

# OIE Collaborating Centres Reports Activities

## *Activities in 2020*

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**ToR: To provide services to the OIE, in particular within the region, in the designated specialty, in support of the implementation of OIE policies and, where required, seek for collaboration with OIE Reference Laboratories**

**ToR: To identify and maintain existing expertise, in particular within its region**

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

Disease control	
Title of activity	Scope
Different immune response to SARS-CoV-2 in adult and paediatric patients	In collaboration with the Paediatric Department of the University Hospital of Padua, the CC analysed sera from sixty (60) family clusters diagnosed with SARS-CoV-2 infection. The samples, which in some cases were collected a few months after the infection, showed stable antibody titres with higher values in paediatric patients rather than in adults. However, by comparing these results with the values obtained by commercially available kits we noted a substantial difference, especially when we tested the collected sera a few months after the infection. This activity provided a considerable contribution to the knowledge of the immune response in different population categories.
Epidemiology, surveillance, risk assessment, modelling	
Title of activity	Scope
Epidemiological surveillance of canine leptospirosis in north-eastern Italy	Since 2013 to 2019, a total of 1631 dog samples were tested by real-time PCR, and leptospires from 193 dogs were subjected to Multilocus Sequence Typing and a Multiple Loci Variable-number Tandem Repeat Analysis. Leptospires were successfully isolated from 15 symptomatic dogs. Six distinct Sequence Types (STs) were found for 135 leptospires, with 3 STs characterizing <i>Leptospira interrogans</i> (ST17, ST198 and ST24), 2 STs characterizing <i>Leptospira kirschneri</i> (ST117 and ST289) and 1 ST characterizing <i>Leptospira borgpetersenii</i> (ST155), revealing the circulation of the serogroups Icterohaemorrhagiae, Australis, Sejroe and Pomona. The Multiple Loci Variable-number Tandem Repeat Analysis of 17 samples did not result in any additional discrimination. Genotypes were compared with those of strains present in the historical internal database, and possible transmission chains were identified from rat, mouse, hedgehog and pig. This study highlights the importance of molecular methods in revealing and identifying circulating <i>Leptospira</i> strains, and it also encourages the evaluation of the ability of commercially available vaccines to reduce the disease burden among dogs.

<p>Serological survey of Hepatitis E in exposed people in north-eastern Italy</p>	<p>To investigate Hepatitis E risk for humans, a serological and epidemiological survey on potentially exposed people (hunters and gamekeepers) was performed in 17 volunteers the Euganean Hills area (Hev virological and serological. At the moment, as regards the outcome of the laboratory analyzes, the examined samples come from Vicenza Province were positive in wild ungulates) and volunteers in apparently Hev-negative area (Vicenza province) which stands as a comparison. all negative while in two subjects from the area of Euganean Hills antibody positivity against IgG was found. This result confirms the circulation of virus and reinforces the need for safe and correct management of game meat.</p>
<p>Rapid identification of ticks species, genotyping and drug sensitivity testing of <i>Borrelia</i> spp. in North Eastern Italy</p>	<p>In 2020 a research has started, named RC IZSVE 08/20, funded by the Italian Ministry of Health, focused on <i>Borrelia</i> and ticks. The bacteria of the genus <i>Borrelia</i> are "fastidious microorganisms" and therefore, given the difficulty of isolation, there are few information on circulating genotypes and their antimicrobial susceptibility. This lack of data makes it difficult to assess the ecology of the infection in the environment, the resulting zoonotic risk and the existence of strains resistant to standard antimicrobial therapy. Given these premises, it is therefore desirable to create a collection of <i>Borrelia</i> spp. in order to study its epidemiology and vector-pathogen relationships. Furthermore, the development of MALDI TOF database for rapid and economical identification of vectors and zoonotic pathogens is of strategic importance. The core area of the project is represented by the province of Belluno, an endemic area for Lyme borreliosis in humans and in which the different <i>Borrelia</i> genospecies have already been identified in their vectors during previous monitoring. The main objectives of the research are therefore: i) the collection of at least 30 <i>Borrelia</i> spp. samples to be subjected to drug-sensitivity tests and genotypic characterization; ii) the creation and population of a mass-spectrometry database of both ticks and <i>Borrelia</i> spp..</p>
<p>Monitoring the focus of <i>Echinococcus multilocularis</i> in red fox</p>	<p>In 2020, the Centre offered a diagnostic service for the search of <i>Echinococcus multilocularis</i> eggs and subsequent molecular characterization in fox feces (<i>Vulpes vulpes</i>) from the area of competence. In total, 533 foxes were examined. The presence of the parasite was confirmed in 6 (1.13%) foxes in the province of Bolzano confirming the presence of the pre-existing outbreak. In October, 2020, the first <i>E. multilocularis</i> positive fox in Trento province were reported; thus, monitoring on foxes were intensified in the focus area, in collaboration with Trento province Forest and Fauna department and MUSE. This will lead to an increased number of samples from the area of interest, while sensitizing the local operators on safe sampling protocols. Between 2018 and 2020 fox fecal samples were collected and genetically characterized at 21 microsatellite loci. The implemented sampling protocol will allow the estimation of fox population density in two areas in Bolzano province, one of which affected by <i>E. multilocularis</i> focus (Alto Isarco district) plus a negative control area (Val d'Ultimo). Comparing the inferred density with spotlight counting will allow to test the efficacy of fox monitoring for sanitary purposes. The molecular characterization of fecal samples led to the identification of 132 individuals: these results will allow to monitor the seasonal evolution of <i>E. multilocularis</i> infection at individual level.</p>
<p>Monitoring mosquito populations for Flaviviridae in north-eastern Italy</p>	<p>In 2020, we placed 77 CDC-CO2 mosquito traps over the area and collected 114170 mosquitoes of 18 different species. Viral search was done in 2478 pooled specimens. West Nile virus was detected in 20 pools and USUTU virus in 31 pools both of <i>Culex pipiens</i>.</p>

Surveillance of Invasive mosquitoes in "Point of entry"	We monitored the entry and spread of invasive species of mosquitoes of the genus <i>Aedes</i> , through the surveillance of certain "Point of entry" such as the port of Marghera (Venice) and the airport of Venice. In the two sites mosquitoes of the <i>Aedes albopictus</i> species have been observed, while at the airport eggs of <i>Aedes koreicus</i> were collected by ovitraps.
Spread of <i>Aedes japonicus japonicus</i> and <i>Ae. koreicus</i> in Italy	The invasive mosquito species, <i>Aedes koreicus</i> and <i>Ae. japonicus japonicus</i> was detected in northeastern Italy for the first time in 2011 and 2015 respectively. An 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 2020, <i>Ae. j. japonicus</i> was found in 34 out of 150 (22.6%) and <i>Ae. koreicus</i> in 81 out of 150 municipalities monitored and before negative. In total, 12.4% and 36.8% of sampling sites were positive for presence of <i>Ae. j. japonicus</i> and <i>Ae. koreicus</i> larvae respectively. The mosquito was collected mainly in artificial containers located in small villages and in rural areas. Both species are well established in Italy and in few years have colonised almost all northeastern Italy displaying rapid spreading throughout hilly and mountainous areas. The further spread of <i>Ae. j. japonicus</i> and <i>Ae. koreicus</i> has the potential to pose new threats of zoonotic agents (i.e. <i>Dirofilaria</i> spp. and West Nile virus) within areas at altitudes previously considered at negligible risk in Italy.
Surveillance of zoonotic dermatophytes in animals involved in animal-assisted interventions (AAIS)	Animal-assisted interventions (AAIs) are based on the establishment of a therapeutic relationship between animals and beneficiaries that is certain to provide positive effects, while currently, it reads as if AAIs aim at exposing stakeholders to potential risk of infection. The surveillance of zoonotic pathogens is necessary for guaranteeing common health. This study investigated the presence of potentially zoonotic parasites, including dermatophytes, in animals involved in AAIs. Between 2015 and 2017, 190 animals (equids, dogs, cats, birds, rabbits, rodents, and goats) were investigated. Anamnestic and management data were recorded. Fur and skin were collected by brushing for mycological investigation. <i>Nannizzia gypsea</i> and <i>Paraphyton mirabile</i> , potential agents of cutaneous mycosis, were isolated in a dog and a horse, respectively. No ectoparasites were found. AAIs might represent a source of infections either directly or via environmental contamination. Thus, active surveillance is necessary and animal screenings should be planned and scheduled according to the risk of exposure.
Analyses performed at the IZSve for rabies diagnosis of lyssaviruses in bats	In 2020, passive surveillance in bats was further enhanced compared to previous years, likely favoured by the spillover in Tuscany of West Caucasian Bat Lyssavirus (WCBV) in a domestic cat. Indeed, 144 of the 596 bat carcasses investigated belonged to the specie <i>Miniopterus schreibersii</i> , the most likely reservoir of WCBV. Among the other analysed hosts, most belonged to the genera <i>Pipistrellus</i> and <i>Hypsugo</i> that have never been associated with species-specific lyssaviruses, while we also analysed a few individuals of the genera <i>Eptesicus</i> (n = 5) and <i>Myotis</i> (n = 5), reservoir for all European lyssaviruses. All bat species were confirmed using molecular techniques targeting the cytochrome oxidase I (COI). All samples tested negative for lyssaviruses. As most samples were of poor quality and/or quantity, all specimens were analysed using molecular techniques only implementing two different protocols: an in house validated one-step RT-PCR and a real time RT-PCR protocol recommended by the OIE Manual of Diagnostic Tests and Vaccines for Terrestrial Animals (2018).

<p>Fatal multiple outbreaks of equine influenza H3N8 in Nigeria, 2019: The first introduction of Florida clade 1 to West Africa</p>	<p>In December 2018, suspected outbreaks of equine influenza (EI) were observed in donkeys in Sokoto State, in northwestern Nigeria. Equine influenza virus (EIV) subtype H3N8 was the etiologic agent identified using real-time RT-qPCR and sequencing of both the partial haemagglutinin (HA) gene and the complete genome. The H3N8 virus spread to 7 of the 19 northern states of Nigeria, affecting both donkeys and horses. Phylogenetic analysis of the partial and complete HA gene revealed the closest nucleotide similarity (99.7%) with EIVs belonging to the Florida clade 1 (Fc-1) of the American lineage isolated in 2018 from Argentina and Chile. Eighty amino acid substitutions were observed in the viral proteins when compared to the OIE-recommended Fc-1 vaccine strains. The HA and neuraminidase proteins respectively had 13 and 16 amino acid substitutions. This study represents the first reported outbreak of EI caused by an Fc-1 virus in Nigeria and in the West Africa sub-region. Extensive disease surveillance in equids is required to establish the circulating lineages and design effective control strategies to protect horses and donkeys in the country.</p>
<p>Surveillance of trichinellosis in domestic animals</p>	<p>In 2020, the Centre offered a diagnostic service for the detection <i>Trichinella</i> spp. on wild and domestic animals. Referring to these last, overall 67924 samples have been tested. In particular muscle tissue from 304 donkeys, 4604 horses, 10 mules, 5 cats, 62757 pigs and 244 ostriches have been analysed. All samples were negative.</p>
<p><b>Zoonoses</b></p>	
<p><b>Title of activity</b></p>	<p><b>Scope</b></p>
<p>BSE surveillance</p>	<p>Confirmation of epidemiological status of negligible BSE risk. We analysed 8081 cattle and none of them tested positive.</p>
<p>Circulation of Mammalian Orthoreovirus in the swine and bat population</p>	<p>Bats are often claimed as a major source for future viral epidemics being associated with several viruses with zoonotic potential. The study describes the high presence and biodiversity of bats associated to intensive pig farms devoted to the production of heavy pigs in northern Italy. Since chiropters or their signs of presence were not found within animal shelters in our study area, we suggest that faecal viruses with high environmental resistance have the highest likelihood for spillover through indirect transmission. We investigated the circulation of mammalian orthoreoviruses (MRVs), coronaviruses (CoVs) and astroviruses (AstVs) in pigs and bats sharing the same environment. Results did not show any bat virus in pigs, thus suggesting that spillover from these animals is rare. However, several AstVs, CoVs and MRVs circulated undetected in pigs. One MRV was a reassortant strain carrying viral genes likely acquired from bats. On the other hand, we found a swine AstV and a MRV strain carrying swine genes in bat guano, indicating that viral exchange at the bat-pig interface might rather occur more frequently from pigs to bats than the other way around.</p>

<p>Characterization of a West Nile virus isolated from a passerine in the Province of Padua</p>	<p>West Nile virus (WNV) is a vector-borne infectious disease, transmitted to birds, horses and humans through the bite of an infected mosquito, usually of the genus <i>Culex</i>. Although WNV is responsible for asymptomatic infections, it can also cause a variety of clinical manifestations ranging from mild fever to neuroinvasive disease. WNV confirmed cases have increased both in EU and Non EU countries, with particular concern for the Mediterranean area. WNV is endemic in north-eastern Italy and particularly dangerous for some risk categories (immunocompromised individuals, the elderly, and children). Developing reliable methods to identify the disease to better manage surveillance systems is indeed a priority. The CC applied a protocol for WNV complete genome amplification via PCR target and Next Generation Sequencing (NGS) approach with Illumina MiSeq and obtained the complete genome of a WNV identified in August 2020 from a passerine in the province of Padua. Results showed that the virus belongs to lineage II and groups with both a WNV identified in Bulgaria in 2018 (99.3% similarity) and with WNVs identified in Greece and Belgium between 2017 and 2019 (99.1% similarity -99.3%).</p>
<p>Characterization of USUTU strains isolated from birds in the Provinces of Padua and Venice</p>	<p>The Usutu virus (USUV) is a flavivirus with a biological cycle similar to West Nile (WNV), whose vector of infection are ornithophilous mosquitoes (mainly <i>Culex</i>) while birds are its reservoir. Initially believed to be a harmless virus with no zoonotic potential, human cases from USUV have been increasing in the last years. For this reason, surveillance plans similar to those prepared for WNV monitoring activities should be implemented in the known endemic areas. The CC applied a protocol to obtain the amplification of the complete genome of USUV by target PCR and Next Generation Sequencing (NGS) with Illumina MiSeq and obtained the complete genome of 3 USUVs identified in August 2020 from two canaries in the Province of Padua and from a blackbird in the Province of Venice. The three Italian viruses are not identical but anyway grouped within the EU2 lineage, in particular in group A, which includes the most recent Italian USUTU viruses.</p>
<b>Wildlife</b>	
<b>Title of activity</b>	<b>Scope</b>
<p>Support to the epidemiology and surveillance of trichinellosis</p>	<p>We monitored 11596 wild animals for <i>Trichinella</i> spp., including wild boars (10153), red foxes (819) wolves (16), golden jackals (11) and mustelids (578). Monitoring is still ongoing, but currently none has tested positive. Preliminary spatial analysis of foxes <i>Trichinella</i> samples collected from 2006 to 2019 have been made in order to identify areas and possible factors of risk that allow its maintenance.</p>

<p>The role of stranded marine mammals in the human-animal interface</p>	<p>Cetacean stranding data can provide baseline information on marine ecosystems and can help us to better understand causes of mortality and factors affecting marine animal health. Disease outbreaks among marine mammals are relatively unexplored compared to those on land, but there are many pathogens that are transmissible to humans and/or come from humans. Among the best known pathogens we find Poxvirus, influenza virus, Calicivirus, West Nile virus, and, potentially, Coronavirus, Papillomavirus, Herpesvirus, Norovirus and Morbillivirus. Marine mammals are also susceptible to pathogenic bacteria, such as <i>Brucella</i> spp., some species of mycoplasmas and to parasites (in particular <i>Toxoplasma gondii</i>). The Italian NRC for Diagnostic Activities in Stranded Marine Mammals (C.Re.Di.Ma.) coordinates surveillance and control activities performed by National Public Health Services of Italy (Istituti Zooprofilattici network) and other RC at the AHI. In 2020 DVM-FLU A analyses were performed on 2 samples collected from <i>Tursiops truncatus</i>. In 2021 the IZSve will be involved in a new research project funded by the Italian Ministry of Health, for the detection of West Nile, Morbillivirus, Betanodavirus, Coronavirus, Astrovirus in samples from stranded cetaceans.</p>
<b>Diagnosis, biotechnology and laboratory</b>	
<b>Title of activity</b>	<b>Scope</b>
<p>Standardization and validation of molecular diagnostic tests for zoonosis</p>	<p>During 2020 a cross examination of three <i>E. multilocularis</i> detection techniques was carried out in collaboration with UNIPI, FEM and UNIPD. 113 foxes were examined using the standard IZSve protocol (sedimentation/filtration and multiplex PCR on positive samples), a qPCR protocol and an intestinal scraping technique used as gold standard. Out of those, <i>E. multilocularis</i> positivity were found in 24 (scraping), 19 (qPCR) and 4 (standard protocol) foxes, suggesting a higher performance for qPCR in detecting the parasite. <i>E. multilocularis</i> specimen found using the scraping technique were collected and will be analyzed for a genetic characterization of the parasitic strain. Also, other cestode species found were collected and will be morphologically analyzed.</p>
<p>Development of SYBR green real-time PCR (rtPCR) for characterization of <i>Prototheca</i> species from cultures and formalin-fixed paraffin-embedded (FFPE) tissue specimens.</p>	<p>Protothecosis is an uncommon disease caused by algae of the genus <i>Prototheca</i> that involves humans and animals. In dogs, the infection is usually first localized to the colon but has the propensity to later disseminate hematogenously to many other organs, with marked tropism for the eyes and central nervous system. Diagnosis is established by culture and/or evidence of <i>Prototheca</i> organisms in cytologic or histologic preparations. Species characterization, however, requires molecular investigations. Our laboratory set up a real-time PCR targeting portion D1/D2 of the 28S rRNA for identification of <i>Prototheca</i> species from both positive cultures (of rectal swabs and urine) and formalin-fixed, paraffin-embedded tissue. <i>Prototheca bovis</i>, <i>P. ciferrii</i>, and <i>P. wickerhamii</i> were characterized in 11 dogs with systemic or cutaneous protothecosis. <i>Prototheca</i> identifications were phylogenetically consistent with the new taxonomy proposed for this genus based on the mitochondrial cytochrome b gene. As a pilot study, we screened feces and rectal scrapes from 200 asymptomatic dogs, using 2 cohorts of stray and owned animals, to determine the prevalence of intestinal carriage of <i>Prototheca</i> spp. The <i>Prototheca</i>-negative results from both cohorts of healthy dogs suggest that predisposing factors related to the host probably contribute more to the acquisition of clinical disease than exposure to contaminated environments.</p>

<p>West Caucasian Bat Lyssavirus (WCBV) detected in a cat in the municipality in Arezzo (Italy)</p>	<p>In July 2020, the CC confirmed the spillover of WCBV in a cat from Arezzo, a city from Tuscany, showing 99% similarity to the original Russian isolate dated 2002. In response, the CC enhanced passive surveillance in bats and implemented eco-epidemiological investigations and active surveillance. Despite the original host of WCBV (<i>M. schreibersii</i>) is a cave dwelling species that was not expected in the area, a transient urban colony of up to 350 bats was found close to the index case between August and October. Cats were photographed going in and out the tunnel. Ecological investigations showed that bats fly away from the tunnel after sunset to feed elsewhere. This should reduce the contacts between cats and healthy bats, although the risk of exposure is still possible when individuals are sick and unable to fly. Around 40% bats showed antibodies neutralizing WCBV but not EBVL-1, as determined through the RFFIT method. Regarding human exposure, the cat bit six people during clinical disease. Despite the vaccine is not predicted to cross-react with WCBV, they all received full post exposure prophylaxis and to date have not displayed any clinical sign of disease.</p>
<p>Development and validation of a high-throughput method for the detection of neutralizing antibodies against SARS-CoV2</p>	<p>In response to the Italian and global SARS-CoV-2 epidemic, the CC developed a virus titration method based on the rapid plaque count that can be performed also on a small sample volume. This approach is defined "high-throughput". This method stands at the basis of the Plaque Reduction Neutralization Assay (PRNT) serological technique, the gold standard method to define the immunological profile of a patient and to quantify the presence of neutralizing antibodies. Furthermore, the PRNT allows verifying the results obtained with other serological methods with a lower degree of specificity. The PRNT method was therefore developed to visualize the viral growth on 96-well plates over about 26 hours by immunocytochemical staining, using the J2 monoclonal antibody, capable of recognizing structures of double-stranded RNA, replicative intermediate of many viruses, including SARS-CoV-2. The choice of this antibody enables to be independent from any fluctuations in the availability of specific antibodies to the SARS-CoV-2 virus. The use of a reduced sample volume (50 microliters of serum) to be serially diluted to obtain a titre makes this an extremely useful method to analyse an exceedingly high number of samples as those generated during the epidemic emergency. This method can be applied both to human and to animal samples and has recently been used to validate a SARS-CoV-2 ELISA test for veterinary use.</p>
<p>Development and validation of a rapid method for collecting, preserving and analysing saliva samples to detect SARS-CoV-2</p>	<p>The use of saliva samples as specimen for the diagnosis of Sars-CoV-2 is an excellent alternative to the nasopharyngeal swabs. The use of self-collected saliva sampling is an easy, convenient, and low-cost approach that does not require the assistance of a healthcare worker. A lyophilized preservative was developed to limit the degradation of the SARS-CoV-2 genome in thermally inactivated saliva samples. Thermal inactivation was validated in order to be able to perform molecular analyses under Biosafety Level 2 (BSL-2) conditions without interfering with the sensitivity of the test and minimizing the level of risk for operators. Moreover, saliva samples subjected to heat treatment with the addition of a preservative have proved to be stable at -80 ° C, + 4 ° C and at room temperature at 24, 48 and 72 hours, which allows a considerable flexibility in the organization and management of the samples.</p>

<p>Development and validation of a method to obtain Zika virus purification to determine lipid composition through lipidomics analysis</p>	<p>In recent years, an increasing number of studies have shown how lipids are able to influence the replicative capacity of flaviviruses in the host cell. Structural lipids of viral and cell membranes are crucial in the early stages of viral replication, such as in receptor binding, in the internalization of virions or in the endosomal fusion. Based on this evidence, the CC investigated the existence of lipid determinants at the viral envelope level capable of defining the replicative phenotype of the Zika virus. This goal was pursued by measuring the amount of cholesterol present on the viral membrane and by characterizing the lipids that make up the virus envelope. To perform the assays necessary to quantify and characterize the lipids on viral envelope, we developed a specific viral purification protocol. The amount of cholesterol in the envelope of purified viruses was determined by an Amplex™ Red Cholesterol Assay, while the overall lipid composition of viral envelope was investigated using a combination of mass spectrometry and liquid chromatography.</p>
<p>Characterizing the viral phenotype of Zika virus in human placental cells</p>	<p>Zika virus strains originating from mammalian cells have a greater capacity to infect rather than those originating from insect cells. In order to investigate the pathogenetic process that determines this difference, the CC decided to characterize the replicative phenotype of the French Polynesia strain in four human placental cell lines. The strain was replicated in mammalian cells (VERO) and insect cells (C6 / 36) to obtain two different viral stocks: FP-V and FP -C6. The applied protocol intended to assess whether this difference was due to a lower initial infecting capacity or to a weak replicative efficiency over time. Results demonstrated that the virus originating from mammalian cells had the capacity to infect a greater number of placental trophoblasts than the one replicated from insect cells; the mechanisms determining this difference were further investigated by means of a binding study, in which the viral infection time was gradually reduced. It turned out that, over time, the batch-to-batch variation had remained the same, meaning that the difference is very likely linked to the efficiency of viral internalization.</p>
<p>Development and validation of biomolecular diagnostic methods to identify SARS-CoV2 from animal and human samples</p>	<p>During the first wave of the COVID-19 pandemic, the CC supported the Health Authorities of the Veneto Region to process an unprecedented number of virological samples by acquiring the WHO protocol for the molecular detection of SARS-CoV-2 (Corman et al. 2020). Technicians and biotechnologists were specifically trained to analyse nasopharyngeal (NF), oro-pharyngeal (OF) and saliva samples of human origin. Performances of the protocol were assessed using reference materials provided by the Reference Laboratory (RL) for COVID-19 of the Veneto Region. The RL rated the CC diagnostic performances as satisfactory. The procedure was also used to detect the presence of SARS-CoV-2 in the samples from companion animals (mainly dogs and cats), whose owners had tested positive and/or had been hospitalized for COVID-19. Intra vitam samples (nasopharyngeal, oro-pharyngeal, faeces, tracheal and rectal swabs) were analyzed; in case of mortality, carcasses underwent necropsy and organs were collected to carry out SARS-CoV-2 analyses. In total, 31.108 human samples and 119 animal specimen were tested at the IZSve laboratories. Moreover, the IZSve assisted the Ministry of Agriculture and Food Supply (Brazil) and the National Veterinary Research Institute of Vom (Nigeria) in the diagnosis of COVID-19, with the provision of the above protocol.</p>

<p>Development and validation of serological diagnostic methods to identify SARS-CoV2 from animal and human samples</p>	<p>Serological analyses were performed by using two commercially available electrochemiluminescent (ECLIA) methods (qualitative and quantitative) on Roche Cobas e601 system at the IZSve laboratories. The qualitative method recognizes the presence of serum total antibodies (IgG, IgM and IgA) against the nucleocapsid protein of SARS COV-2 virus, while the quantitative method is able to detect the concentration of serum IgG antibodies reactive against the spike RBD SARS-CoV-2. Both methods are double-antigen sandwich immunoassays employing a ruthenium and biotin-labelled antigen. Analytical performances were evaluated according to the CLSI EP15-A3 protocol (CLSI User verification of precision and estimation of bias; approved guideline—third edition. Clinical and Laboratory Standards Institute, Wayne, PA (2014) CLSI EP15- A3. Data were also compared to the neutralization activity using the plaque reduction neutralization test (PRNT). Both methods proved to be potentially useful for different animal species, and were used for serological analyses in cats and dogs. A commercially available double-antigen ELISA kit, targeted to SARS COV-2 N-protein and detecting total IgG antibodies was also used to test human and animal sera, with results similar to the ECLIA methods.</p>
<p>Diagnosis of Echinococcus multilocularis in red fox</p>	<p>In 2020, the Centre offered a diagnostic service for the search of Echinococcus multilocularis eggs and subsequent molecular characterization in fox feces (Vulpes vulpes) from the area of competence. In total, 354 foxes were examined. The presence of the parasite was confirmed in 7 (2%) foxes in the province of Bolzano, confirming the presence of the pre-existing outbreak and in 1 (0.3%) fox in the province of Trento.</p>
<p><b>Other (Name the category)</b></p>	
<p><b>Title of activity</b></p>	<p><b>Scope</b></p>
<p>Development of a Webgis named “Visore”</p>	<p>In 2020, a Webgis named “Visore” was developed for the georeferencing of the samples and the visualization of the data collected through a dynamic online map and their theming (for example, for year of discovery). The Webgis using the JS OpenLayers3 framework, for the front-end part, and in Java for the back-end side. The software is published through the Tomcat 7 application server, on a Linux server.</p>
<p>Inter-annual variability of the effects of intrinsic and extrinsic drivers affecting West Nile virus vector Culex pipiens population dynamics in northeastern Italy</p>	<p>WNV epidemiology is difficult to predict due to the complexity of the environment-host-vector-pathogen interaction. The analyses of ecological drivers responsible for the earlier WNV reactivation and transmission are pivotal; in particular, variations in the vector population dynamics may represent a key point of the recent success of WNV. We investigated the variations of Cx.pipiens population abundance using environmental, climatic and trapping data obtained from 2010 to 2018 through the WNV entomological surveillance conducted in northeastern Italy. An information theoretic approach and model-averaging algorithms were implemented to examine the relationship between the seasonal mosquito population growth rates and both intrinsic and extrinsic predictors, to identify the most significant combinations of variables outlining the Cx.pipiens population dynamics. Population abundance and length of daylight were the predominant factors regulating the mosquito population dynamics; however, other drivers encompassing environmental and climatic variables also had a significant impact. The analyses of datasets, and the comparison with the results obtained from the overall model highlighted remarkable differences in coefficients magnitude, sign and significance. These outcomes indicate that different combinations of factors might have distinctive, and sometimes divergent, effects on mosquito population dynamics.</p>

<p>The common European mosquitoes <i>Culex pipiens</i> and <i>Aedes albopictus</i> are unable to transmit SARS-CoV-2, after a natural-mimicking challenge with infected blood</p>	<p>On March 11 2020, the World Health Organization (WHO) declared COVID-19 outbreak a global pandemic. As the mosquito season progressed, the understandable concern that such insects could transmit the virus began to spread, despite the WHO had already stated that there was no evidence for it. In response to this request, the vector competence for SARS-CoV-2 of <i>Culex pipiens</i> and <i>Aedes albopictus</i>, the two most common species of vector mosquitoes in Europe, was investigated. In order to evaluate the capacity to transmit the virus, mosquitoes of both species were allowed to take up an infectious blood meal. Mosquitoes were collected and analysed at 0, 3, 7 and 10 days post-feeding. Due to the peculiar feeding behaviour, the role of <i>Aedes albopictus</i> in a potential mechanical transmission of the virus was also evaluated. Both mosquito species were found not competent for SARS-CoV-2 and in addition <i>Aedes albopictus</i> was unable to mechanically transmit the virus.</p>
<p>Development and validation of primary cells or of human placental explants to characterize Zika virus phenotypes</p>	<p>Within the framework of the Horizon 2020-funded ZIKAction project, we developed and validated the use of placental explants for the study of Zika viruses. Data obtained from previous experimental trials revealed that Zika viruses cultured in mammalian cells (VERO) are able to replicate more efficiently than the ones cultured in insect cells (C6/36). We decided to investigate whether such difference was due to factors related to the viral structure itself or to the type of infected cell. To support this latter assumption, the CC decided to characterize the Zika virus phenotype in the single cells of the placental tissue. Viral replication was investigated at the level of the most representative placental cells, already recognized as being the targets of infection for this virus.</p>
<p>Genetic analyses on three different clusters of SARS-CoV-2 identified in the Provinces of Padova-Vicenza (part 1)</p>	<p>Padova-Vicenza cluster: The SARS-CoV-2 sequences obtained from 4 nasopharyngeal swabs taken from human patients in the provinces of Padua and Vicenza were analysed and turned out to be identical. This means that there exists a probable epidemiological connection between the four cases. The viruses belong to the B.1.1 lineage and are closely related to those identified in Serbia and Switzerland. Results are accessible from the following link: <a href="https://www.izsvenezie.it/sequenziamento-genoma-sars-cov2-cluster-serbia/">https://www.izsvenezie.it/sequenziamento-genoma-sars-cov2-cluster-serbia/</a></p>
<p>Genetic analyses on three different clusters of SARS-CoV-2 identified in the Provinces of Venice and Treviso (part 2)</p>	<p>Venice cluster: The Regional Health Authority sent 44 nasopharyngeal swabs from individuals hosted in a reception facility in Jesolo (Province of Venice), from which six SARS-CoV-2 samples were tested and complete genome sequences analysed. All six viruses are grouped in the phylogenetic tree within lineage B.1.1. In particular, it seems that four viruses are identical, while two differ for 1 and 5 nucleotide substitutions, thus suggesting the presence of more viral variants in this sampled group. The genomic sequences also revealed the highest identity with the strains identified in Portugal at the beginning of March 2020. Treviso cluster: Ten nasopharyngeal swabs from individuals hosted in the former army barracks in the municipality of Casier (Province of Treviso) were tested and the complete genome sequences of seven selected SARS-CoV-2 samples revealed there had been two distinct viral introductions into the facility in different time periods. One virus belongs to lineage B.1.1, while the second one falls within lineage B.1.1.1. However, the low number of swabs subjected to sequencing (7) compared to the total of positives (over 200) does not allow excluding the co-circulation of both viruses.</p>
<p>Characterization of the whole viral genome of Zika virus strains and their derivatives in cells of different origin</p>	<p>Zika virus strains (Honduras 2015, French Polynesia 2013 and MR-766) replicated in mammalian cells are able to infect human placenta explants more efficiently than the same strains replicated and collected from insect cell lines. The CC conducted a study to understand if such difference was due to one or more mutations deriving from the replication of the viruses in their respective cell lines. By comparing the sequences of the same strain in the two cell lines (FP-V vs FP-C6) no significant differences were found. If we exclude the genome and the related proteins, the only element capable of determining the structure of the virus and its interaction with the host cell is the lipid envelope that derives from a re-arrangement of the endoplasmic reticulum of the host cell during viral replication. One of the future objectives of the CC is to study the lipid composition of the viral envelope in search of phenotypic determinants.</p>

Characterization of the lipid composition of the viral envelope	<p>In recent years, an increasing number of studies have revealed the importance of lipids in the replicative cycle of flaviviruses that are able to reorganize the host cell lipid metabolism to create a favourable environment for viral multiplication. These viruses obtain their lipid envelope from the endoplasmic reticulum of the infected host cell. Evidence demonstrate that specific lipids determine the phenotypic difference between strains originating from different cell lines and for this reason the CC carried out a study to better understand the lipid composition of the viral membranes of these strains. Results showed that for the same viral protein batches from mammal cells contain at least 1.6 times more cholesterol than the batches cultivated from insect cells. Should this hypothesis be confirmed by the presence of further differences observable in the amount and type of lipids at the level of the viral envelope, the potential pathogenetic determinants of the Zika virus at the human placenta level could be better defined. The identification of these factors would make it possible not only to identify additional markers of Zika placental tropism, but would help to define a possible correlation between the role of lipids and the mother-fetus vertical transmission of this virus.</p>
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***ToR : To propose or develop methods and procedures that facilitate harmonisation of international standards and guidelines applicable to the designated specialty***

**2. Proposal or development of any procedure that will facilitate harmonisation of international regulations applicable to the surveillance and control of animal diseases, food safety or animal welfare**

Proposal title	Scope/Content	Applicable area
xx	xx	<input type="checkbox"/> Surveillance and control of animal diseases <input type="checkbox"/> Food safety <input type="checkbox"/> Animal welfare

***ToR: To establish and maintain a network with other OIE Collaborating Centres designated for the same specialty, and should the need arise, with Collaborating Centres in other disciplines***

***ToR: To carry out and/or coordinate scientific and technical studies in collaboration with other centres, laboratories or organisations***

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

Yes

Name of OIE CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose

Aedes Invasive Mosquitoes (AIM-COST)	Europe	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	<p>COST Action CA17108. A transboundary network across Europe to establish a cost effective management of the risk of introduction and spread of Exotic Invasive Aedes Mosquito Borne Viruses.</p> <p>Partners from 19 countries.</p>
Versatile Emerging Infectious Disease Observatory (VEO)	Europe	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	<p>VEO's vision is to establish a versatile emerging infectious diseases forecasting, nowcasting, and tracking system that serves as an interactive virtual observatory for the generation and distribution of high-quality actionable information for evidence-based early warning, risk assessment and monitoring of emerging infectious disease (EID) threats by public health actors and researchers in the One Health domain. Funded by the European Union's Horizon 2020 research and innovation programme under grant agreement No. 874735.</p> <p>20 partners from 12 European countries.</p>
National Centre for Foreign Animal Disease of the Canadian Food Inspection Agency (NCFAD)	Winnipeg (Canada)	<input type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input type="checkbox"/> Europe <input type="checkbox"/> Middle East	<p>Research studies focusing, among the others, on investigating zoonotic viral agents including animal influenza viruses</p>

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

Yes

Name of OIE CC/RL/other organisation(s)	Location	Region of networking Centre	Purpose
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<p>Medical Research Council, University of Glasgow Centre for Virus Research - CVR</p> <p>(OIE CC Viral Genomics and Bioinformatics)</p>	<p>Glasgow (United Kingdom)</p>	<p><input type="checkbox"/>Africa <input checked="" type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input checked="" type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>OIE-ad hoc group on high throughput sequencing,</p> <p>Bioinformatics and computational Genomics (HTS-BCG).</p>
<p>Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna "Bruno Ubertini"- IZSLER</p> <p>(OIE CC Veterinary Biologicals Biobank)</p>	<p>Brescia (Italy)</p>	<p><input type="checkbox"/>Africa <input checked="" type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input checked="" type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>OIE-ad hoc group on high throughput sequencing,</p> <p>Bioinformatics and computational Genomics (HTS-BCG).</p>
<p>Australian Animal Health Laboratory</p> <p>; CSIRO Livestock Industries (OIE CC Laboratory Capacity Building)</p>	<p>Victoria (Australia)</p>	<p><input type="checkbox"/>Africa <input type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>OIE-ad hoc group on high throughput sequencing,</p> <p>Bioinformatics and computational Genomics (HTS-BCG).</p>
<p>Irish Equine Centre (IEC)(OIE RL for equine influenza)</p>	<p>Kildare (Ireland)</p>	<p><input type="checkbox"/>Africa <input checked="" type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input checked="" type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>FAO-OIE Advisory Group on viral evolution of SARS-CoV-2 in animals.</p>
<p>Royal Veterinary College (RVC)</p> <p>(OIE CC for Risk Analysis &amp; Modelling)</p>	<p>London (UK)</p>	<p><input type="checkbox"/>Africa <input checked="" type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input checked="" type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>FAO-OIE Advisory Group on viral evolution of SARS-CoV-2 in animals.</p>
<p>Val d'Hebron University Hospital (Spain)</p> <p>ZIKAction, Horizon2020 - Grant Agreement 734857 of the EU Commission DG for research and innovation</p>	<p>France</p>	<p><input type="checkbox"/>Africa <input checked="" type="checkbox"/>Americas <input checked="" type="checkbox"/>Asia and Pacific <input checked="" type="checkbox"/>Europe <input type="checkbox"/>Middle East</p>	<p>Interdisciplinary program of research studies to address key knowledge gaps related to ZIKA epidemiology, natural history and pathogenesis, focusing on maternal and child health.</p>

PRIMA CALL - Medirab	Spain, Tunisia, Morocco, Italy	<input checked="" type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Strategies for the control of Lyssaviruses in North African Mediterranean countries and the prevention of importation into Europe.
BIO-CRIME Interreg VA Italy-Austria	Austria, Italy	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Implementation of joint actions and policy exchanges to fight against zoonoses and illegal pet trade.
<p>Global Laboratory Leadership Programme (GLLP)</p> <p>FAO- OIE -WHO;</p> <p>The Association of Public Health Laboratories (APHL);</p> <p>The Centers for Disease Control and Prevention (CDC);</p> <p>The European Centre for Disease Prevention and Control (ECDC)</p>	Worldwide	<input checked="" type="checkbox"/> Africa <input checked="" type="checkbox"/> Americas <input checked="" type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input checked="" type="checkbox"/> Middle East	To outline the essential competencies needed by laboratory leaders to build and direct sustainable national laboratory systems for disease detection, control and prevention. To ensure a multisectoral One Health approach addressing the entire laboratory system that includes human, animal, environmental, agricultural, food, aquatic and chemical laboratories in support of health systems.
EUREGIO Project - ConBAT, Combining BAT Conservation and spillover Control	Italy	<input type="checkbox"/> Africa <input type="checkbox"/> Americas <input type="checkbox"/> Asia and Pacific <input checked="" type="checkbox"/> Europe <input type="checkbox"/> Middle East	Investigating the ecology of Myotis myotis throughout the EUREGIO area with the aim of studying LYSV.

**ToR: To place expert consultants at the disposal of the OIE.**

**5. Did your Collaborating Centre place expert consultants at the disposal of the OIE?**

Yes

Name of expert	Kind of consultancy	Subject
Monne Isabella	Meeting of the FAO-OIE Advisory Group on viral evolution of SARS-CoV-2 in animals	<p>Purpose of the group is to advise on risks related to the evolution of SARS-CoV-2 in animal populations, in addition to liaising with the WHO viral evolution group.</p> <p>Specifically: to monitor and assess the latest information on SARS-CoV-2 viral evolution in animals; keep an inventory of observed mutations and assess their implications for animal and/or public health; list knowledge gaps and priority research areas in relation to SARS-CoV-2 viral evolution</p>

***ToR: To provide, within the designated specialty, scientific and technical training to personnel from OIE Member Countries***

**6. Did your Collaborating Centre provide scientific and technical training, within the remit of the mandate given by the OIE, to personnel from OIE Member Countries?**

Yes

- a) Technical visits: 0
- b) Seminars: 2
- c) Hands-on training courses: 0
- 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
B	On-line course: "Arthropod vectors of pathogens to humans and animals: mosquitoes"	Italy	338
B	On-line course: "Arthropod vectors of pathogens to humans and animals: ticks"	Italy	340

***ToR: To organise and participate in scientific meetings and other activities on behalf of the OIE***

**7. Did your Collaborating Centre organise or participate in the organisation of scientific meetings on behalf of the OIE?**

No

**ToR: To collect, process, analyse, publish and disseminate data and information relevant to the designated specialty**

**8. Publication and dissemination of any information within the remit of the mandate given by the OIE that may be useful to Member Countries of the OIE**

a) Articles published in peer-reviewed journals: 36

Parry R, Naccache F, Ndiaye EH, Fall G, Castelli I, Lühken R, Medlock J, Cull B, Hesson JC, Montarsi F, Failloux AB, Kohl A, Schnettler E, Diallo M, Asgari S, Dietrich I, Becker SC. Identification and RNAi Profile of a Novel Iflavirus Infecting Senegalese *Aedes vexans arabiensis* Mosquitoes. *Viruses*. 2020 Apr 14;12(4):440.

Pacienti M, Sinigaglia A, Franchin E, Pagni S, Lavezzo E, Montarsi F, Capelli G, Barzon L. Human West Nile Virus Lineage 2 Infection: Epidemiological, Clinical, and Virological Findings. *Viruses*. 2020 Apr 18;12(4):458.

Fornasiero D, Mazzucato M, Barbujani M, Montarsi F, Capelli G, Mulatti P. Inter-annual variability of the effects of intrinsic and extrinsic drivers affecting West Nile virus vector *Culex pipiens* population dynamics in northeastern Italy. *Parasit Vectors*. 2020 May 29;13(1):271.

Panarese R, Iatta R, Latrofa MS, Zatelli A, Ćupina AI, Montarsi F, Pombi M, Mendoza-Roldan JA, Beugnet F, Otranto D. Hyperendemic *Dirofilaria immitis* infection in a sheltered dog population: an expanding threat in the Mediterranean region. *Int J Parasitol*. 2020 May 29;S0020-7519(20)30114-4.

Boccolini D, Menegon M, Di Luca M, Toma L, Severini F, Marucci G, D'Amato S, Caraglia A, Maraglino FP, Rezza G, Romi R, Gradoni L, Severini C; Italian Malaria Surveillance Group. Non-imported malaria in Italy: paradigmatic approaches and public health implications following an unusual cluster of cases in 2017. *BMC Public Health*. 2020 Jun 5;20(1):857.

Simonato G, Marchiori E, Marcer F, Ravagnan S, Danesi P, Montarsi F, Bononi C, Capelli G, Pietrobelli M, Cassini R. Canine Leishmaniosis Control through the Promotion of Preventive Measures Appropriately Adopted by Citizens. *Journal of Parasitology research*. 2020. Article ID 8837367:7.

Buezo Montero S, Gabrieli P, Montarsi F, Borean A, Capelli S, De Silvestro G, Forneris F, Pombi M, Breda A, Capelli G, Arcà B. IgG Antibody Responses to the *Aedes albopictus* 34k2 Salivary Protein as Novel Candidate Marker of Human Exposure to the Tiger Mosquito. *Front Cell Infect Microbiol*. 2020 Jul 29;10:377.

Pombi M and Montarsi F. Mosquitoes (Culicidae) for the Encyclopedia of Infection and Immunity. 2020, doi.org/10.1016/B978-0-12-818731-9.00019-7.

Lazzarini L, Barzon L, Foglia F, Manfrin V, Pacienti M, Pavan G, Rattu M, Capelli G, Montarsi F, Martini S, Zanella F, Padovan MT, Russo F, Gobbi F. First autochthonous dengue outbreak in Italy, August 2020. *Euro Surveill*. 2020 Sep;25(36):2001606.

Simonato, G., Danesi, P., Regalbono, A.F.D., Dotto, G., Tessarin, C., Pietrobelli, M., Pasotto, D. Surveillance of zoonotic parasites in animals involved in animal-assisted interventions (AAIS)(2020) *International Journal of Environmental Research and Public Health*, 17 (21), art. no. 7914, pp. 1-11.

Danesi, P., Falcaro, C., Dukik, K., Jiang, Y., Rizzoli, A.P., Allavena, R., Simpson, V., Ravagnan, S., Zanardello, C., Capelli, G., de Hoog, G.S. Molecular Diagnosis of *Emmonsia*-Like Fungi Occurring in Wild Animals. (2020) *Mycopathologia*, 185 (1), pp. 51-65.

Masuda, M., Jagielski, T., Danesi, P., Falcaro, C., Bertola, M., Krockenberger, M., Malik, R., Kano, R. Protothecosis in Dogs and Cats—New Research Directions. (2020) *Mycopathologia*.

Simonato, G., Marchiori, E., Marcer, F., Ravagnan, S., Danesi, P., Montarsi, F., Bononi, C., Capelli, G., Pietrobelli, M., Cassini, R. Canine Leishmaniosis Control through the Promotion of Preventive Measures Appropriately Adopted by Citizens (2020) *Journal of Parasitology Research*. art. no. 8837367.

Cocchetto A., Briola C., Furlanello T., Danesi P., Ciria A., 6 and Menchetti M. 3-T MRI of protothecosis encephalic lesions in a Scottish shepherd dog. *Veterinary Record Case Reports*. DOI: 10.1136/vetreccr-2020-001145.

Bertasio C, Boniotti MB, Lucchese L, Ceglie L, Bellinati L, Mazzucato M, Furlanello T, D'Incau M, Natale A. Detection of New *Leptospira* Genotypes Infecting Symptomatic Dogs: Is a New Vaccine Formulation Needed? *Pathogens*. 2020 Jun 18;9(6):484. doi: 10.3390/pathogens9060484.PMID: 32570803

Iatta R, Trerotoli P, Lucchese L, Natale A, Buonavoglia C, Nachum-Biala Y, Baneth G, Otranto D. Validation of a new immunofluorescence antibody test for the detection of *Leishmania infantum* infection in cats. *Parasitol Res*. 2020 Apr;119(4):1381-1386. doi: 10.1007/s00436-020-06627-1. Epub 2020 Feb 27.PMID: 32107620

Morosetti G, Toson M, Trevisiol K, Idrizi I, Natale A, Lucchese L, Michelutti A, Ceschi P, Lorenzi G, Piffer C, Fiorentino E, Bongiorno G, Gradoni L. Canine leishmaniosis in the Italian northeastern Alps: A survey to assess serological prevalence in dogs and distribution of phlebotomine sand flies in the Autonomous Province of Bolzano - South Tyrol, Italy. *Vet Parasitol Reg Stud Reports*. 2020 Jul;21:100432. doi: 10.1016/j.vprsr.2020.100432. Epub 2020 Jul 4.PMID: 32862903

Lucchese L, Ravagnan S, Da Rold G, Toniolo F, Wurzbürger W, Mion M, Carminato A, Fournier PE, Capelli G, Natale A, Vascellari M. Survival of *Rickettsia conorii* in artificially contaminated whole and leukoreduced canine blood units during the storage period. *Parasit Vectors*. 2020 Apr 21;13(1):118. doi: 10.1186/s13071-020-3991-9.PMID: 32312308

Basurco A, Natale A, Capello K, Fernández A, Verde MT, González A, Yzuel A, Giner J, Villanueva-Saz S. Evaluation of the performance of three serological tests for diagnosis of *Leishmania infantum* infection in dogs using latent class analysis. *Rev Bras Parasitol Vet*. 2020 Dec 4;29(4):e018020. doi: 10.1590/S1984-29612020105. eCollection 2020.PMID: 33295380

Iatta R, Natale A, Ravagnan S, Mendoza-Roldan J, Zatelli A, Cavalera MA, Nachum-Biala Y, Baneth G, Otranto D. Zoonotic and vector-borne pathogens in tigers from a wildlife safari park, Italy. *Int J Parasitol Parasites Wildl*. 2020 Mar 28;12:1-7. doi: 10.1016/j.ijppaw.2020.03.006. eCollection 2020 Aug.PMID: 32280584

Ades, A. E., Soriano-Arandes, A., Alarcon, A., Bonfante, F., Thorne, C., Peckham, C. S., & Giaquinto, C. (2020). Vertical Transmission of Zika Virus and Its Outcomes: A Bayesian Synthesis of Prospective Studies. *The Lancet Infectious Diseases*. [https://doi.org/10.1016/S1473-3099\(20\)30454-0](https://doi.org/10.1016/S1473-3099(20)30454-0).

Cavicchio, L., Tassoni, L., Laconi, A., Cunial, G., Gagliazzo, L., Milani, A., Campalto, M., Di Martino, G., Forzan, M., Monne, I., & Beato, M.S. (2020). Author Correction: Unrevealed genetic diversity of GII Norovirus in the swine population of North East Italy. *Scientific Reports*, 10, 12522.

Cavicchio, L., Tassoni, L., Zamperin, G., Campalto, M., Carrino, M., Leopardi, S., Benedictis, P.D., & Beato, M.S. (2020). Unexpected Genetic Diversity of Two Novel Swine MRVs in Italy. *Viruses*, 12

Gallocchio, F., Biancotto, G., Moressa, A., Pascoli, F., Pretto, T., Toffan, A., Arcangeli, G., Montesi, F., Peters, R., & Ricci, A. (2020). Bioaccumulation and in vivo formation of titanium dioxide nanoparticles in edible mussels. *Food Chemistry*, 323, 126841. doi: <https://doi.org/10.1016/j.foodchem.2020.126841>

Giobbe, G., Bonfante, F., Zambaiti, E., Gagliano, O., Jones, B., Luni, C., Laterza, C., Perin, S., Stuart, H., Pagliari, M., Bortolami, A., Mazzetto, E., Manfredi, A., Colantuono, C., Filippo, L., Pellegata, A., Li, V., Eaton, S., & Thapar, N. (2020). SARS-CoV-2 infection and replication in human fetal and pediatric gastric organoids.

Laconi, A., Cavicchio, L., Tassoni, L., Cunial, G., Milani, A., Ustulin, M., Di Martino, G., Forzan, M., Campalto, M., Monne, I., & Beato, M.S. (2020). Identification of two divergent swine Noroviruses detected at the slaughterhouse in North East Italy. *Porcine health management*, 6, 9-020-00147-1. eCollection 2020.

Leopardi, S.; Priori, P.; Zecchin, B.; Zamperin, G.; Milani, A.; Tonon, F.; Giorgiutti, M.; Beato, M.S.; Benedictis, P. De Interface between Bats and Pigs in Heavy Pig Production. *Viruses* 2021, 13, 1–18, doi:<https://dx.doi.org/10.3390/v13010004>.

Leopardi, S., Terregino, C., & Paola, D.B. (2020). Silent circulation of coronaviruses in pigs. *Veterinary Record*, 186, 323-323. doi:10.1136/vr.m932

Mazzetto, E., Bortolami, A., Fusaro, A., Mazzacan, E., Maniero, S., Vascellari, M., Beato, M.S., Schiavon, E., Chiapponi, C., Terregino, C., Monne, I., & Bonfante, F. (2020). Replication of Influenza D Viruses of Bovine and Swine Origin in Ovine Respiratory Explants and Their Attachment to the Respiratory Tract of Bovine, Sheep, Goat, Horse, and Swine. *Frontiers in Microbiology*, 11, 1136.

Padoan, A., Bonfante, F., Sciacovelli, L., Cosma, C., Basso, D., & Plebani, M. (2020). Evaluation of an ELISA for SARS-CoV-2 antibody testing: clinical performances and correlation with plaque reduction neutralization titer. *Clinical chemistry and laboratory medicine*, DOI: <https://doi.org/10.1515/cclm-2020-1096>

Padoan, A., Zuin, S., Cosma, C., Basso, D., Plebani, M., Bonfante, F. (2020). Clinical performances of an ELISA for SARS-CoV-2 antibody assay and correlation with neutralization activity. *Clinica Chimica Acta*. <https://doi.org/10.1016/j.cca.2020.08.024>

Padoan, A., Bonfante, F., Pagliari, M., Bortolami, A., Negrini, D., Zuin, S., Bozzato, D., Cosma, C., Sciacovelli, L., Plebani, M. (2020). Analytical and clinical performances of five immunoassays for the detection of SARS-CoV-2 antibodies in comparison with neutralization activity. *EBioMedicine*, 62, 103101.

Shittu, I., C. A. Meseko, L. P. Sulaiman, B. Inuwa, M. Mustapha, P. S. Zakariya, A. A. Muhammad, U. Muhammad, Y. J. Atuman, I. J. Barde, B. Zecchin, E. G. Quaranta, D. Shamaki, O. Alabi, I. Monne, A. Fusaro, and T. M. Joannis. Fatal multiple outbreaks of equine influenza H3N8 in Nigeria, 2019: The first introduction of Florida clade 1 to West Africa. *Vet. Microbiol.* 248:108820. 2020.

Schwarz, E.R., Oliveira, L.J., Bonfante, F., Pu, R., Pozor, M.A., Maclachlan, N.J., Beachboard, S., Barr, K.L., & Long, M.T. (2020). Experimental Infection of Mid-Gestation Pregnant Female and Intact Male Sheep with Zika Virus. *Viruses*, 12, 10.3390/v12030291.

Zucca P, Rossmann MC, Osorio JE, Karem K, De Benedictis P, Haißl J, De Franceschi P, Calligaris E, Kohlweiß M, Meddi G, Gabrutsch W, Mairitsch H, Greco O, Furlani R, Maggio M, Tolomei M, Bremini A, Fischinger I, Zambotto P, Wagner P, Millard Y, Palei M, Zamaro G. (2020). The "Bio-crime model" of cross-border cooperation among Veterinary Public Health, Justice, Law Enforcements and Customs to tackle the Illegal Animal Trade/Bio-terrorism and prevent the spreading of Zoonotic Diseases among Human Population. *Frontiers in Veterinary Science*, 7, 855.

Turchetto, S, Obber, F, Rossi, L, D'Amelio S, Cavallero S, Poli, A, Parisi, F, Lanfranchi, P, Ferrari N, Dellamaria, D, Citterio, CV. Sarcoptic Mange in Wild Caprinae of the Alps: Could Pathology Help on Filling the Gaps in Knowledge. *Front. Vet Sci.* 2020 7:193

b) International conferences: 0

c) National conferences: 0

d) Other

(Provide website address or link to appropriate information): 41  
Youtube and facebook, contents produced by IZSve (Italian)

De Benedictis, P., Leopardi, S. "Are bats really harmful to other species?" (Quanto sono davvero pericolosi i pipistrelli)

[https://www.youtube.com/watch?time\\_continue=6&v=3FNQjYV98AY&feature=emb\\_logo](https://www.youtube.com/watch?time_continue=6&v=3FNQjYV98AY&feature=emb_logo)

<https://www.facebook.com/izsvenezie/posts/2689918081326445>

Leopardi, S. "Wuhan novel Coronavirus: how does an epidemic start?" (Wuhan novel Coronavirus: come nasce un'emergenza epidemica)

<https://www.facebook.com/izsvenezie/posts/2552512441733677>

<https://www.linkedin.com/feed/update/urn:li:activity:6628558795029139456/>

Beato, MS. "Hunting for Mammalian orthoreovirus (MRV) in bats, swine and humans" (A caccia di Mammalian orthoreovirus (MRV) tra pipistrelli, suini e uomo)

<https://www.facebook.com/izsvenezie/posts/2709767662674820>

<https://www.linkedin.com/feed/update/urn:li:activity:6691286476061196288/>

News in the IZSve website

Update on the genetic characteristics of SARS-CoV-2 identified in Veneto Region (Aggiornamento sulle caratteristiche genetiche di SARS-CoV-2 identificati in Veneto)

<https://www.izsvenezie.it/caratteristiche-genetiche-sars-cov-2-veneto-novembre-2020/>

Sequencing of the SARS-CoV-2 genome belonging to the cluster of viruses identified in Serbia (Sequenziamento del genoma di SARS-CoV-2 appartenenti al cluster dei virus identificati in Serbia)

<https://www.izsvenezie.it/sequenziamento-genoma-sars-cov2-cluster-serbia/>

COVID-19, mosquitoes do not transmit the virus (COVID-19, le zanzare non trasmettono il virus)

<https://www.izsvenezie.it/covid-19-le-zanzare-non-trasmettono-il-virus/>

The genome of the SARS-CoV-2 virus circulating in Veneto has been sequenced (Sequenziato il genoma del virus SARS-CoV-2 circolante in Veneto) <https://www.izsvenezie.it/sequenziato-genoma-virus-sars-cov-2-veneto/>

Case of a Belgian cat positive for SARS-CoV2 (Caso di un gatto belga positivo per SARS-CoV2)

<https://www.izsvenezie.it/caso-gatto-belga-positivo-sars-cov2/>

New Coronavirus and pets: frequently asked questions and useful information (Nuovo Coronavirus e animali da compagnia: domande frequenti e informazioni utili) <https://www.izsvenezie.it/coronavirus-animali-da-compagnia/>

How much does the tiger mosquito bite? The immune response as an indicator of human exposure to the insect (Quanto punge la zanzara tigre? La risposta immunitaria come indicatore dell'esposizione umana all'insetto)

<https://www.izsvenezie.it/quanto-punge-la-zanzara-tigre/>

What happens to mosquitoes in winter? An app can help you find out (Che fine fanno le zanzare d'inverno?)

Un'app può aiutare a scoprirlo <https://www.izsvenezie.it/zanzare-inverno-mosquito-alert-app/>

IZSve press release - 02/2020

The IZSve laboratories already operational for analyse Covid-19 swabs (I laboratori dell'IZSve già operativi per le analisi Covid-19 sui tamponi)

<https://www.izsvenezie.it/documenti/comunicazione/area-stampa/comunicati-stampa/2020/CS-02-2020-tamponi-coronavirus.pdf>

Media contents produced by other editors (Italian) De Benedictis, P. (edited by ABOUTPHARM) "Humans, bats and other animals in the time of coronavirus" (Uomini, pipistrelli e altri animali ai tempi del coronavirus)

<https://www.aboutpharma.com/blog/2020/04/27/uomini-pipistrelli-e-altri-animali-ai-tempi-del-coronavirus/>

De Benedictis, P. (edited by Radio3 Scienza) "Coronavirus infection in minks" (Il visone che non ti aspetti)

<https://www.raipplayradio.it/audio/2020/11/Il-visone-che-non-ti-aspetti-cda9b1d0-8f21-4463-8bb8-56093b99d828.html>

De Benedictis, P. (edited by CafeTV24) "Coronavirus" (Stammi bene - Il coronavirus),

<https://www.youtube.com/watch?v=KZS752Em5Io>

Leopardi, S. (edited by "Alto Adige")

"All you need to know about bats, disease and coronavirus" (Pipistrelli e Covid-19, tutto quello che bisogna sapere)

<https://www.altoadige.it/cultura-e-spettacoli/pipistrelli-e-covid-19-tutto-quello-che-bisogna-sapere-1.2314069>

Leopardi, S. (edited by "Radio Popolare" - 10/2/2020)

"Consider the Armadillo - Relationship between bats and coronavirus" (Che relazione c'è tra coronavirus e pipistrelli?)

<https://www.radiopopolare.it/che-relazione-ce-tra-coronavirus-e-pipistrelli/>

Leopardi, S. (edited by RAI3 - 28/4/2020)

TGR Leonardo

Coronavirus and bats (Coronavirus e pipistrelli)

<https://www.rainews.it/tgr/rubriche/leonardo/index.html?/tgr/video/2020/04/ContentItem-8f5b7f0b-8cac-41b8-be90-46a41c985aab.html>

Leopardi, S (edited by Focus)

"Give it to the greaser" (Dagli all'untore)

<https://www.izsvenezie.it/documenti/comunicazione/area-stampa/rassegna-stampa/2020/2020-04/2020-04-focus.pdf>

Leopardi, S. (edited by Le Scienze)

“The next spillover” (Il prossimo spillover)

<https://www.izsvenezie.it/documenti/comunicazione/area-stampa/rassegna-stampa/2020/2020-05/2020-05-le-scienze.pdf>

Leopardi, S. (edited by ASVIS, association for the sustainable development)

“The Sustainable Development Festival 2020. One health: towards a new vision of health”

<https://www.radioradicale.it/scheda/617570>

Leopardi, S. (edited by “Radio Popolare”)

“Consider the Armadillo” (M’ammalia 2020 – CONSIDERA L’ARMADILLO – noi e altri animali)

<https://www.mammiferi.org/progetti/mammalia-settimana-dei-mammiferi/mammalia-2020-2/>

<https://www.mammiferi.org/eventi/mammalia-2020-virus-autostoppisti-della-biosfera-2/>

Leopardi, S. (edited by MUSE – Science Museum in Trento)

“Bats, fears and pandemics” (M’ammalia 2020 – PPP: pipistrelli, paure e pandemie)

<https://www.mammiferi.org/eventi/mammalia-2020-ppp-pipistrelli-paure-e-pandemie-2/>

Terregino, C. (edited by “Venerdì di Repubblica”)

“Gorillas also at risk from coronavirus” (Povero gorilla ci mancava la paura dell’epidemia)

<https://www.izsvenezie.it/documenti/comunicazione/area-stampa/rassegna-stampa/2020/2020-10/2020-10-02-venedi-repubblica.pdf>

Ricci, A. e Terregino, C. (edited by del “Corriere del Veneto”)

Research in Veneto Region: new coronavirus is not transmitted through mosquito bites (Coronavirus in Veneto, ricerca sulle zanzare: non trasmettono il virus)

[https://corrieredelveneto.corriere.it/veneto/cronaca/20\\_giugno\\_26/ricerca-zanzarenon-trasmettono-virusche-non-piu-debole-e1ebb962-b786-11ea-ba74-dd0d825f1870.shtml](https://corrieredelveneto.corriere.it/veneto/cronaca/20_giugno_26/ricerca-zanzarenon-trasmettono-virusche-non-piu-debole-e1ebb962-b786-11ea-ba74-dd0d825f1870.shtml)

Ricci, A. e Terregino, C. (edited by A3 News)

COVID-19 Not Transmitted by Mosquitoes (Le zanzare non trasmettono il coronavirus)

<https://www.youtube.com/watch?v=d-xabGu-g3U>

Monne, I. (edited by RAI 3 - 19/11/2020)

Why do we sequence coronaviruses?

<https://www.rainews.it/tgr/veneto/notiziari/index.html?tgr/video/2020/11/ContentItem-7de021bd-374e-4153-9ef4-fbe2717de99d.html>

Fusaro, A. (edited by RAI 3 - 22/12/2020)

New Covid-19 mutation is unlikely to have an impact on vaccine efficacy

<https://www.rainews.it/tgr/veneto/notiziari/index.html?tgr/video/2020/12/ContentItem-b54408da-af4d-44b7-90d5-d0a4efba0ecf.html>

Other Links:

Links

NRL and OIE Collaborating Centre for diseases at the Animal/Human Interface (IZSVE)

<http://www.izsvenezie.com/reference-laboratories/diseases-at-the-animalhuman-interface/>

IZSVE, Next Generation Sequencing (NGS): sezione dedicate alle attività di sequenziamento e in particolare alle attività su SARS-CoV-2

<https://www.izsvenezie.it/sequenziato-genoma-virus-sars-cov-2-veneto/>

<https://www.izsvenezie.it/sequenziamento-genoma-sars-cov2-cluster-serbia/>

IZSVE’s section on bats (Italian)

<https://www.izsvenezie.it/temi/animali/pipistrelli/>

National reference centre for animal assisted intervention (pet therapy)

<http://www.izsvenezie.com/reference-laboratories/pet-therapy/>

ZikAction - Preparedness, research and action network on maternal-paediatric axis of Zika virus infection in Latin America and the Caribbean

<http://penta-id.org/news.html>

Interreg V A Italy-Austria "BIO CRIME"  
<http://www.biocrime.org/>

CHAFEA/2016/BTSF/03: Organisation and implementation of training activities on controls of movements of dogs and cats  
<http://www.foodinfo-europe.com/training-programs/modc2017-2019>

### **9. Additional comments regarding your report:**

During 2020, IZSVe staff did not participate in any national and international conferences due to the persistence of the health emergency linked to COVID-19. All communication and dissemination activities are carried out remotely and added in section d) Other.