Activities in 2023

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Centre Information

Title of WOAH Collaborating Centre	WOAH Collaborating Centre for Diseases at the Animal/Human Interface
Address of WOAH Collaborating Centre	VIALE DELL'UNIVERSITA' 10,
Tel.:	049 8084391
E-mail address:	gcattoli@izsvenezie.it
Website:	https://www.izsvenezie.com/reference-laboratories/diseases-at-the-animalhuman-interface/
Name Director of Institute (Responsible Official):	Dr Antonia Ricci, Director General
Name (including Title and Position) of Head of the Collaborating Centre (WOAH Contact Point):	Dr Giovanni Cattoli, Director of Science
Name of the writer:	Dr Giorgia Angeloni

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
Epidemiology, surveillance, risk assessment, (true)	Entomological surveillance for West Nile and Usutu viruses in north-eastern Italy	In 2022, 85 CDC-CO2 mosquito traps were placed over the area and 146,482 mosquitoes of 17 different species were collected. The viral search was done in 2,854 pooled specimens. West Nile virus was detected in 27 pools of Culex pipiens, and in 1 pool of Aedes albopictus. USUTU virus was found in 17 pools of Cx. pipiens and in 1 pool of Aedes albopictus.
Zoonoses (true)	Zoonosis in dog and cat shelters: study and development of an integrated strategy for effective health management	To ensure the correct health and relational management of animals in shelters through training and communication actions, dogs and cats in shelters were screened for Influenza virus type A, Norovirus, Rotavirus, Cowpox virus, Reovirus, Hepatitis E virus, Dermatophytosis, C. canimorsus, intestinal parasites, antibiotic-resistant bacteria, Bartonella henselae, Leishmania, Leptospira, Brucella canis and SARS-CoV-2.
Diagnosis, biotechnology and laboratory (true)	Detection of Trichinella spp. in domestic animals	Swine, equine and wild boars regularly slaughtered (n=8838) have been controlled for the presence of Trichinella larvae in muscle samples. All samples were negative. Diagnosis, biotechnology and laboratory

Epidemiology, surveillance, risk assessment (true)	Surveillance of Invasive mosquitoes in "Points of entry	Monitoring of the entry and spread of invasive species of mosquitoes of the genus Aedes, through the surveillance of selected "Points of entry", such as the port of Marghera (Venice) and the airports of Venice and Treviso (northeast Italy). Aedes albopictus species have been collected in all sites, while no other invasive species were found.
Epidemiology, surveillance, risk assessment (true)	Surveillance of Aedes japonicus japonicus and Ae. koreicus in Italy	The invasive mosquito species, Aedes koreicus, and Ae. japonicus japonicus were detected in northeastern Italy for the first time in 2011 and 2015, respectively. Active monitoring has been carried out since their introduction to assess the spreading and occurrence of these species. The presence of invasive mosquitoes was checked in all possible breeding sites through collections of larvae. The mosquitoes were identified morphologically and molecularly. In 2023, Ae. j. japonicus was found in 11 out of 30 (37%) and Ae. koreicus in 17 out of 20 (85%) municipalities monitored. The mosquito was collected mainly in artificial containers located in small villages and in rural areas.
Epidemiology, surveillance, risk assessment (true)	Surveillance of sand flies Phlebotomine for Leishmania and Toscana virus	In 2021, the first circulation of Toscana virus (TOSV) (Phlebovirus) was recorded in northeast Italy, with three human cases and one pool of positive vectors to TOSV found in the same area. In 2023, two sites were monitored biweekly collecting sand flies by CDC-CO2 light traps. Insects were tested for TOSV and Leishmania screening. In total, 1,619 sand flies were collected, and 71 pools were tested; one pool was positive for Leishmania infantum, one for TOSV and one for Punique virus. Circulation of TOSV was also confirmed in 2023 with four human cases and the detection of the virus in vectors in the same circulation area of the previous year.
Epidemiology, surveillance, risk assessment (true)	Assessing the presence of West Nile virus in overwintering mosquitoes	Mosquito samplings were performed in February and March 2023 in areas with WNV circulation in the previous year to assess the virus presence (as a form of virus overwintering). In total, 25 sites were monitored, and 1,527 Culex pipiens were collected. All polled mosquitoes were negative for WNV.
Epidemiology, surveillance, risk assessment (true)	BSE surveillance	Confirmation of epidemiological status of negligible BSE risk. A total of 6743 cattle were analysed, and none of them tested positive.
Diagnosis, biotechnology and laboratory (true)	Detection of Dermatophytes in domestic animals	Skin specimens from pet and domestic animals (n=1928) have been tested for the presence of dermatophytes. Trhichophyton mentagrophytes (n=3), Microsporum canis (n=14) and Nannizia gypsea (ex Microsporum gypseum, n=4) were isolated and identified from animals.
Diagnosis, biotechnology and laboratory (true)	Diagnostic activity for Coxiella burnetii	We tested 6647 ruminant sera and 753 samples (e.g., aborted foetuses and tank milk) with real-time PCR. We also organized the annual Proficiency testing for the diagnosis of Q fever by ELISA, CFT, and Real- Time PCR.
Diagnosis, biotechnology and laboratory (true)	Diagnostic activity for Leptospira	We tested 1,441 farm animals' sera, 588 companion animals' sera with MAT and 474 samples (i.e. urine, organs, blood, culture) with real-time PCR.

Diagnosis, biotechnology and laboratory (true)	Diagnostic activity for Brucellosis	Local application of the national surveillance programme to confirm the official free status by means of serology and abortion surveillance. We analysed 32983 ruminant sera, 412 aborted foetuses and 240 bulk tank milk samples. Since March 2023, the Veneto region stopped the monitoring program on bulk tank milk
Diagnosis, biotechnology and laboratory (true)	Beyond COVID - By COVID project	The Portal launched in April 2020 to bring together datasets and data-sharing tools with the aim of accelerating research on SARSCOV-2. Allows researchers to upload, access and analyse data on COVID-19. The initiative is part of the BY-COVID project, a consortium of institutes and research facilities in the field of biomedical sciences funded by the European Union's Horizon 2020 programme, in which the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) also participates.
Diagnosis, biotechnology and laboratory (true)	EVAGlobal project	Within the framework of the European research programme Horizon 2020, the project provides for development procedures and information tools in line with international standards and began an intensive collaboration with the WOAH Collaborating Centre for Veterinary Biologicals biobanks at the Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna (IZSLER). Recent IZSVe initiatives consist of practical and theoretical proposals, including the development and acquisition of IT tools for archiving biological samples, training in 'Access and Benefit Sharing', and participation in conferences, working groups and European networks on the subject of biobanking.
Diagnosis, biotechnology and laboratory (true)	ISIDORe: Integrated Services for Infectious Disease Outbreak Research	ISIDORe's main objective is to foster the interchange of resources between Europe's many research groups in order to make the scientific community's response to current and future epidemic emergencies synergistic. In pursuit of this mission, ISIDORe has established an extensive catalogue of products and services for which researchers can apply free of charge, complementing their research projects in the area of infectious diseases with epidemic potential.
Diagnosis, biotechnology and laboratory (true)	Noroviruses in swine populations	Identification and characterization methods have been developed to face the emerging risk of animal- human recombination. The research project aimed at improving the scientific data on the spread of genogroups and genotypes in the same geographic area by developing new diagnostic and sequencing tools to detect and characterize NoVs affecting animals, specifically swine
Epidemiology, surveillance, risk assessment (true)	Lyssavirus in cats	Implementation of the syndromic surveillance of possible Lyssavirus in cats with neurological disorders (RC 07/22). Proposal for a diagnostic algorithm to include lyssaviruses infection in cats as a possible differential diagnosis in cases with specific clinical, epidemiological, and anamnestic features.
	WOALI Callaborative Contro Deposite Activities 2022	Following the COVID-19 emergency, the Ministry of Health strategic research funds (RCS 2020) to carry out studies on mammals as a possible reservoir, incidental host and/or model of emerging coronaviruses, with a particular focus on SARS-CoV-2 as the aetiological agent of the current pandemic. The project, in which IZSVe is the lead partner, involves the collaboration of all the Italian National Health Service Institutes (IIZZSS). During the

Zoonoses (true)	Susceptibility of mammals to SARS-COV-2: risks of reverse zoonosis and possibilities in translational medicine	reporting year, the IZSVe coordinated all the working groups involved at different levels in the project activities and periodically collected the data obtained in the field of serological surveillance in domestic animals (received from all the IIZZSSs), virological surveillance in wildlife (received from all the IIZZSSs) and immune studies on the hamster model (IZSVe, IZS Sassari - Sardinia). The research continued during the reporting period, during which some trials were completed and the final data analysed. The results were published in the main journals of the sector and disseminated at conferences. All data obtained at completion of the activities of WP2 "Translational research. Sex differences in SARS-CoV-2 immunopathogenesis using the golden hamster animal model" were published in the journal Viruses (Castellan, M.; Zamperin, G.; Franzoni, G.; Foiani, G.; Zorzan, M.; Drzewnioková, P.; Mancin, M.; Brian, I.; Bortolami, A.; Pagliari, M.; et al. (2023) Host Response of Syrian Hamster to SARS-CoV-2 Infection including Differences with Humans and between Sexes. Viruses 2023, 15, 428. https://doi.org/10.3390/v15020428).
Diagnosis, biotechnology and laboratory (true)	Development and validation of serological tests for the detection of SARS-CoV-2 in susceptible animals	The use of the Focus Reduction Neutralization Test (FRNT) methodology was used to analyse sera from wild ungulate species. To detect the circulation of the SARS-CoV-2 virus in this population, approximately 60 sera collected during the 2021-2022 hunting season were examined. Analyses were performed using both pre-Omicron variants of SARS-CoV-2 (Alpha and Delta) and viruses belonging to the Omicron family (BA.1 and BA.2) to maintain a high sensitivity for the test. Thirteen positive samples (titer ≥ 1:40) were detected in the FRNT test. Considering the anomalous result, the sera were then analysed using two serological tests capable of detecting specific antibodies against the Receptor Binding Domain (RBD) of the SARS-CoV-2 virus: LIPS-S and cPass™. The first is an immunoprecipitation-based test, already tested for various animal species, while the second is a commercial kit based on a technology capable of detecting the presence of neutralising antibodies that specifically block the interaction between the purified RBD portion of the spike protein and its ACE2 receptor. It is a highly sensitive and specific method, with the advantage of being species-independent and not requiring the use of live viruses, which would need to be handled within biosafety level 3 containment facilities (Tan, C. W. et al. Nat. Biotechnol. 2020 and Embregts, C. W. E. et al. One Heal. 2021). The kit allows for the use of RBDs belonging to different variants of SARS-CoV-2; therefore, purified RBDs from the parental virus and the Omicron variant BA.2 were used for the analyses, respectively designed on the corresponding portion of the spike protein of the two variants. These additional tests did not confirm the results obtained in FRNT. Such discrepancies are likely attributed to the poor storage conditions of the sera and the possible presence of high levels of cross-neutralising antibodies capable of interfering with methodologies using the entire virus. Therefore, confirming the preliminary result obtained in FRNT was impossible.
		For the study of antigenic correlation among different variants of SARS-CoV-2 and for the production of reference materials useful for future

Diagnosis, bi	otechnology a	and laboratory	(true)

Production of a panel of hyperimmune sera in different animal species against different variants of the SARS-CoV-2 virus

validation studies of serological methods, in 2022, hyperimmune sera were produced in ferrets (Mustela putorius furo), hamsters (Mesocricetus auratus), and rabbits (Oryctolagus cuniculus) for the Parental (B.1), Beta, Delta, Omicron BA.1, BA.2, and BA.5 variants. The sera were produced by infecting animals of the first two species naturally (via the oro-nasal route) as part of various experimental studies, while rabbits were immunized by administering a high concentration of virus inactivated using betapropiolactone. The produced sera were then subjected to titration analysis of the achieved antibody titer and cross-neutralization tests using FRNT methods to study the antigenic characteristics of the various circulating variants. The results obtained from the neutralizations highlighted how the highest antibody titers for each variant were present in homologous sera, while when the sera were exposed to viruses belonging to different variants from those used for infection or immunization, notable differences in titers were observed, consistent with observations in some previous studies conducted in the hamster species. Results were analyzed using the online software ACMACS (https://acmacs-web.antigenic-

cartography.org/), which was used to generate antigenic maps differentiated by species. The maps show the considerable antigenic distance between the Omicron variants (BA.1, BA.2, BA.5, and BQ.1.1) and the pre-Omicron variants (Parental, Beta, and Delta), as well as the continuous and rapid antigenic evolution of the Omicron variants. For the evaluation of the translational potential of each serum donor species, the mean differences of antigenic distances (expressed as Antigenic Units, AU) between the datasets of each analyzed species and a reference dataset based on human-origin sera available in the literature were calculated to assess whether the animal models tended to underestimate or overestimate the distances between viruses, assuming the map generated with human sera as the reference standard. It was observed that the hamster model tended to underestimate the antigenic distances by 1.30 AU (-1.30 ± 1.62), while, conversely, the ferret model tended to overestimate the distances by 1.75 AU (± 1.45). The rabbit model recorded the lowest observed mean difference, equal to 0.51 ± 1.87 AU, compared to the human sera dataset used as a comparison (Wang, Qiong et al. 2019

https://doi.org/10.1007/s12250-020-00212-7). These results represent a starting point and offer a possible solution to the inability to use human sera i) for the definition of a reference serum panel for the study of the antigenic evolution of SARS-CoV-2 viruses and ii)

for the evaluation of the immune response to vaccines. The hyperimmune sera produced in hamsters, ferrets, and rabbits for the SARS-CoV-2 virus have also been used to create a panel of sera to

be sent to various national and international laboratories with the aim of providing samples with known titers to harmonize the results obtained from different neutralization methods. This need arose from the difficulty encountered in obtaining standard sera used as calibrators and produced by the WHO. For the future, comparative analyses are planned to identify which serum may be the best to use as a reference serum with a calibrator function for

		neutralization methods or the development of serological kits.
Epidemiology, surveillance, risk assessment (true)	Characterisation of USUTU viruses identified in the Veneto region (Northeastern Italy) in 2023	USUTU virus (USUV) is an emerging arbovirus first isolated in South Africa in 1959 AND maintained in the environment through a typical enzootic cycle involving mosquitoes and birds. Mosquitoes also transmit the virus to susceptible mammals, including humans, sporadically causing neuroinvasive disease. Previous surveillance has highlighted the endemic nature of the USUV in Northeastern Italy. To characterise the viruses circulating in the Veneto region in 2023, the complete or partial genome of 9 viruses, collected between July and November 2023 in the provinces of Padua (N=2), Treviso(N=1), Verona(N=3), Venice(N=2) and Vicenza (N=1), was obtained. The samples, identified in pools of mosquitoes (N=5) and birds (N=4), were subjected to full USUV genome amplification protocols and the resulting amplicons were sequenced using a Next Generation Sequencing (NGS) approach. The phylogenetic analysis revealed that these viruses show a similarity ranging between 99.28% and 99.89% and fall within the EU2-A lineage, which includes samples collected in Veneto and Friuli Venezia Giulia from 2013 to 2023 and other sequences from Italy, Hungary, Austria, Germany collected from 2009 to 2018. The nine viruses analysed cluster within four distinct groups together with viruses circulating in the Veneto region in the past years, demonstrating the continuous circulation of this virus in our Regions.
Epidemiology, surveillance, risk assessment (true)	racterisation of West Nile viruses identified in the Veneto and Friuli Venezia Giulia regions (Northeastern Italy) in 2023	West Nile virus (WNV) is a vector-borne Flavivirus that mainly infects mosquitoes, birds, horses, and humans. In humans, WNV is responsible for asymptomatic infections but can also cause clinical manifestations ranging from mild febrile states to neuroinvasive disease. The West Nile virus has been circulating every summer in the Veneto region and other Northeastern Italian regions for several years. In 2022, most of the human cases of West Nile associated with neuroinvasive forms in Europe were recorded in the Veneto region, where a co-circulation of WNV lineage 1 (WNV-1) and WNV lineage 2 (WNV- 2) was observed. In 2023, in order to characterise the viruses circulating in the Veneto and Friuli Venezia Giulia regions, the complete or partial genome of 28 viruses (14 WNV-1 and 14 WNV-2) identified in pools of mosquitoes (N=12), birds (N=13) and humans (N=3) between July and November 2023 was obtained. Of these 28 viruses, 26 were collected in the Veneto region and 2 in Friuli Venezia Giulia. All samples were subjected to full WNV genome amplification protocols using PCR targets specific to the two lineages, and the resulting amplicons were sequenced using a Next Generation Sequencing (NGS) approach. WNV-1 - The 14 samples belonging to lineage 1 collected from the provinces of Padua (N=7), Rovigo (N=2), Venice (N=4) and Vicenza (N=1) in 2023 show a similarity ranging between 99.81% and 100%. They cluster within a monophyletic group together with the samples collected in Northeastern Italy in 2021-2022, with no genetic grouping according to species or province of origin. WNV-2 - The 14 samples from lineage 2 belong to three distinct clusters: - The first cluster includes virus

sequences collected a) in 2018-2023 in the province of Verona; b) in 2016-2023 in the province of Rovigo; c) in 2022 in the province of Vicenza; d) in 2022-2023 in the province of Venice and e) in 2022-2023 in the province of Padua. This cluster includes all the WNV-2 samples taken in 2023 in the province of Padua (N=3) and Rovigo (N=2), 1 out of 5 samples from the province of Venice, 1 out of 2 samples from the province of Verona. - The second cluster comprises two distinct groups: the first contains one sample collected in the province of Verona in 2023 and samples collected in Italy from 2020 to 2022; the second group consists only of samples collected in 2023, 4 from the province of Venice and 1 from the province of Udine. - The third cluster includes 1 out of 2 samples from Friuli Venezia Giulia collected in late 2023 (November), one sample identified in 2021 from Hungary and samples collected in 2017-18 from Greece, Belgium and Serbia. This indicates a possible new introduction from Eastern countries.

To provide insights into the evolutionary and epidemiological viral dynamics during the current COVID-19 pandemic in the Italian Northeastern region of Veneto, genetic surveillance of SARS-CoV-2 has been implemented since the beginning of 2020. The complete genome sequences of about 3820 viruses of human origin were sequenced between January and December 2023. All sequences obtained by Next Generation Sequencing on Illumina MiSeq and NextSeq platforms are deposited in the GISAID database (www.gisaid.org/) and the Italian National Institute of Health platform ICoGen

(https://irida.iss.it/). The reporting period (January 2023 - December 2023) was characterised by the presence of only one variant in Veneto, the Omicron variant, which is characterized by five main lineages

(BA.1, BA.2, BA.3, BA.4 and BA.5) and several sublineages. Among these, the European Centre for Disease Prevention and Control (ECDC) has classified BA.2, BA.4 and BA.5 and their sublineages as VOC until the 3rd of March 2023. Since then, no SARS-CoV-2 variant has been classified as VOC. Between January- June 2023, the BA.5 lineage (and

sublineages), which accounted for almost 90% of the sequences obtained in December 2022, decreased from 81.8% (January) to 2.9% (June). On the contrary, a new variant (XBB) increased in frequency thanks to a higher transmissibility rate and to a greater capacity for immune evasion. XBB, which appeared in Veneto in the first half of November 2022, is a recombinant of the BJ.1 (BA.2.10.1.1) e BM.1.1.1 (BA.2.75.3.1.1.1) sublineages. In June 2023, XBB (and sublineages) totalled 89.8% of the sequences obtained in the Veneto region and, over the months, differentiated itself into several sublineages. Among these, the most widespread in the Veneto region, as in the rest of the world, were XBB.1.5 (and sublineages) and XBB.1.9 (and sublineages), whose increased diffusion may have been due to the distribution both in vaccinated subjects and in those who had recovered from a previous infection thanks to a greater capacity for immune evasion. XBB.1.5 was most common in the first half of 2023, whereas XBB.1.9, and its

the first half of 2023, whereas XBB.1.9, and its descendant EG.5, was widespread in the second half of 2023. During the reporting period, the BA.2 lineage and sublineages were present, with a frequency

Epidemiology, surveillance, risk assessment (true)

Genetic surveillance of SARS-CoV-2 in Northeastern Italy in 2023

between 2.8% and 51.6% over the months. Two main lineages were dominant: BA.2.75 (and sublineages)
and BA.2.86 (and sublineages). The first disappeared in our region in December 2023, while the second began to grow exponentially in November after its first appearance in September 2023. In December 2023, the BA.2.86 lineage and its descendant JN.1 (BA.2.86 + S: L455S) made up 51.6% of the sequences obtained in the Veneto region, increasing by 37 percentage points in only one month. BA.2.86 is a descendant lineage of BA.2, with the earliest two samples collected on July 24, 2023, in Denmark and South Africa. It differed from BA.2 as well as from other variants by over 30 mutations in the spike protein and was quickly designated as a variant under monitoring after its emergence, garnering global attention. Later, at the end of July 2023, it became a variant of interest. BA.2.86 showed an increased ACE2 binding affinity compared with current dominant variants, such as EG.5.1 and HK.3 (both descendants of XBB.1.9.2.5.1 lineage). This high binding affinity, coupled with its distinct antigenicity, enabled BA.2.86 to accumulate immune-evasive mutations during low-level population transmission. With only one additional receptor binding domain mutation (L455S) compared to its predecessor, BA.2.86, the JN.1 variant rapidly became globally predominant. Due to this rapidly increasing spread, at the end of August 2023, the WHO classified JN.1 as a separate variant of interest (VOI) from the parent lineage BA.2.86. During the reporting period, we sequenced one spillover case in animals. In April 2023, a virus identified in a mink in the Lombardy region was characterized by a positive nasal swab collected from an employer working at the mink farm. The analyses of the sequences obtained from the employer and the mink revealed 100% identity. Both viruses belonged to the Omicron XBB.1.5 sublineage and possessed the same additional amino-acid mutation in the RBD of the Spike protein (P330S). At the time of the analyses, this mutation was present on a global scale in 0.04% of the XBB.1.5 sequences, and its impact on the biologic
We coordinated nine partners from Italy to perform passive surveillance for coronaviruses in wildlife. All laboratories were harmonized in the target species/tissue and molecular protocol to be used, able to detect all species of coronaviruses. The collection of samples lasted from 2021 to the end of 2022, and statistical and phylogenetic analyses were conducted in early 2023. Briefly, we investigated 87 individuals infected with coronaviruses among the 3311 samples analysed. The highest prevalence was found in the European hedgehog, followed by Chiroptera, Carnivora, Rodentia and Arctiodactyla. Most viral species were already known to circulate in the same host species or in the domestic counterpart. Novel viruses were described in mustelids and the crested porcupine. The pilot study, granted by the Italian Ministry of Health (RCS01/20), showed the critical role of passive surveillance in monitoring the circulation of coronaviruses in wildlife and helped to identify animal groups of particular interest, such as mustelids, that could be targeted for surveillance in the long term to monitor the diversity of coronaviruses and possible spill back events of

Epidemiology, surveillance, risk assessment (true)

Passive surveillance for coronaviruses in Italian wildlife

		human coronaviruses.
Epidemiology, surveillance, risk assessment (true)	Characterization of coronaviruses at the interface between swine, people and bats	In the framework of the project Convergence (ICRAD - Grant agreement N° 862605, ID 95), the circulation of coronaviruses was investigated to characterize the specie-specific CoVs and detect spillover cases from bats and humans, including SARS-CoV-2. We investigated 18 swine farms from Northeastern Italy by pan-coronavirus molecular screening. We collected data on management, production strategies and biosafety measures to investigate risk factors influencing the prevalence of detected coronaviruses. In addition, we investigated the diversity and frequency of bats within farms using bioacoustics. We performed fieldwork between 2021 and 2023 and conducted analyses in 2023. We found evidence only for swine coronaviruses, including PHEV and Alphacoronavirus 1. Phylogenetic analyses showed low variability for both viruses and clustering based on farms for PHEV. The prevalence was mostly influenced by farm size and animal category, with weaning animals being particularly affected. Farmers reported no increase in symptomatic cases, suggesting these viruses are endemic and of no particular concern at the moment. We found no evidence of infection with SARS-CoV-2 or other spillover viruses in humans or bats. Bioacoustics showed that bats are widely circulating in most farms, with biodiversity ranging from 2 to 8 species confirmed. These data will be modelled to investigate environmental, structural, and managerial parameters influencing the presence of these wild animals, which are considered potential sources for novel viruses.

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

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

No

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
National Reference Centre for Foreign Diseases of Animals	Teramo, Italy	Europe	Diagnosis confirmation
VEO Action Consortium – Horizon 2020.			

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	- Dis. Animai/Human Inter		
Versatile Emerging infectious disease Observatory	Rotterdam, Netherlands	Europe	Research project
EYWA Project Consortium - EarlY WArning System for Mosquito-Borne Diseases and a game changer in the domain of epidemics	Athens, Greece	Europe	Research project
National Reference Laboratory for Arboviruses. Department of Infectious Diseases. Istituto Superiore di Sanità	Rome, Italy	Europe	Research project
WOAH Reference Laboratory for Brucellosis	Teramo, Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
National Reference Centre for Leptospirosis	Brescia, Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
National Reference Centre for Antrax (Centro di Referenza Nazionale per l'Antrace (Ce.R.N.A.)	Foggia, Italy	Europe	Diagnosis confirmation, proficiency testing
National Reference Centre for Leishmaniosis (C.RE.NA.L)	Sicilia, Italy	Europe	Diagnosis confirmation,proficiency testing
WOAH (OIE) Reference Laboratory for Swine Influenza	Parma, Italy	Europe	Collaboration, research project

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
lstituto Zooprofilattico Sperimentale del Lazio e della Toscana "M. Aleandri"	Rome, (Italy)	Europe	National Surveillance activities for West Caucasian Bat Lyssavirus (WCBV) in the Tuscany region
Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise (National Reference Centre for Whole Genome Sequencing of microbial	Teramo (Italy)	Europe	Serological characterization of animal sera for the detection

	- Dis. Animal/Human Inter		
pathogens: database and bioinformatic analysis/ FAO Reference Centre for Zoonotic Coronaviruses, in collaboration with IZSVe)			of SARS-CoV-2 antibodies in wild mammals
Ospedale Sacro Cuore Don Calabria (IRCCS - Scientific Institute for Research, Hospitalization and Healthcare)	Verona (Italy)	Europe	SARS-COV-2 sequencing data and analysis support; Intra- host variation and evolutionary dynamics of SARS-CoV-2 in patients; Comparison of saliva and nasopharyngeal swab testing methods
University of Padua	Padua, (Italy)	Europe	The hidden replication of SARS-CoV-2 in the gastrointestinal system - novel perspectives into virus transmission and therapeutics - GICOVID
Fondazione Biotecnopolo di Siena	Siena, (Italy)	Europe	Among the many objectives of the collaboration: i) setting up working groups to draft national and international research projects and related activities; ii) consultancy and advisory group on different issues and according to the needs; iii) implementing activities of common interest and production of literature
University of Padua	Padua, (Italy)	Europe	Cell shielding to REduce Sars- cov sPreading intO humaN boDy (RESPOND project)
Department of Medicine DIMED (University of Padua)	Padua, (Italy)	Europe	Resource recovery from recycling of personal protective items (PPI)
University of Venice – in the frame of the project "FISR 2020 Life Sciences "RELIEVED""	Venice, (Italy)		In vitro studies in a BSL3 confined environment aimed at testing the efficacy of an experimental drug against SARS-CoV-2 In vivo studies in the Sprague-Dawley animal model and in the ferret
University of Liverpool	Liverpool (UK)	Europe	Research collaboration for diagnostic and scientific purposes on animal and human viral agents
H2020 "OneBAT" Consortium - A One Health approach to the study and prevention of bat-borne viral emergencies HORIZON-HLTH-2022- DISEASE-07	Cyprus France Hungary Italy Spain Ukraine UK USA	Americas Europe	Project aim: to explore the complex interaction between host, pathogens, and environment with a view to identify factors that can trigger viral spillover from European bats to humans or

	- Dis. Animal/Human Inter		
			domestic animals.
FAO and IAEA Centre of Nuclear Techniques in Food and Agriculture	Vienna, (Austria)	Europe	To generate, validate, standardize and make available reference material for the antigenic surveillance in animals of circulating and newly emerging strains of SARS-CoV-2
European Commission	Europe	Europe	"Better training for Safer Food" - Organisation and implementation of training activities on controls of movements of dogs and cats: i.e. intra-Union trade, imports and non-commercial movements
Department of Molecular Medicine, University of Padova. Microbiology and Virology Unit, Padova University Hospital	Padova, (Italy)	Europe	Through the EVAg network, the IZSVe participates in the consortium of the ISIDORe project, which includes 17 European research infrastructures to offer integrated services for combatting current and future infectious disease outbreaks. Research collaboration for diagnostic and scientific purposes on arbovirus
Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna "Bruno Ubertini"- IZSLER (WOAH CC Veterinary Biologicals Biobank	Brescia, (Italy)	Europe	WHOA-ad hoc group on high throughput sequencing, Bioinformatics and computational Genomics (HTS-BCG)
ConVErgence Consortium - Assessing swine as potential hosts for emerging Coronaviruses - Era-Net ICRAD	Italy, The Netherlands, United Kingdom		Investigating the process of the emergence of coronaviruses in the pig industry, focusing on bats and humans as the most likely sources of infection
"VERDI" Consortium - SARS-coV2 variants Evaluation in pRegnancy and paeDlatrics cohorts	Europe, Switzerland, United Kingdom, South Africa, Thailand, Haiti, USA	Africa Americas Asia and Pasific Europe MiddleEast	Improving the understanding of the epidemiology, transmission, disease progression and treatment of variants of SARS-CoV-2 among children and pregnant women
"ORCHESTRA Consortium -Connecting European Cohorts to Increase Common and Effective Response to SARS- CoV-2 Pandemic""	European Cohorts to Increase Common and Effective Response to SARS-		Providing an innovative method to study the pandemic and deliver recommendations for future health crises: performs data analysis to integrate epidemiological, clinical, microbiological and genotypic aspects of population-based cohorts with environmental and

			socioeconomic elements. Through the EVAg network, the IZSVe participates in the consortium of the ISIDORe
ISIDORe Consortium - Integrated Services for Infectious Disease Outbreak	Bulgaria Croatia Czech Republic Finland France Italy Latvia Luxembourg Netherlands Norway Portugal Slovenia Spain Sweden	Europe	project, which includes 17 European research infrastructures to offer integrated services for combatting current and future infectious disease outbreaks.

TOR6: EXPERT CONSULTANTS

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

Yes

tes		
NAME OF EXPERT	KIND OF CONSULTANCY	SUBJECT
Bonfante Francesco	Participation in meeting (Saudi Arabia 25-30/11/2023)	The biennial Quadripartite Global Technical Meeting on MERS-CoV and Other Emerging Zoonotic Organised by: FAO, UNEP, WHO, and WOA), in partnership with the Public Health Authority and Ministry of Health, Kingdom of Saudi Arabia

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? Yes

a) Technical visit : 4

b) Seminars : 0

c) Hands-on training courses: 13

d) Internships (>1 month) : 1

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
Α	Cell culture and cell production; avian virology; virology in mammalian and virology for rabies	Italy	2
с	Activities in the frame of the Convergence project "Evaluation of the pig as an intermediate host of coronaviruses emerging from bats and/or humans"	ltaly	1
с	Training on entomological surveillance, vector identification and pathogen screening	Kosovo	2
D	Laboratory tests for diagnosis of mycosys in animals	Poland	1
с	Introduction to cell culture and isolation (viral and bacterial) feasible on Biosafety	Kosovo	2

Laboratory 2+

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?

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:

28

1. Angeloni G, Bertola M, Lazzaro E, Morini M, Masi G, Sinigaglia A, Trevisan M, Gossner CM, Haussig JM, Bakonyi T, Capelli G, Barzon L. Epidemiology, surveillance and diagnosis of Usutu virus infection in the EU/EEA, 2012 to 2021. Euro Surveill. 2023;28(33):pii=2200929.

2. Auer A., Bortolami A., Berguido F.J., Bonfante F., Terregino C., Natale A., Fincato A., Colitti B., Rosati S., Lamien C.E., Cattoli G. (2023) The Luciferase Immunoprecipitation System (LIPS) Targeting the Spike Protein of SARS-CoV-2 Is More Accurate than Nucleoprotein-Based LIPS and ELISAs for Mink Serology. Transboundary and Emerging Diseases 2023:1318901.

3. Balboni A, D'Incau M, Zamagni S, Lucchese L, Mazzotta E, Marchione S, Battilani M, Natale A. Identification of the most effective serovars to be included in the MAT antigen panel to optimize the serodiagnosis of Leptospira infection in Northern Italy. Vet Res Commun. 2023 Mar 16.

4. Barzon L, Masi G, Sinigaglia A, Trevisan M, Angeloni G, Bertola M, Crovato S, Lazzaro E, Montarsi F, Pinto A, Ricaldi G, Tiozzo B, Capelli G. Surveillance, prevention and control of West Nile virus and Usutu virus infections in the EU/EEA. ECDC and EFSA publications. doi: 10.2900/844421.

5. Bellinati L, Campalto M, Mazzotta E, Ceglie L, Cavicchio L, Mion M, Lucchese L, Salomoni A, Bortolami A, Quaranta E, Magarotto J, Favarato M, Squarzon L, Natale A. One-Year Surveillance of SARS-CoV-2 Exposure in Stray Cats and Kennel Dogs from Northeastern Italy. Microorganisms. 2022 Dec 31;11(1):110.

6. Belluco S, Bertola M, Montarsi F, Di Martino G, Granato A, Stella R, Martinello M, Bordin F, Mutinelli F. Insects and Public Health: An Overview. Insects 2023, 14, 240 7. Castellan M., Zamperin G., Franzoni G., Foiani G., Zorzan M., Drzewnioková P, Mancin M., Brian I., Bortolami A., Pagliari M., Oggiano A., Vascellari M., Panzarin V., Crovella S., Monne I., Terregino C., De Benedictis P, Leopardi S. (2023) Host Response of Syrian Hamster to SARS-CoV-2 Infection including Differences with Humans and between Sexes. Viruses 15(2):428.

8. Ciocchetta S, Frentiu FD, Montarsi F, Capelli G, Devine GJ Investigation on key aspects of mating biology in the mosquito Aedes koreicus. Med Vet Entomol. 2023 Aug 25. doi: 10.1111/mve.12687.

9. Di Chiara, C., Boracchini, R., Sturniolo, G., Barbieri, A., Costenaro, P., Cozzani, S., De Pieri, M., Liberati, C., Zin, A., Padoan, A., Bonfante, F., Kakkar, F., Cantarutti, A., Donà, D., & Giaquinto, C. (2023). Clinical features of COVID-19 in Italian outpatient children and adolescents during Parental, Delta, and Omicron waves: a prospective, observational, cohort study. 11, 1193857. Frontiers in Pediatrics, doi:10.3389/fped.2023.1193857

 Grassi L, Franzo G, Grillo S, Mondin A, Drigo M, Barbarino F, Comuzzo C, Legnardi M, Bertola M, Montarsi F, Menandro ML. Survey of Tick-Borne Zoonotic Agents in Ixodes Ticks Carried by Wild Passerines during Postbreeding Migration through Italy. Transboundary and Emerging Diseases Volume 2023, Article ID 1399089, 9 pages.
Johnson LR, Hulsebosch SE, Viall AK, Danesi P, Woolard KD, Cook SE, Maggs DJ, Leonard BC. Oculosystemic pneumocystosis in 2 sibling Chihuahuas. J Vet Intern Med. 2023 37(3):1179-1185.

 Leopardi, S., Breugem, T. I., Kim, Y., Festa, F., Lamers, M. M., Haagmans, B., Nouvellet, P. and De Benedictis, P.(2023). Assessing swine as potential hosts for emerging Coronaviruses. International Coordination of Research on Infectious Animal. Diseases (ICRAD) First Call. GMPC TOP. 3(2). pp. 7. https://doi.org/10.51585/gtop.2023.2.0034
Leopardi, S., Desiato, R., Mazzucato, M., Orusa, R., Obber, F., Averaimo, D., Berjaoui, S., Canziani, S., Capucchio, M.T., Conti, R., di Bella, S., Festa, F., Garofalo, L., Lelli, D., Madrau, M.P., Mandola, M.L., Martin, A.M.M., Peletto, S., Pirani, S., Robetto, S., Torresi, C., Varotto, M., Citterio, C., & Terregino, C. (2023a). One health surveillance strategy for coronaviruses in Italian wildlife - CORRIGENDUM. 151, e104. Epidemiology and Infection, -06-27 doi:10.1017/S0950268823001000

14. Leopardi, S., Desiato, R., Mazzucato, M., Orusa, R., Obber, F., Averaimo, D., Berjaoui, S., Canziani, S., Capucchio, M.T., Conti, R., di Bella, S., Festa, F., Garofalo, L., Lelli, D., Madrau, M.P., Mandola, M.L., Moreno Martin, A.M., Peletto, S., Pirani, S., Robetto, S., Torresi, C., (2023b). One health surveillance strategy for coronaviruses in Italian wildlife. 151, e96. Epidemiology and Infection, -06-01 doi:10.1017/S095026882300081X

15. Lo Presti, A., Di Martino, A., Ambrosio, L., De Sabato, L., Knijn, A., Vaccari, G., Di Bartolo, I., Morabito, S., Terregino, C., Fusaro, A., Monne, I., Giussani, E., Tramuto, F., Maida, C. M., Mazzucco, W., Costantino, C., Rueca, M., Giombini, E., Gruber, C. E. M., Capobianchi, M. R., On Behalf Of The Italian Genomic Laboratory Network (2023). Tracking the Selective Pressure Profile and Gene Flow of SARS-CoV-2 Delta Variant in Italy from April to October 2021 and Frequencies of Key Mutations from Three Representative Italian Regions. Microorganisms, 11(11), 2644. https://doi.org/10.3390/microorganisms11112644

16. Malik R., Martin P., Danesi P., Tong L., Krokenberger M. Fungal disease: an update Perspective N. 157. 2023. Issue 310: 32-48.

 Manzi S, Nelli L, Fortuna C, Severini F, Toma L, Di Luca M, Michelutti A, Bertola M, Gradoni F, Toniolo F, Sgubin S, Lista F, Pazienza M, Montarsi F, Pombi M. A modified BG-Sentinel trap equipped with FTA card as a novel tool for mosquito-borne disease surveillance: a field test for flavivirus detection Sci Rep. 2023 Aug 8;13(1):12840.
Marchiori E, Obber F, Celva R, Marcer F, Danesi P, Maurizio A, Cenni L, Massolo A, Citterio CV, Cassini R. Comparing copromicroscopy to intestinal scraping to monitor red fox intestinal helminths with zoonotic and veterinary importance. Front Vet Sci. doi: 2023 11;10:1190058. 10.3389/fvets.2023.1190058.

19. Mazzotta E, Bellinati L, Bertasio C, Boniotti MB, Lucchese L, Ceglie L, Martignago F, Leopardi S, Natale A. Synanthropic and Wild Animals as Sentinels of Zoonotic Agents: A Study of Leptospira Genotypes Circulating in Northeastern Italy. Int J Environ Res Public Health. 2023 Feb 20(5):3783.

20. Mazzotta E, De Zan G, Cocchi M, Boniotti MB, Bertasio C, Furlanello T, Lucchese L, Ceglie L, Bellinati L, Natale A. Feline Susceptibility to Leptospirosis and Presence of Immunosuppressive Co-Morbidities: First European Report of L. interrogans Serogroup Australis Sequence Type 24 in a Cat and Survey of Leptospira Exposure in Outdoor Cats. Trop Med Infect Dis. 2023 Jan 10;8(1):54.

Mencattelli G., Silverj A., Iapaolo F., Ippoliti C., Teodori L., Di Gennaro A., Curini V., Candeloro L., Conte A., Polci A., Morelli D., Perrotta M.G., Marini G., Rosà R., Monaco F., Segata N., Rizzoli A., Rota-Stabelli O., Savini G., West Nile W.G. (2023) Epidemiological and Evolutionary Analysis of West Nile Virus Lineage 2 in Italy. Viruses 15(1)
Meseko C, Milani A, Inuwa B, Chinyere C, Shittu I, Ahmed J, Giussani E, Palumbo E, Zecchin B, Bonfante F, Maniero S, Angot A, Niang M, Fusaro A, Gobbo F, Terregino C, Olasoju T, Monne I, Muhammad M. The Evolution of Highly Pathogenic Avian Influenza A (H5) in Poultry in Nigeria, 2021-2022. Viruses. 2023 Jun 17; 15(6):1387.

23. Modise BM, Mpoloka SW, Settypalli TBK, Hyera J, Natale A, Ceglie L, Gcebe N, Marobela-Raborokgwe C, Viljoen GJ, Cattoli G, Lamien CE. A novel multiplex qPCR HRM

assay for the simultaneous detection of four abortive zoonotic agents in cattle, sheep, and goats. Sci Rep. 2023 Jul 28;13(1):12282.

24. Peruzzo A, Vascellari M, Massaro A, Mancin M, Stefani A, Orsini M, Danesi P, Petrin S, Carminato A, Santoro MM, Speranza R, Losasso C, Capelli G. Giardia duodenalis Colonization Slightly Affects Gut Microbiota and Hematological Parameters in Clinically Healthy Dogs. Animals (Basel). 2023 7;13(6):958.

25. Pietroluongo G, Centelleghe C, Sciancalepore G, Ceolotto L, Danesi P, Pedrotti D, Mazzariol S. Environmental and pathological factors affecting the hatching success of the two northernmost loggerhead sea turtle (Caretta caretta) nests. Sci Rep. 2023 20;13(1):2938. doi: 10.1038/s41598-023-30211-z.

26. Soresinetti L, Arnoldi I, Negri A, Naro G, Michelutti A, Montarsi F, Mosca A, Bandi C, Gabrieli P, Epis S. . Development of microsatellite markers for the invasive mosquito Aedes koreicus. Parasit Vectors. 2023 Jul 6;16(1):223.

27. Zadra N, A. Tatti, A. Silverj, R. Piccinno, J. Devilliers, C. Lewis, D. Arnoldi, F. Montarsi, P. Escuer, G. Fusco, V. De Sanctis, R. Feuda, A. Sanchez-Gracia, A. Rizzoli, O. Rota-Sabelli. Shallow Whole-Genome Sequencing of Aedes japonicus and Aedes koreicus from Italy and an Updated Picture of Their Evolution Based on Mitogenomics and Barcoding. Insects 2023, 14, 904.

28. Zamperin G., Festa F., Palumbo E., Quaranta E., Monne I., Terregino C., De Benedictis P., Leopardi S. (2023) Discovery of a coronavirus in the Eurasian badger (Meles meles) belonging to a putative new genus. Infect Genet Evol 109:105406.

b) International conferences:

14

1. Bellinati L., Ceglie L., Mazzotta E., Lucchese L., Natale A. (2023) One-year surveillance of Chlamydia spp. infection in Stray Cats from northeastern Italy. 6th European Meeting of Animal Chlamydioses & Zoonoses and 1st European Meeting of Intracellular Abortifacient Pathogens. Edinburgh, 28th November 2023

2. Caputo B, Virgillito C, Longo E, De Marco CM, Micocci M, Venturini S, Serini P, Zucchelli MV, Lencioni V, Paoli F, Michelutti A, Montarsi F, Severini F, Palmer J, Bartumeus F, Della Torre A. Mosquito Alert ITALIA 2020-2022: citizen engagement, achievements and criticisms. Journal of the European Mosquito Control Association. Suppl 1 - XIth International EMCA Conference: 34. Palma (Spain), 7-10 November.

3. E. G. Quaranta, A. Fusaro, E. Giussani, E. Palumbo, A. Schivo, B. Zecchin, A. Drago, K. Cecchettin, F. Gobbo, F. Montarsi, P. Danesi, A. Sinigaglia, E. Dal Molin , M. Pacenti, L. Barzon, I. Monne, G. Capelli. (2023) Extensive genetic diversity and evolution of West Nile Virus in northeastern Italy. In: 8th European Congress of Virology 2023. Gdansk, Poland, 04-07/05/2023

4. Francesca Festa, Giulia Chiarello, Maria Varotto, Paola De Benedictis, Stefania Leopardi (2023). Eco-epidemiology and diversity of coronaviruses in the Kuhli's pipistrelle (Pipistrellus kuhlii). NIDO 2023- XVIth International Nidovirus Symposium, 14-18 May 2023, Montreux, Switzerland

5. Martina Castellan, Gianpiero Zamperin, Giulia Franzoni, Greta Foiani, Maira Zorzan, Petra Drzewnioková, Marzia Mancin, Irene Brian, Alessio Bortolami, Matteo Pagliari, Annalisa Oggiano, Marta Vascellari, Valentina Panzarin, Sergio Crovella, Isabella Monne, Calogero Terregino, Paola De Benedictis and Stefania Leopardi (2023). Host response of Syrian hamster to SARS-CoV-2 infection, including differences with humans and between sexes. NIDO 2023- XVIth International Nidovirus Symposium, 14-18 May 2023, Montreux, Switzerland

6. Mazzotta E., Lucchese L., Ceglie L., Campalto M., Cavicchio L., Bellinati L., Mion M., Carrino M., Corrò M., Spagnolo E., Danesi P., Natale A. (2023) Zoonoses in dog and cat shelters: study and development of an integrated strategy (epidemiology, social research, training and risk communication) for effective health management. 48th World Small Animal Veterinary Association Congress and the 28th FECAVA Eurocongress, p. 159-161. Lisbon, Portugal 27-29 September 2023.

7. Michelutti A, Gradoni F, Sgubin S, Danca L, Carlin S, Toniolo T, Poletto E, Porcellato E, Palumbo E, Zecchin B, Monne I, Danesi P, Gobbo F, Montarsi F. Results of entomological surveillance 2022 for West Nile and Usutu virus in northeastern Italy. Journal of the European Mosquito Control Association. Suppl 1 - XIth International EMCA Conference: 40. Palma (Spain), 7-10 November.

8. Michelutti A, Negri A, Soresinetti L, Arnoldi D, Corona C, Berrone E, Tessarolo C, Accorsi A, Listorti V, Gradoni F, Sgubin S, Poletto E, Visentin P, Gobbo F, Drago A, Rizzoli A, Mosca A, Gabrieli P, Epis S, Montarsi F. Spreading of invasive mosquito Aedes japonicus japonicus and Aedes koreicus in Italy. Journal of the European Mosquito Control Association. Suppl 1 - XIth International EMCA Conference: 18. Palma (Spain), 7-10 November.

9. Michelutti A, Vettore S, Gradoni F, Carlin S, Micocci M, Bonetto D, Drago A, Martini S, Montarsi F. Pilot study to evaluate alternative and eco-friendly methods for larval mosquito control in an urban area in northeast Italy. Journal of the European Mosquito Control Association. Suppl 1 - XIth International EMCA Conference: 70. Palma (Spain), 7-10 November.

10. Quaranta EG, Fusaro A, Giussani E, Palumbo E, Schivo A, Zecchin B, Drago A, Cecchettin K, Gobbo F, Montarsi F, Danesi P, Sinigaglia A, Dal Molin E, Pacenti M, Barzon L, Monne I, Capelli G. Extensive genetic diversity and evolution of West Nile Virus in northeastern Italy. 8th European Congress of Virology 2023. Abstracts. pag 504. Gdańsk, Poland. 4–7 May 2023.

11. Soresinetti L, Arnoldi I, Negri A, Naro G, Montarsi F, Bandi C, Gabrieli P, Epis S. Introduction and spread of the invasive mosquito Aedes koreicus in Italy: insights from population genetics. Journal of the European Mosquito Control Association. Suppl 1 - XIth International EMCA Conference: 5. Palma (Spain), 7-10 November.

12. Tim Breugem, Rik Ruijten, Debby Schipper, Stefania Leopardi, Mart Lamers, Bart Haagmans (2023). Investigating domestic pigs as potential reservoir for emerging and reemerging coronaviruses using porcine organoid models. NIDO 2023- XVIth International Nidovirus Symposium, 14-18 May 2023, Montreux, Switzerland

13. Zamperin: G.; Quaranta, E.; Gastaldelli, M. (2023) A tool for predicting lineages and recombinants of Infectious Bronchitis virus using a combination of multiple correspondence analysis and neural network. NIDO 2023- XVIth International Nidovirus Symposium, 14-18 May 2023, Montreux, Switzerland

14. Angeloni Giorgia, Lisa Guardone, Nicoletta Buono, Elena Lazzaro, Cosmin Marius Ivascu, Alain Abi Rizk, Dimitrios Skordos, Jasna Prodanov-Radulović, Dessislava Dimitrova, Michele Nori - Mixed human migrations and transboundary animal diseases

spread: the Western Balkan route case, 15th EPIZONE Annual Meeting, Novi Sad, Serbia 26 to 28 April 2023.

c) National conferences:

9

1. Fortuna C, Severini F, Marsili G, Toma L, Amendola A, Argentini C, Boccolini D, Casale F, Bernardini I, Venturi G, Fiorentini C, Michelutti A, Toniolo F, Sgubin S, Carlin S, Dal Molin E, Pagliari M, Bonfante F, Montarsi F, Di Luca M. Rischio di focolai di dengue in Italia: valutazione della competenza vettoriale di popolazioni italiane di Aedes albopictus per DENV-1. XXVII Congresso Nazionale di Entomologia (CNIE 2023): 247. Palermo, 12-16 Giugno.

 Danca L, Gradoni F, Pavan G, Sgubin S, Toniolo F, Bernardini I, Fortuna C, Bongiorno G, Menandro ML, Michelutti A, Montarsi F. Rilevamento di Toscana virus e Leishmania infantum grazie alla sorveglianza dei flebotomi in nord-est Italia. XXVII Congresso Nazionale di Entomologia (CNIE 2023): 253. Palermo, 12-16 Giugno.
Gradoni F, Carlin S, Bertola M, Danca L, Poletto E, Toniolo F, Sgubin s, Michelutti A, Montarsi F. La diffusione di Aedes koreicus (Diptera: Culicidae) verso sud aumenta il rischio di trasmissione di malattie trasmesse dalle zanzare? XXVII Congresso Nazionale di Entomologia (CNIE 2023): 252. Palermo, 12-16 Giugno.
Bertola M, Gradoni F, Albano I, Magnaghi S, Di Martino G, Belluco S, Montarsi F. Gli infestanti nella filiera degli insetti edibili: stato dell'arte e possibili opzioni di trattamento. XXVII Congresso Nazionale di Entomologia (CNIE 2023): 317. Palermo, 12-16 Giugno. 5. Bongiorno G, Bernardini I, Bianchi R, Mangiapelo C, Fiorentino E, Di Muccio T, Scalone A, Orsini S, Fortuna C, Venturi G, Magliano A, De Lesto I, De Liberato C, Mosca A, Michelutti A, Montarsi F, Foxi C, Calzolari M, Dottori M, Satta G, Gradoni L, Angelini P. Indagini entomologiche condotte in sette regioni italiane hanno evidenziato hot spot per la circolazione di malattie trasmesse da flebotomi. XXVII Congresso Nazionale di Entomologia (CNIE 2023): 238. Palermo, 12-16 Giugno.

6. Sgubin S, Danca L, Gradoni F, Bertola M, Carlin S, Toniolo F, Poletto E, Porcellato E, Palumbo E, Zecchin B, Monne I, Gobbo F, Danesi P, Montarsi F, Michelutti A. Risultati della sorveglianza entomologica 2022 nell'ambito del piano di sorveglianza regionale di West Nile e Usutu virus in nord-est Italia. XXII Congresso Nazionale Sidilv 2023, 11-13 ottobre, Brescia pag. 13-14.

7. Da Rold G, Drigo I, Guolo A, Obber F, Celva R, Dalla Libera E, Gradoni F, Sgubin S, Montarsi F, Citterio CV, Bano L. Impiego del Maldi Tof MS per l'identificazione di specie di zecche rilevanti per la trasmissione di patogeni zoonotici. XXII Congresso Nazionale Sidilv 2023, 11-13 ottobre, Brescia pag. 594-596.

8. Belluco S, Bertola M, Pinarelli Fazion J, Marzoli F, Cento G, Barco L. Persistenza di Salmonella Infantis in Acheta domesticus e Tenebrio molitor. XXII Congresso Nazionale Sidilv 2023, 11-13 ottobre, Brescia pag. 55-56.

9. Spagnolo E., Corrò M., Campalto M., Carrino M., Mazzotta E., Natale A. (2023) Studio sulla presenza di Capnocytophaga spp in cani e gatti di canili e colonie feline del triveneto e valutazione dei metodi di isolamento ed identificazione. XX National Conference Società di Diagnostica di Laboratorio Veterinaria (SIDILV), p. ///, Brescia, Italy, 11-13th October 2023.

d) Other (Provide website address or link to appropriate information):

81

1. Reports produced by other organisations in collaboration with IZSVe (n° 1) EU-EFSA The European Union One Health 2022 Zoonoses Report https://www.efsa.europa.eu/en/efsajournal/pub/8442

https://efsa.onlinelibrary.wiley.com/doi/epdf/10.2903/j.efsa.2023.844

Presentations as invited speaker (n° 4)

2. Angeloni G. (2023) "Conflicts and veterinary medicine: old and new challenges for the one health". Symposium WG Migrants, One Health and Peace War: interconnections, effects and public health tasks; Italian Association of Epidemiology, Pisa, 19th April 2023

3. Leopardi S. (2023). "Climate change and Health risks. Title of event: 3^ edizione di Ecologicamente, rassegna culturale sul clima e l'ambiente, 04/11/2022 Monselice, Italy 4. Terregino C. (2023). "One Health approach to veterinary health issues caused by emerging and re-emerging viruses". Title of event: One Health and Veterinary medicine: Parasitoses and emerging infectious diseases. Ordine dei Medici Veterinari della Provincia di Bologna, 13/09/2023 - Bologna, Italy

5. Zamperin, G. (2023). "Discovery of a coronavirus in the Eurasian badger (Meles meles) belonging to a putative new genus". International Conference on Livestock, Companion Animals and Wildlife Coronaviruses. University of Belfast, School of Medicine, Dentistry and Biomedical Science, 24-26/05/2023 - Belfast, Ireland

National training courses organized by IZSVe (n° 1)

6. Updates on emerging and re-emerging diseases at the human-animal-environment interface

https://www.izsvenezie.it/documenti/formazione/corsi-convegni/2023/2023-12-07-aggiornamenti-malattie-emergenti/programma.pdf

Presentations (accepted) (n° 2)

7. Bonfante F. (2023). "Standardization SARS-CoV-2 Serological Assays in animals". The biennial Quadripartite Global Technical Meeting on MERS-CoV and Other Emerging Zoonotic, organised by: FAO, UNEP, WHO, and WOA), in partnership with the Public Health Authority and Ministry of Health, Kingdom of Saudi Arabia 25-30/11/2023 & Bonfante F. (2023). "Animal models for antigenic distance mapping for SARS-CoV-2". The biennial Quadripartite Global Technical Meeting on MERS-CoV and Other Emerging Zoonotic, organised by: FAO, UNEP, WHO, and WOA), in partnership with the Public Health Authority and Ministry of Health, Kingdom of Saudi Arabia 25-30/11/2023

Links from IZSVe's site

9. NRL and WHOA Collaborating Centre for diseases at the Animal/Human Interface (IZSVE) http://www.izsvenezie.com/reference-laboratories/diseases-at-theanimalhuman-interface/

10. DGRV 1424/2020 Veneto Region project: sequencing of SARS-CoV-2 (Italian) https://www.izsvenezie.it/categoria/covid-19/

11. IZSVe's section on bats (Italian) https://www.izsvenezie.it/temi/animali/pipistrelli/

12. IZSVe's section on fish, crustacean and mollusc pathology https://www.izsvenezie.com/reference-laboratories/fish-crustacean-and-mollusc-pathology/

Research and news on vectors and vector-borne diseases:

13. 04/04/2023 https://www.izsvenezie.it/insetti-manifesto-salute-pubblica/

14. 11/05/2023 https://www.izsvenezie.it/mosquito-alert-fondi-pnrr/

15. 19/06/2023 https://www.izsvenezie.it/attenzione-animali-pericolosi/

16. 20/06/2023 https://www.izsvenezie.com/insects-manifesto-public-health/

17. 31/07/2023 https://www.izsvenezie.it/west-nile-primo-caso-umano-veneto-sorveglianza/

Research and news on animal reservoir and infectious diseases

18. 23/01/2023 https://www.izsvenezie.it/progetto-eva-global-izsve-2023/

19. 07/03/2023 https://www.izsvenezie.com/how-are-veterinary-epidemic-emergencie-managed-video/ [ENG]

20. 14/03/2023 https://www.izsvenezie.it/progetto-connetticat/

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32. 19/01/2023 https://www.izsvenezie.it/sequenziata-vari	ante-xbb-1-5/
33. 19/01/2023 https://www.izsvenezie.it/varianti-sars-cov	r-2-veneto-sorveglianza-iss-10-gennaio-2023/
34. 20/02/2023 https://www.izsvenezie.it/varianti-sars-cov	-2-veneto-sorveglianza-iss-7-febbraio-2023/
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36. 03/01/2023 Influenza aviaria, Sars-CoV-2 e West Nile: I	
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38. 19/01/2023 Sequenziata la variante XBB.1.5	
39. 21/04/2023 Lyssavirus nei pipistrelli, la trasmissibilità d	el virus raddoppia dopo il parto
40. 11/05/2023 I fondi PNRR per la ricerca sulle zanzare pro	omuovono la scienza partecipata attraverso l'app
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41. 31/07/2023 West Nile, dopo il primo caso umano in Ven	neto continua la sorveglianza in zanzare e uccelli
42. 25/09/2023 Giornata mondiale contro la rabbia: worksh	nop internazionale all'IZSVe per i Paesi del
Mediterraneo	
43. 28/09/2023 Gestione "One health" delle emergenze san	itarie: le sfide globali passano per il Veneto
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44. 28/03/2023 "MRV, nuovo studio coinvolge cani e gatti" ((IN link)
45. 23/04/2023 "Connetti-Cat, circolazione di Lyssavirus ne	i gatti di proprietà" (FB link; IN link)
46. 04/04/2023 "Insetti, un manifesto per la salute pubblico	a" (FB link; IN link)
47.28/04/2023 "Lyssavirus nei pipistrelli, trasmissibilità rad	doppia dopo il parto" (FB link; IN link)
48. 19/06/2023 "Attenzione animali pericolosi" (FB link)	
49. 13/07/2023 "Prima segnalazione di Leptospira interrogo	ans in gatto" (FB link; IN link)
50. 31/07/2023 West Nile, dopo il primo caso umano in Ven	neto" (FB link; IN link)
51. 28/09/2023 "World rabies day" (FB link; IN link)	
52. 02/11/2023 "Virus e pipistrelli: una relazione pericolosa"	?" [VIDEO] (FB link)
53. 05/12/2023 "OneBAT. Un approccio One Health per lo st	tudio e la prevenzione di emergenze virali dai
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60. 05/03/2023 Corriere Veneto (PRESS OFFICE IZSVe)	

61 25/03/2023 Telenuovo Tg Padova: https://tgpadova.telenuovo.it/attualita/2023/03/25/siccita-caldowest-nile-sara-unestate-di-emergenze-video

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sola-36e0e2d0-f343-4e62-94ca-22de64e00d2e.html

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71. 04/08/2023 Sole 24 Ore - Sanità24 (PRESS OFFICE IZSVe)

72. 02/08/2023 Repubblica Salute (PRESS OFFICE IZSVe)

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- 75. 04/11/2023 VVOX: https://www.youtube.com/watch?v=D8H6BuYHrUQ
- 76. 10/10/2023 L'Arena (PRESS OFFICE IZSVe)
- 77. 18/10/2023 Adnkronos salute: https://www.adnkronos.com/cronaca/zecche-e-sindrome-alfa-gal-cose-
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- 78. 11/10/2023 Il Post: https://www.ilpost.it/2023/10/11/cimici-dei-letti-rischio-italia/
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- 80. 18/10/2023 Radio3 scienza: https://www.raiplaysound.it/audio/2023/10/Radio3-Scienza-del-
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- 81. 19/10/2023 Radio Roma Sound (PRESS OFFICE IZSVe)
- 11. What have you done in the past year to advance your area of focus, e.g. updated technology?
- Confocal microscopy has been implemented with optimiz3ed immunofluorescence protocols for the visualization of viral and host proteins in several animal tissues (e.g. Syrian hamsters, bats, cats). Moreover, the technique has been successfully adapted and used for the localization of monoclonal antibodies at the cell surface or inside the cells in in vitro studies.

12. Additional comments regarding your report: