WOAH Collaborative Centre Reports Activities 2023

Activities in 2023

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Centre Information

Title of WOAH Collaborating Centre	Detection and identification in Humans of emerging Animal Pathogens and Develoment of Tools for their Diagnoses			
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Name Director of Institute (Responsible Official):	Yasmin BELKAID			
Name (including Title and Position) of Head of the Collaborating Centre (WOAH Contact Point):	Dr Jean-Claude MANUGUERRA DVM, PhD, HDR - Research director - Head of the 'Environment and infectious risks" and of the Laboratory for urgente response to biological threats - Deputy head of the French National reference centre for hantaviruses			
Name of the writer:	Jean-Claude MANUGUERRA			

TOR1 AND 2: SERVICES PROVIDED

1. Activities as a centre of research, expertise, standardisation and dissemination of techniques within the remit of the mandate given by WOAH

Category	Title of activity	Scope
Training, capacity building (true)	1/ Regional Workshop on Multidisciplinary field outbreak investigation" 2/ Workshop «Metagenomic Technologies» for the MediLabSecure Network 3/ Training on serosurveillance of emerging viruses in wildlife avifauna	1/ A workshop on Mobile laboratories and field diagnostic was organized in Tunis in September 2023 in the framework of the MediLabSecure project. This workshop included human virologists (4) and medical entomologist (4) from 3 countries of North Africa (Tunisia, Libya, and Algeria). The workshop was dedicated to the detection and surveillance of WNV using point-of-Care diagnostic tools and NGS sequencing. 2/Two workshops on "Metagenomic Technologies " were held at Institut Pasteur in Paris in April and May 2023. The objective was to train scientists on sequencing and data analysis using metagenomic approaches. These workshops included 22 participants from animal virology (10), human virology (10) and medical entomology (2) sectors from 16 countries belonging to MediLabSecure network. 3/ A 2-week training course on the serological screening of sentinel wild bird populations using MMIA (Multiplex Microspherebased immune-assay) was provided to the Institut Pasteur of French Guiana.
		Orthoebolavirus in porcine populations of Guinea -

Zoonoses (true)

1/ Sero-surveys and molecular screening of zoonoses at the human-animal interface

Pigs are naturally susceptible to Reston virus and experimentally to Ebola virus (EBOV), but their role in Orthoebolavirus ecology remains unknown. We tested 888 serum samples collected from pigs in Guinea during 2017-2019 (between the 2013-16 epidemic and its resurgence in 2021) by indirect ELISA and in house MMIA against EBOV nucleo- and glycoproteins. We identified 2 hotspots of possible pig exposure by IgG titer levels: the northern coast had 48.7% of positive serum samples, and Forest Guinea, bordering Sierra Leone and Liberia, where the virus emerged and reemerged, had 50% of positive serum samples. Those results are consistent with previous observations of the circulation of Orthoebolavirus species in pig farming regions in Sierra Leone and Ghana, suggesting potential risk for Ebola virus disease in humans, especially in Forest Guinea. • Orthopoxviruses in domestic animals and cattle of Guinea - Following 3 sample collection campaigns conducted in 2023, sera from over 300 pigs, 400 dogs, 299 Caprines, 111 ovines and 157 bovines were collected from different regions of Guinea. The biobank was screened using an in-house multiplex immunoassay targeting antibodies against 32 surface proteins of human pathogenic orthopoxviruses, including MonkeyPox virus. The analysis of seroprevalence rates in the different host populations is currently ongoing. • Rift Valley fever virus in wild and domestic animals in Gabon Although the Rift Valley fever virus (RVFV) transmission cycle has been well documented across Africa in savanna ecosystems, little is known about its transmission in tropical rainforest settings, particularly in Central Africa. We therefore conducted a survey in northeastern Gabon to assess RVFV circulation among wild and domestic animals. Among 163 wildlife samples tested using RVFVspecific RT-qPCR, four ruminants belonging to subfamily Cephalophinae were detected positive. The phylogenetic analysis revealed that the four RVFV sequences clustered together with a virus isolated in Namibia within the well-structured Egyptian clade. A cross-sectional survey conducted on sheep, goats and dogs living in villages within the same area determined the IgG RVFV-specific antibody prevalence. Out of the 306 small ruminants, an overall antibody prevalence of 15.4% was observed with a higher rate in goats than in sheep (20.1% versus 3.3%). RVFV-specific antibodies were detected in a single dog out of the 26 tested. Our findings highlight sylvatic circulation of RVFV for the first time in Gabon. • Japanese encephalitis in pigraising communities in Bangladesh - Japanese encephalitis virus (JEV) circulates endemically in Bangladesh and the country is set to introduce JEV vaccine. However, knowing how best to deploy the vaccine has been hampered by an insufficient understanding of key aspects of JEV ecology, including the spatial heterogeneity in risk, and risk factors for infection. We conducted a national seroprevalence study where we visited 110 communities around the country and collected blood from randomly selected individuals (N=2938). The blood was tested for anti-JEV IgG antibodies using a novel in house MMIA test that limits crossreactivity with dengue virus. We found 3.4% of participants had antibodies against JEV, and

estimated that on average 215,000 people get infected each year. Infection risk was greatest around pig-raising communities. This study provides the basis to identify regions in the country where vaccine deployment would be most beneficial and, will allow us to assess the impact of different approaches in terms of health outcomes (infections, cases, deaths, and disability life-years averted) per doses used. • Urban rat-associated zoonotic pathogens The objective was to document the presence and diversity of zoonotic pathogens among urban brown rat populations (Rattus norvegicus) and to determine the rat associated public health risks. Tissue samples from 700 brown rats trapped in seven French cities (2021-2024) in the framework of three scientific projects: ARMAGUEON (Assessment of Rats Management Associated to a Genomics-Urban Ecology-Disease Occurrence Network in Paris; ANR funded), Rat en ville -Eurométropole de Strasbourg (CNR Hantaviruses funded) and RATVAR (Evaluation of the receptivity, susceptibility and transmission potential of the Murinae subfamily to SARS-CoV-2 variants; ANRS-MIE funded), will be tested for infection with bacteria (including Leptospira interrogans, Yersinia spp, Streptobacillus moniliformis, Rickettsia typhi, Borrelia spp.) and viruses (including Hantaviruses (particularly Seoul virus), rat hepatitis E virus, coronaviruses, orthopoxviruses and Lymphocytic choriomeningitis. virus). Work is still in progress. 1/ We developed and evaluated direct shotgun metagenomic and amplicon-based approaches using Nanopore technology for the sequencing of monkeypox virus from clinical specimens. Balière C, Hourdel V. Kwasiborski A. Grassin O. Feher M. Hoinard D. Vanhomwegen J. Tajeb F. Consigny PH. Manuguerra JC, Leclercq I, Batéjat C, Caro V. Complete Genome Sequences of Monkeypox Virus from a French Clinical Sample and the Corresponding Isolated Strain, Obtained Using Nanopore Sequencing. Microbiol Resour Announc. 2023 Apr 18:12(4):e0000923 Kwasiborski A. Hourdel V. Balière C, Hoinard D, Grassin Q, Feher M, De La Porte Des Vaux C, Cresta M, Vanhomwegen J, Manuguerra J-C, Batéjat C, Caro V. Direct metagenomic and amplicon-based Nanopore sequencing of French human monkeypox from clinical specimen. Microbiol Resour Announc, 2024 Jan 17;13(1):e0081123. doi: 10.1128/MRA.00811-23. 2/ We developed and evaluated two assays to quantify neutralizing antibodies (NAbs) in sera from control, 1/ Monkeypox virus Next generation sequencing MPXV-infected, or modified vaccinia Ankara -Diagnosis, biotechnology and laboratory (true) approaches 2/Monkeypox virus Serology 3/ SARSvaccinated individuals. Hubert M, Guivel-Benhassine CoV-2 RT-PCR primer design tool F, Bruel T, Porrot F, Planas D, Vanhomwegen J, Wiedemann A. Burrel S. Marot S. Palich R. Monsel G. Diombera H, Gallien S, Lopez-Zaragoza JL, Vindrios W, Taieb F, Fernandes-Pellerin S, Delhaye M, Laude H, Arowas L, Ungeheuer MN, Hocqueloux L, Pourcher V, Prazuck T, Marcelin AG, Lelièvre JD, Batéjat C, Lévy Y, Manuguerra JC, Schwartz O. Complement-dependent mpox-virus-neutralizing antibodies in infected and vaccinated individuals. Cell Host Microbe. 2023 Jun 14;31(6):937-948.e4. doi: 10.1016/j.chom.2023.05.001. 3/ We developed and evaluated an Innovative AIbased primer design tool for precise and accurate detection of SARS-CoV-2 variants of concern. Perez-

Romero CA, Mendoza-Maldonado L, Tonda A, Coz E,
Tabeling P, Vanhomwegen J, MacSharry J, Szafran J,
Bobadilla-Morales L, Corona-Rivera A, Claassen E,
Garssen J, Kraneveld AD, Lopez-Rincon A. An
Innovative AI-based primer design tool for precise
and accurate detection of SARS-CoV-2 variants of
concern. Sci Rep. 2023 Sep 22;13(1):15782. doi:
10.1038/s41598-023-42348-y.

TOR3: HARMONISATION OF STANDARDS

2. Proposal or development of any procedure that will facilitate harmonisation of international regulations applicable to the main fucus area for which you were designated

Proposal title	Scope/Content	Applicable area	
Heat inactivation of monkeypox virus	Different kinds of media spiked with monkeypox virus (MPXV) were subjected to heat inactivation at different temperatures for various periods of time. The results showed that MPXV was inactivated in less than 5 min at 70 °C and less than 15 min at 60 °C, with no difference between viruses from the West African and Central African clades. The present findings could help laboratory workers to manipulate MPXV in optimal biosafety conditions and improve their protocols.	Laboratory expertise	

3. In exercising your activities, have you identified any regulatory research needs* relevant for WOAH?

Nο

4. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres (CC), Reference Laboratories (RL), or organisations designated for the same specialty, to coordinate scientific and technical studies?

Yes

Name of WOAH CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
Friedrich-Loeffler-Institut,(FLI) Institute of Novel and Emerging Infectious Diseases	Insel RiemserGermany	Europe	FLI and I. Pasteur are 2 core members of the new project for the European Health Emergency Preparedness and Response Authority (HERA): Delivering a Unified Research Alliance of Biomedical and public health Laboratories against Epidemics.

TOR4 AND 5: NETWORKING AND COLLABORATION

5. Did your Collaborating Centre maintain a network with other WOAH Collaborating Centres, Reference laboratories, or organisations in other disciplines, to coordinate scientific and technical studies?

Yes

Name of WOAH CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
WOAH Collaborating Centre for Risk Analysis and Modelling (UK's Animal and Plant Health Agency (APHA) and the Royal Veterinary College)	London, UK	Europe	Contact have been continued to explore opportunities for collaboration to achieve expected deliverables more effectively.

TOR6: EXPERT CONSULTANTS

6. Did your Collaborating Centre place expert consultants at the disposal of WOAH?

Yes

NAME OF EXPERT	KIND OF CONSULTANCY	SUBJECT
1/ Jean-Claude MANUGUERRA 2/ Jean-Claude MANUGUERRA and Jessica VANHOMWEGEN	1/ WOAH ad hoc group: Covid-19 at the animal-human interface 2/ Principal drafters of the WOAH case definition: Crimean-Congo Haemorrhagic Fever	

TOR7: SCIENTIFIC AND TECHNICAL TRAINING

 $7.\ Did\ your\ Collaborating\ Centre\ provide\ advice/services\ to\ requests\ from\ Members\ in\ your\ main\ focus\ area?$

No

8. Did your Collaborating Centre provide scientific and technical training, within the remit of the mandate given by WOAH, to personnel from WOAH Members?

a) Technical visit : 1b) Seminars : 0

c) Hands-on training courses: 1

d) Internships (>1 month): 0

TYPE OF TECHNICAL TRAINING PROVIDED (A, B, C OR D)	CONTENT	COUNTRY OF ORIGIN OF THE EXPERT(S) PROVIDED WITH TRAINING	NO. PARTICIPANTS FROM THE CORRESPONDING COUNTRY
А	Multiplex microsphere-based immuno- French Guiana assay for zoonotic virus serology		3
С	Multiplex microsphere-based immuno- assay for zoonotic virus serology	French Guiana	3

TOR8: SCIENTIFIC MEETINGS

9. Did your Collaborating Centre organise or participate in the organisation of scientific meetings related to your main focus area on behalf of WOAH?

Yes

NATIONAL/INTERNATIONAL	TITLE OF EVENT	CO-ORGANISER	DATE (MM/YY)	LOCATION	NO. PARTICIPANTS
International	Symposium International sur les Maladies Zoonotiques Emergentes et Réémergentes : focus sur les Fièvres Hémorragiques Virales en Afrique (Etiologie- Epidémiologie- Surveillance et Prévention)	WOAH, IRD, CIRAD	2023-10-10	Mbour, Senegal	100

TOR9: DATA AND INFORMATION DISSEMINATION

10. Publication and dissemination of any information within the remit of the mandate given by WOAH that may be useful to Members of WOAH a) Articles published in peer-reviewed journals:

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1: Perez-Romero CA, Mendoza-Maldonado L, Tonda A, Coz E, Tabeling P, Vanhomwegen J, MacSharry J, Szafran J, Bobadilla-Morales L, Corona-Rivera A, Claassen E,

Garssen J, Kraneveld AD, Lopez-Rincon A. An Innovative AI-based primer design tool for precise and accurate detection of SARS-CoV-2 variants of concern. Sci Rep. 2023 Sep 22;13(1):15782. doi: 10.1038/s41598-023-42348-y. PMID: 37737287; PMCID: PMC10516913.

- 2: Tendu A, Kane Y, Li R, Omondi V, Chen Y, Mastriani E, Lan J, Hughes AC, Berthet N, Wong G. Virome characterization and identification of a putative parvovirus and poxvirus in bat ectoparasites of Yunnan Province, China. One Health. 2023 Oct 13;17:100641. doi: 10.1016/j.onehlt.2023.100641. PMID: 38024255; PMCID: PMC10665160.
- 3: Mendiboure V, Teiti I, Aubry M, Teissier A, Paoaafaite T, Vanhomwegen J, Manuguerra JC, Fontanet A, Cao-Lormeau VM, Madec Y. SARS-CoV-2 seroprevalence and associated factors of infection before and after the Delta wave in French Polynesia: a cross-sectional study. BMC Public Health. 2024 Feb 5;24(1):382. doi: 10.1186/s12889-024-17869-4. PMID: 38317107; PMCID: PMC10840228.
- 4: Kane Y, Chen J, Li L, Descorps-Declère S, Wong G, Berthet N. Diverse single-stranded DNA viruses from viral metagenomics on a <i>cynopterus</i> bat in China. Heliyon. 2023 Jul 17;9(8):e18270. doi: 10.1016/j.heliyon.2023.e18270. PMID: 37520955; PMCID: PMC10374907.
- 5: Becquart P, Bohou Kombila L, Mebaley TN, Paupy C, Garcia D, Nesi N, Olive MM, Vanhomwegen J, Boundenga L, Mombo IM, Piro-Mégy C, Fritz M, Lenguiya LH, Ar Gouilh M, Leroy EM, N'Dilimabaka N, Cêtre-Sossah C, Maganga GD. Evidence for circulation of Rift Valley fever virus in wildlife and domestic animals in a forest environment in Gabon, Central Africa. PLoS Negl Trop Dis. 2024 Mar 1;18(3):e0011756. doi: 10.1371/journal.pntd.0011756. PMID: 38427694; PMCID: PMC10936825.
- 6: Kwasiborski A, Hourdel V, Balière C, Hoinard D, Grassin Q, Feher M, De La Porte Des Vaux C, Cresta M, Vanhomwegen J, Manuguerra J-C, Batéjat C, Caro V. Direct metagenomic and amplicon-based Nanopore sequencing of French human monkeypox from clinical specimen. Microbiol Resour Announc. 2024 Jan 17;13(1):e0081123. doi: 10.1128/MRA.00811-23. Epub 2023 Dec 4. PMID: 38047654; PMCID: PMC10793249.
- 7: Balière C, Hourdel V, Kwasiborski A, Grassin Q, Feher M, Hoinard D, Vanhomwegen J, Taieb F, Consigny PH, Manuguerra JC, Leclercq I, Batéjat C, Caro V. Complete Genome Sequences of Monkeypox Virus from a French Clinical Sample and the Corresponding Isolated Strain, Obtained Using Nanopore Sequencing. Microbiol Resour Announc. 2023 Apr 18;12(4):e0000923. doi: 10.1128/mra.00009-23. Epub 2023 Mar 27. PMID: 36971577; PMCID: PMC10112124.

b) International conferences:

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QCMD Board Meeting, Glasgow, February 2023

• The importance of External Quality Assessments in preparedness and response to emerging vector borne diseases: the MediLabSecure experience

Conférence du Conseil Scientifique de l'Institut Pasteur de Tunis, Tunis, Friday 28 April2023

· Faire face aux défis du diagnostic biologique au début de l'émergence de maladies nouvelles ou résurgentes

8th European Congress of Virology 2023, Gdansk, Poland, Friday 5 May 2023

• Innovative diagnostics in virus surveillance

London Calling, Oxford Nanopore Technologies, London (UK), 17-19 May 2023

• Operational strategy for rapid detection and characterization of emergent viral pathogens using third next-generation sequencing technologies

10th European Meeting on Viral Zoonoses, St-Raphael (France), 23-26 September 2023

• Persistence of Mpox virus on various surfaces

Medical Biodefense Conference, Munich, October 2023

• Network for promoting a One Health approach to mitigate biological risks related to emerging vector borne viruses in the Mediterranean, Black Sea & Sahel regions

International Symposium on Emerging and Re-emerging Zoonotic Diseases, Mbour (Sénégal), 9-11 october 2023

- Detecting and differentiating past exposure to zoonotic viruses using microsphere immunoassays: applications in hyperendemic areas
- Operational strategy for rapid detection and characterization of emergent zoonotic viral pathogens using third next-generation sequencing technologies.

28th UN Climate Change Conference (COP28), Dubai, United Arab Emirates, 30 November – 12 December 2023

• The Institut Pasteur, a key player in tomorrow's biomedical research

Meeting to advance research for Zika and arboviruses, Wellcome Trust, London (UK), 4-6 December 2023

· Building laboratory networks: Overview of European arbovirus research networks, initiatives, and biorepositories

c) National conferences:

Microbes, SFM (French Society for Microbiology) annual meeting, Rennes, France, October 2023

- Network for promoting a One Health approach to mitigate biological risks related to emerging vector borne viruses in the Mediterranean, Black Sea & Sahel regions
- d) Other (Provide website address or link to appropriate information):

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11. What have you done in the past year to advance your area of focus, e.g. updated technology? See section 1

12. Additional comments regarding your report: *None*