liquid interphase cultures of several animal species will be infected with SARS-CoV-2.

- c) Ex vivo organ cultures,
 - d) Air liquid interface
- Viruses replicating in these systems will be characterized with respect to genome analysis, viral growth and host responses





Task 2.2 Deliverables

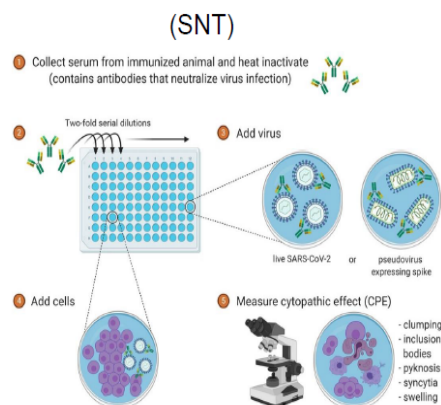
D2.2.1 Report on cell line sensitivities – species and virus growth characteristics.

D2.2.2 Report on assessment of VNA techniques and comparison with ELISA

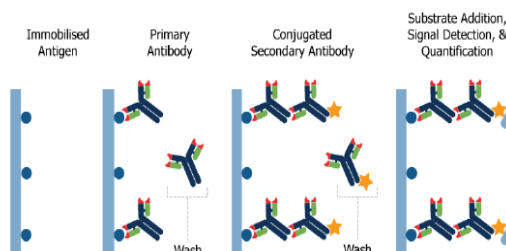
D2.2.3 Report on complex culture viral characterisation.



Virus Neutralisation Assay (VNA)

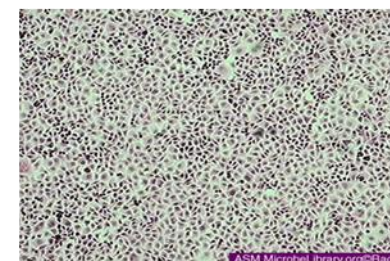


Enzyme-Linked Immunosorbent Assay (ELISA)

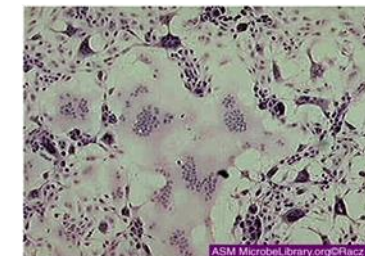


Delahay et al., "Assessing the Risks of SARS-CoV-2 in Wildlife"
<https://www.preprints.org/manuscript/202012.0283/v3>

- 179 Human sera and 260 cats and dog sera tested for validation.



Uninfected cells



Infected cells (CPE)



Task 2.3 - Development, optimization and harmonization of animal models for SARS-CoV2 characterization

Lead: APHA (P21) (Sharon Brookes)

Participants: ANSES (P1), FLI (P10), IZSAM (P28), WBVR (P31), NVI (P33)

Animal models; species type for veterinary health and animal models for human disease including zoonoses.

- a) Exchange of protocols and experimental designs (infection, transmission, therapeutic intervention etc)
- b) Explore and share pathology parameters (virus, receptors etc).
- c) Undertake host response and cellular biomarkers analyses – innate and adaptive (humoral and cellular).



WVP

Covid 19 in farmed mink, Netherlands

Research objectives

- Spread of the infection in the minks
- Spread of the infection in the farms and between the farms
- Viruscontamination in the farms and the environment (exposure assessment)
- Association between the infections in the mink and infections in humans
- Association between the infections in the mink and other animals, in particular stray cats.





Task 2.3 Deliverables

D2.3.1 Catalogue of animal models in use, pros and cons, and designed protocol sharing and harmonisation.

D2.3.2 Report on pathology per species and investigative toolboxes.

D2.3.3 Report on virus-host interaction parameters across susceptible species.

- Review the literature and perform *in silico* analysis for susceptible host species range.
- Use *in vitro* assessments of susceptibility.
- Aim to bridge knowledge gaps relevant to reverse-zoonotic reservoir risk.

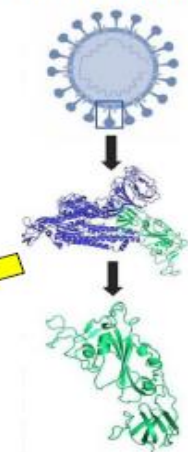
In silico analysis



RISK ASSESSMENT



Functional analysis



HUMAN VS FERRET CLINICAL SIGNS AND SYMPTOMS OF INFECTION

HUMANS

FERRETS



Fever



Anorexia



Weight loss



Sneezing



Nasal Discharge



Lethargy





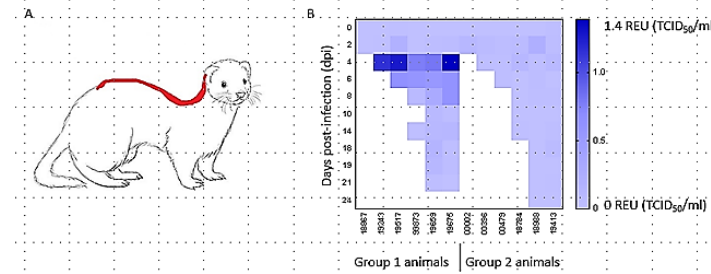
Task 2.4 Analyses of virus traits related to zoonotic and/or reverse zoonotic transmission

Lead: AGES (P2) (Barbara Holzer)

Participants: ANSES (P1), FLI (P10), APHA (P21), UoS (P23), IZSAM (P28), WBVR (P31), NVI (P33)

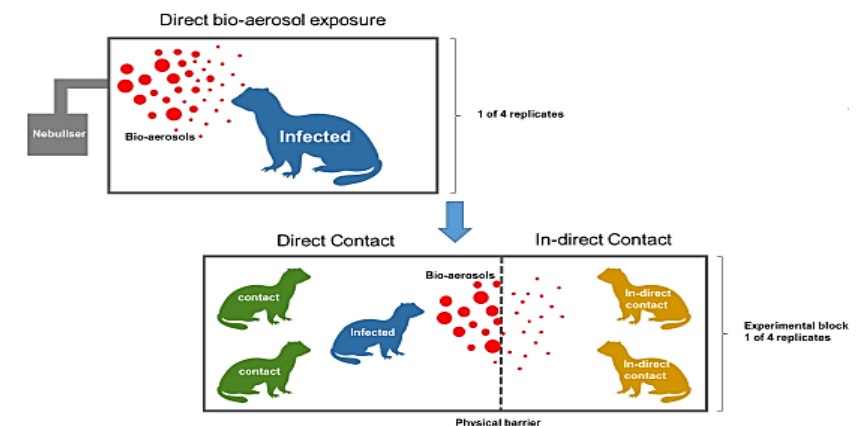
Outcomes and materials from this and other WPs will allow:

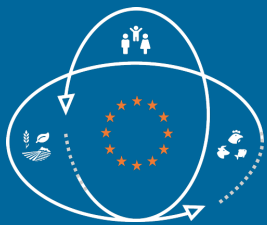
- Variant analyses on host species change progeny viruses
- Host cell ACE2 receptor virus interaction analyses.
- Antigenic site modifications determination including cartography.
- A variant virus in vivo investigation.



Everett HE, *Viruses*. 2021 Jan 15;13(1):113. doi: 10.3390/v13010113. PMID: 33467732; PMCID: PMC7830262.

Investigate bio-aerosol infection parameters and zoonotic and reverse-zoonotic transmission using ferret infection models.





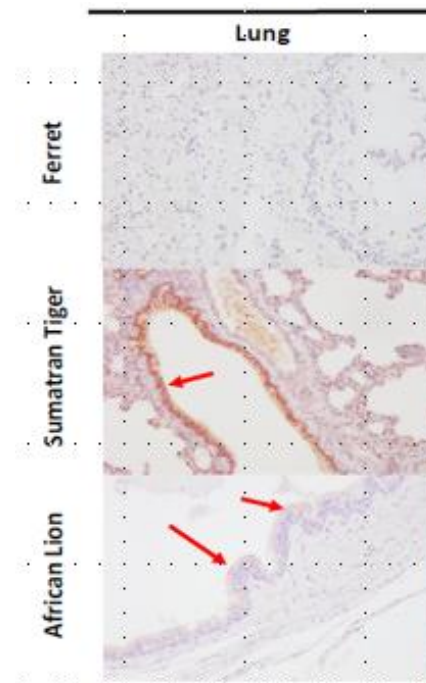
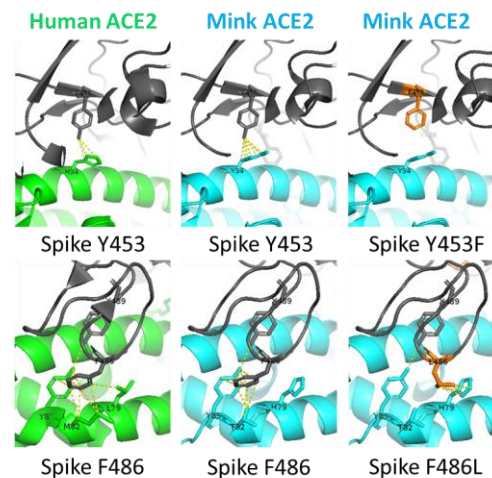
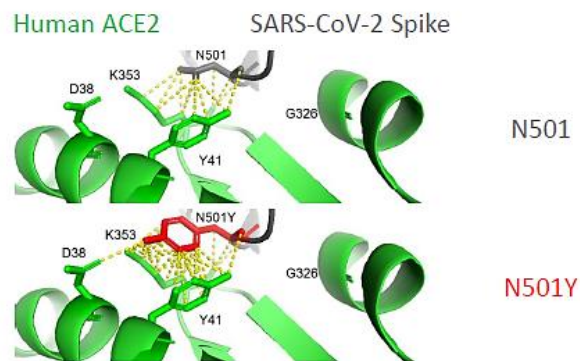
Task 2.4 Deliverables

D2.4.1 Collated partner outcomes of virus trait change as a result of species change including cell receptor affinity.

D2.4.2 Report on in silico and antigenic cartography analysis of antigenic site adaptation traits.

D2.4.3 Undertake and report on a virus variant in vivo follow-up study.

		SARS-CoV-2 Spike Protein																			
		417				453				484				501							
		K417		K417T		K417N		Y453		Y453F		E484		E484K		N501		N501Y			
ACE2 Protein	Human	D30	H34	D30	H34	D30	H34	H34	H34	K31	E35	K31	E35	Y41	D38	G326	K353	Y41	D38	G326	K353
	Mink	E30	Y34	E30	Y34	E30	Y34	Y34	Y34	K31	E35	K31	E35	Y41	E38	G326	K353	Y41	E38	G326	K353
	Ferret	E30	Y34	E30	Y34	E30	Y34	Y34	Y34	K31	E35	K31	E35	Y41	E38	G326	K353	Y41	E38	G326	K353
	Dog	E30	Y34	E30	Y34	E30	Y34	Y34	Y34	K31	E35	K31	E35	Y41	E30	E326	K353	Y41	E38	E326	K353
	Cat	D30	H34	D30	H34	D30	H34	H34	H34	K31	E35	K31	E35	Y41	D30	G326	K353	Y41	E38	G326	K353
	Pig	E30	L34	E30	L34	E30	L34	L34	L34	K31	E35	K31	E35	Y41	D30	G326	K353	Y41	D38	G326	K353
	Horse	E30	S34	E30	S34	E30	S34	S34	S34	K31	E35	K31	E35	H41	E38	G326	H41	E38	G326	K353	
	Mouse	N30	Q34	N30	Q34	N30	Q34	Q34	Q34	N31	E35	N31	E35	Y41	D30	G326	H353	Y41	D38	G326	H353
	Rat	N30	Q34	N30	Q34	N30	Q34	Q34	Q34	K31	E35	K31	E35	Y41	D38	G326	H353	Y41	D38	G326	H353
	Chicken	A30	V34	A30	V34	A30	V34	V34	V34	K31	R35	K31	R35	Y41	D30	G326	K353	Y41	D38	G326	K353





Deliverable time lines

Task	2021				2022				2023	
	37-39	40-42	43-45	46-48	49-51	52-54	55-57	58-60	61-63	64-66
T 2.1			D2.1.1	D2.1.2		D2.1.3				
T 2.2				D2.2.1	D2.2.2		D2.2.3			
T2.3			D2.3.1		D2.3.2			D2.3.3		
T2.4						D2.4.1	D2.4.2			D2.4.3

Deliverables

- WP deliverable reports
- Reporting Year Annual Reports: 1st Jan to 31st Dec.
- Annual Scientific Meeting – 2021, 2022, 2023
- Partner(s) peer-review publications
- OHEJP and Partner blogs

Other collaborative funding opportunities:

- Horizon Europe or International partner country grants



Main Challenges:

- variable COVID restrictions in partner countries
- virtual / live networking
- other disease outbreaks e.g. AIV, ASFV etc

Draw backs:

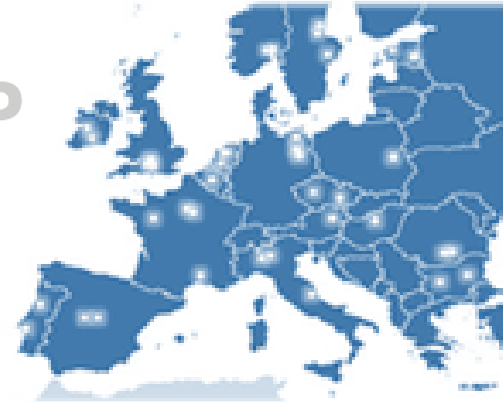
- Two years, reduced budgets (STM)
- Additional partners – one year



Stakeholders & Connections

OH-EJP

In country partner support



World Organisation for Animal Health



International Veterinary Vaccinology Network



STAR-IDAZ International Research Consortium on Animal Health



BSL4ZNet



#APHascience



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company/aphagovuk

Thank you for your attention!



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COVRIN

CoronaVirus Research Integration

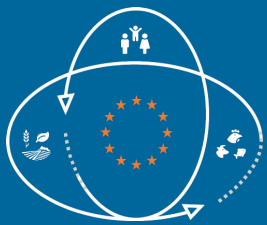
WP3 - SARS-CoV2 Risk assessment and surveillance

Joaquin Prada
Mirjam Kretzschmar



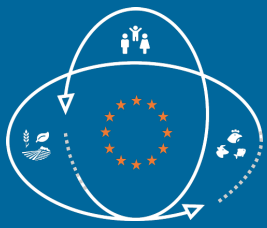
WP3 Objectives

- Main goal
 - 1) Integration of data into an aligned One-Health surveillance system for SARS-CoV-2.
 - 2) This aligned surveillance will be combined with WP1/WP2 outputs to inform risk assessment.
- Outcomes of WP3 will provide evidence for decision-makers and other stakeholders to understand risk from a OH perspective.



WP3 Tasks

- Tasks
 1. T3.1 Integration of surveillance activities
 2. T3.2 Mapping of surveillance data
 3. T3.3 Risk factors for virus transmission
 4. T3.4 Models for transmission routes and risk assessment (in a OH perspective)



WP3 Workplan

	Project Months									
	2021		2022						2023	
	M37-39	M40-42	M43-45	M46-48	M49-51	M52-54	M55-57	M58-60	M61-63	M64-66
WP3, Risk Assessment&Surveillance										
T3.1 Integration of surveillance activities		D3.3.1								
ST3.1.1 Design format/procedure for surveillance data		D3.3.1								
ST3.1.2 Collection of surveillance data						D3.3.2				
ST3.1.3 Identification additional sources of surveillance data							D3.3.3			
T3.2 Mapping of surveillance data		D3.2.1								
ST3.2.1 Evaluation of current surveillance activities				D3.2.1						
ST3.2.2 Identification of key stakeholders									D3.2.2	
T3.3 Identification of risk factors for virus transmission		D3.3.1								
ST3.3.1 Analyses of transmission in pets						D3.3.1				
ST3.3.2 Study of epidemiology and risk factors in pets									D3.3.2	
T3.4 Models for transmission routes and risk assessment		D3.4.1								
ST3.4.1 Listing of existing models			D3.4.1							
ST3.4.2 Reviewing transmission parameters						D3.4.2				
ST3.4.3 Listing of susceptible hosts and relative risks								D3.4.3		
ST3.4.4 Reviewing of challenge experiments										D3.4.4
ST3.4.5 Description of transmission characteristics in mink					D3.4.5					



WP3 Deliverables

1.T3.1 Integration of surveillance activities

D.3.1.1. Report on the format and procedure for data integration.

D.3.1.2. Database on sampling on wildlife, food producing animals, pets, and the environment.

D.3.1.3. Report on data sources and possibilities of integration into a common framework.

1.T3.2 Mapping of surveillance data

2.T3.3 Risk factors for virus transmission

3.T3.4 Models for transmission routes and risk assessment (in a OH perspective)



WP3 Deliverables

- 1.T3.1 Integration of surveillance activities
- 2.T3.2 Mapping of surveillance data
 - 1.D.3.2.1. Review of surveillance activities carried out by member countries.
 - 2.D.3.2.2. Report on key stakeholders across member countries and opportunities for alignment of One Health surveillance activities.
- 3.T3.3 Risk factors for virus transmission
- 4.T3.4 Models for transmission routes and risk assessment (in a OH perspective)



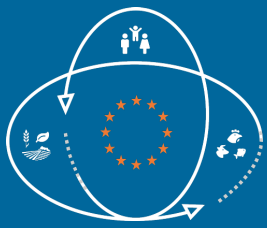
WP3 Deliverables

- 1.T3.1 Integration of surveillance activities
- 2.T3.2 Mapping of surveillance data
- 3.T3.3 Risk factors for virus transmission
 - 1.D.3.3.1. Report on epidemiological survey design and clinical data (including anamnesis and lab results).
 - 2.D.3.3.2. Report on the epidemiological survey results and risk factor assessment for pet-human SARS-Cov-2 transmission.
- 4.T3.4 Models for transmission routes and risk assessment (in a OH perspective)



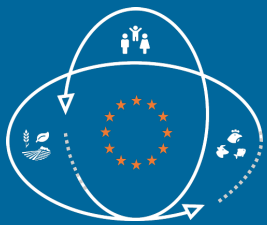
WP3 Deliverables

- 1.T3.1 Integration of surveillance activities
- 2.T3.2 Mapping of surveillance data
- 3.T3.3 Risk factors for virus transmission
- 4.T3.4 Models for transmission routes and risk assessment (in a OH perspective)
 - 1.D.3.4.1 List of existing models and required parameters that need quantification.
 - 2.D.3.4.2 Systematic review report and quantification of transmission parameters for different animal species.
 - 3.D.3.4.3 List of susceptible hosts and relative risk ranking of susceptibility.
 - 4.D.3.4.4 Report on the review of challenge experiments across different host species.
 - 5.D3.4.5 Report describing the transmission characteristics of the mink outbreaks for the countries where data was available.



WP3 Team

- Lead: Joaquin Prada (UoS)
- Deputy: Mirjam Kretzschmar (RIVM)
- Task Leads:
 1. T3.1 Integration of surveillance activities: Cecilia Mia Wolff (NVI)
 2. T3.2 Mapping of surveillance data: Joaquin Prada (UoS)
 3. T3.3 Risk factors for virus transmission: Irene Iglesias (INIA)
 4. T3.4 Models for transmission routes and risk assessment (in a OH perspective): Jose Gonzalez (WBVR)
- 1. Sub-Task leads: ST3.1.2 Franz Conrath (FLI)
 - ST3.1.3 and ST3.2.2 Lapo Mughini Gras (RIVM)
 - Other partner institutes: ANSES, Ages, Sciensano, VRI, UCM, APHA, ISS, IZZSAM, IZSLER, PIWET, INIAV, SVA



WP3 Stakeholder and collaborations

The tripartite



European authorities



Overlap with past/ongoing OHEJP projects such as MATRIX and ORION





WP3 Challenges and Opportunities

- Challenges
 - Short project
 - Ensure fluid communication (and stakeholder engagement)
 - Quick turnover for some deliverables
- Opportunities
 - Existing links to other projects (i.e. with MATRIX)
 - Teams in place with multidisciplinary expertise

Thank you for your attention!



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COVRIN - CoronaVirus Research Integration

WP4 – Coronavirus preparedness



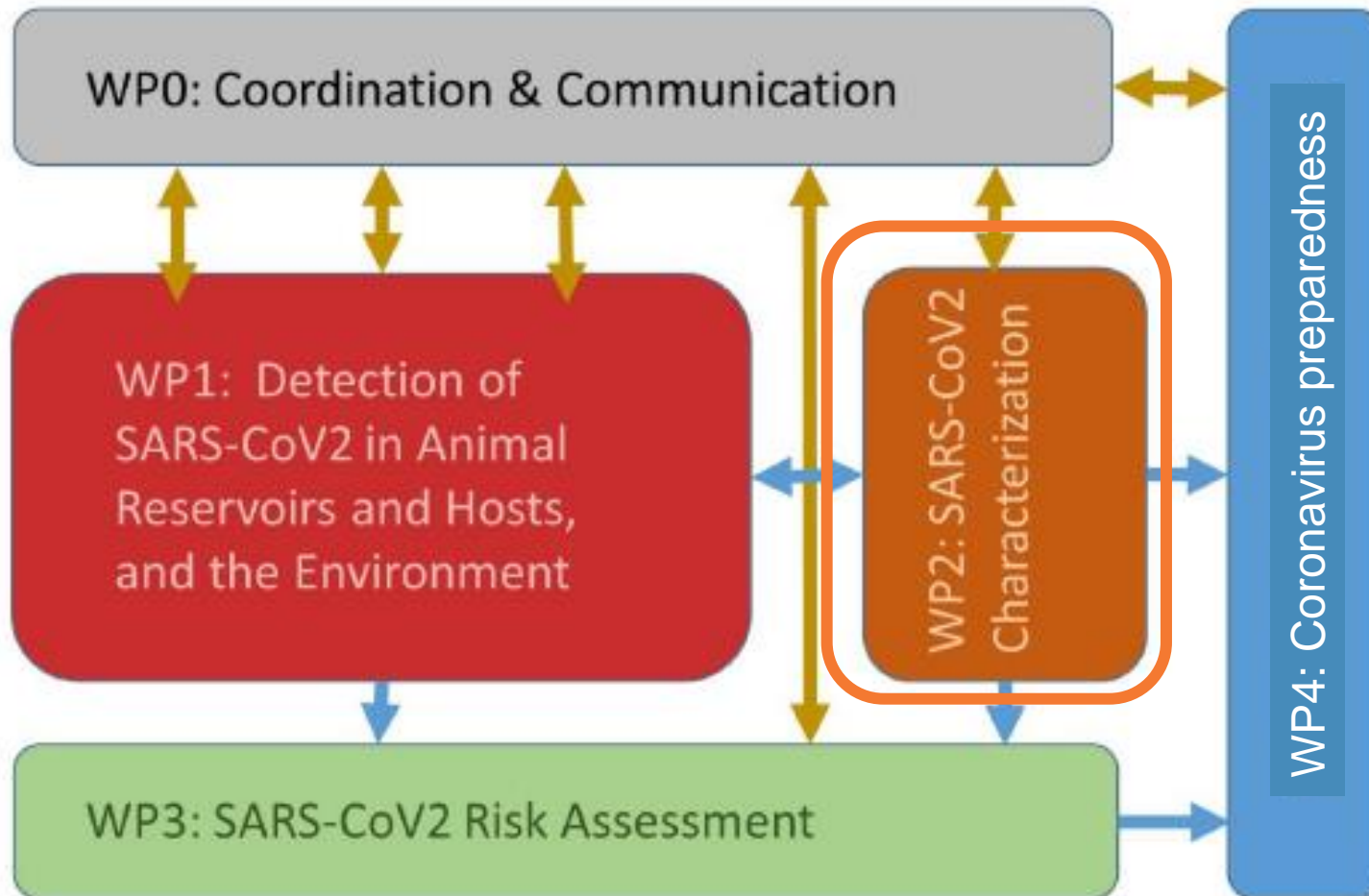
Nicolas Eterradosi – Anses P1
Wim van der Poel – WBVR P31

March, 2021



WP4: Coronavirus preparedness

SARS-CoV2 Research Integration & Preparedness COVRIN 2.0



- Develop common COVID-19 protocols that support OHEJP collaborations
- Develop common infrastructure for COVID-19 research
- Integrate COVRIN deliverables into the work processes of OHEJP partners
- Reduce overlaps of COVID-19 research within OHEJP
- Develop a common OHEJP structure on Coronavirus preparedness



WP4 Objectives: Coronavirus preparedness

- i) to enhance preparedness for future novel coronavirus emergence from animal populations,
 - ii) to understand the drivers for such emergence
 - iii) to integrate results from the different WPs and modelize the risk of coronavirus emergence in different virus host interaction situations
- Study virus host interactions of non-Sars-Cov-2 coronaviruses to better understand which determinants are critical for infection of humans or susceptible animal species, (*Felidae*, *Mustelidae*, *Cricetidae* etc...)
 - Investigate under natural and experimental conditions the adaptive potential of relevant animal CoVs, and identify possible molecular mechanisms of evolution and host adaptation
 - Analyze the phylodynamics of coronaviruses to assess which ones have the greatest potential for cross-species interactions, to identify early zoonotic and reverse zoonotic adaptations and to highlight ecological opportunities and human practices that have a direct impact on coronaviruses evolution
 - Integrate the results to model coronavirus emergence risks in different virus-host interaction situations.



WP4 – Coronavirus preparedness

Nicolas Eterradossi, Anses (P1)

Wim van der Poel, WBVR (P31)

- **T4.1 Virus host interactions**
 - ST4.1.1 *In vivo* and *in vitro* studies
 - ST4.1.2 *In vitro* and *ex vivo* studies
 - ST4.1.3 Virus isolation from wildlife (i.e. hedgehogs)
- **T4.2 Drivers of virus emergence**
 - ST4.2.1 Global time and geographical scales phylodynamics
 - ST4.2.2 Trace relevant virus mutations and recombinations
 - ST4.2.3 Evaluate the impact of ecological factors and human interventions
- **T4.3 Virus emergence risk modelling**
 - ST4.3.1 Follow coronavirus contamination in bats
 - ST4.3.2 Follow coronavirus contamination in cats
 - ST4.3.3 Follow coronavirus contamination in wildlife (hedgehogs)
 - ST4.3.4 Risk assessment and modelling



WP4 Tasks / Subtasks and Leads

T4.1 Virus-Host interactions

ST4.1.1 Perform in vivo and in vitro studies

ST4.1.2 Perform in vitro and ex vivo studies

ST4.1.3 Isolate virus from wildlife (hedgehogs)

Paul Brown (ANSES); Marcin Smreczak (PIWET)

Paul Brown (ANSES)

Falko Steinbach (APHA)

Elodie Monchatre-Leroy (ANSES)

T4.2 Drivers of virus emergence

ST4.2.1 Global time and geographical scale phylodynamics

ST4.2.2 Trace relevant virus mutations and recombinations

ST4.2.3 Evaluate the impact of ecological factors and human interventions

Wim van der Poel (WBVR); Paul Brown (ANSES)

Paul Brown (ANSES)

Maud Contrant (ANSES)

Wim van der Poel (WBVR)

T4.3 Virus emergence risk modelling

ST4.3.1 Follow coronavirus contamination in bats (colony)

ST4.3.2 Follow coronavirus contamination in cats (breeding center)

ST4.3.3 Follow coronavirus contamination in wildlife (hedgehog shelter)

ST4.3.4 Risk assessment and modelling

Alessio Lorusso (IZSAM); Elodie Monchatre-Leroy (ANSES)

Marcin Smreczak (PIWET)

Sophie Le Poder (ANSES)

Davide Lelli (IZSLER)

Matthias Filter (BfR)



Task 4.1 – Virus-host interactions

Lead: Anses (P1) (Paul BROWN), Co-lead : PIWET (P34) (Marcin SMRECZAK)

Participants: ANSES (P1), VRI (P8), FLI (P10), APHA (P21), ISS (27), IZSAM (P28), IZSLER (P29), WBVR (P31), PIWET (P34)

Experimental infections under controlled conditions *in vivo*, *in vitro* and *ex-vivo*, using different coronaviruses from domestic and wild animals, to assess the evolutionary and adaptative potential of animal coronaviruses.

- a) Animal coronaviruses will be passaged *in vitro* and *in vivo* (Paul Brown, Anses) or *in vitro* and *ex-vivo* (F. Steinbach, APHA), in their homologous host or in alternate animal hosts, cells or tissues.
 - Genetic changes in virus populations (consensus and minor variants) associated with propagation in heterologous hosts will be determined by NGS.
- b) Experimental co-infections will be performed *in vitro* or *ex-vivo* and the genetic make-up of viral progeny will be investigated by deep sequencing
 - Frequency and possible strain specificity of recombination events will be reported
- c) Isolation of hedgehog coronavirus will be attempted and zoonotic potential of possible isolates will be assessed experimentally using animal models of Covid19 (Hamster / ferrets)
 - Zoonotic potential of hedgehog betacoronavirus will be precised

DELIVERABLES : Reports on animal experiments / full length genomes of viruses from a, b and c.



Task 4.2 – Drivers of virus emergence

Lead: WVBR (P31) (Wim VAN DER POEL); Co-Lead: Anses (P1) (Paul BROWN)

Participants: ANSES (P1), FLI (P10), APHA (P21), ISS (27), IZSLER (P29), WBVR (P31), PIWET (P34), INIAV (P35) + Associated partner (own budget) : CHU Caen, FR

Improve our understanding of factors affecting coronavirus genetic diversity and evolution in domestic animals and wildlife,

- a) Global time and geographical phylodynamics of animal coronaviruses
 - ➔ Phylogenetic relationships between coronaviruses will be analyzed between animal species, and within one coronavirus species in different breeding facilities or operations
- b) Detect relevant mutations and recombination events
 - ➔ Insights into genetic variation under “natural” conditions (as compared with 4.1.a and 4.1.b)
- c) Investigate how the observed genetic changes may correlate with ecological factors (species interactions, habitat...) and human interventions (vaccination, trading of animals), and how factors may impact on coronavirus evolution (evolution rates, composition of recombinants, possible contribution of vaccine viruses).
 - ➔ Role of ecological factors and human interventions

DELIVERABLES : Report on most relevant sample types and populations (metanalysis) / Harmonized methods for detection – metagenomics – Phylogenetics / Report on correlation between CoV evolution and environment (ecological factors – human interventions)



Task 4.3 – Virus emergence risk modelling

Lead IZSAM (P28) (Alessio LORUSSO), Co-lead : Anses (P1) (Elodie MONCHATRE-LEROY)

Participants: ANSES (P1), BfR (P9), FLI (P10), APHA (P21), ISS (27), IZSAM (P28), IZSLER (P29), WBVR (P31), PIWET (P34)

Specific animal communities will be followed over a predefined period of time (RT-PCR, NGS) to monitor intra-community CoV genetic variation. Data from other WPs and other WP4 tasks will be used to assess the potential of CoV genetic variation on future emergences (for animal species and humans).

- a) High frequency sampling of bat colonies in natura, and of cats in domestic environment.
 - Longitudinal study of genetic variation under ‘natural’ conditions (to be compared with 4.1 ad 4.2).
- b) Monthly fecal sampling of cats and kittens under breeding farm conditions
 - Impact of human interventions (link with 4.2.c)
- c) Frequent sampling of animals hosted for prolonged periods in wildlife shelters (incl. hedgehogs)
 - Impact of modified interactions on the evolution of wildlife coronaviruses (link with 4.2.c)
- d) Integrating data from WPs 1, 2, 3 and WP4 tasks to model which animal species / conditions offer the highest potential for future emergences.

DELIVERABLES : Reports on best techniques for long term community monitoring
Reports on coronavirus contamination in studied communities
Report on relevance of the studied animal models in assessing the risk for CoV emergence



Stakeholders & Connections

Cf. Sharon's slide

+

PREventing ZOonotic Diseases Emergence, PREZODE

Thank you for your attention!



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