WOAH Collaborative Centre Reports Activities 2025

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CENTRE INFORMATION

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TOR 1 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
		The PAIR project (Pandemic Information to Support Rapid Response, GA 101133191), funded under HORIZON-HLTH-2023-TOOL-05-08 (HORIZON Innovation Action), officially started in January 2024 with a kick-off meeting in Copenhagen and involves 20 partners from seven countries. PAIR aims to strengthen European pandemic preparedness and response by integrating rapid, reliable diagnostics with advanced predictive modelling within a One Health framework. The project develops two interconnected technological pillars. The first is PANPOC, a portable point-of-care diagnostic system based on RT-LAMP for rapid detection of respiratory RNA viruses with pandemic potential, including human Influenza A, avian influenza virus (AIV), swine influenza A virus (IAV-S/SIV), influenza B, and betacoronaviruses (bCoV) such as SARS-CoV-2 variants and emerging strains. PANPOC will be validated using animal, environmental, and clinical

Disease control (true)	PAIR Project – “PAndemic Information to support rapid Response”	samples and demonstrated in real end-user settings (hospitals, general practitioners, veterinary and public health authorities, border control points, airports, and other high-risk environments). The second pillar is PANRISK, an AI-based prognostic platform designed to predict the emergence and spread of the target viruses. PANRISK combines a pathogen genomic drifting model, estimating the risk of animal pathogens evolving toward human infectivity, with epidemiological models that forecast geographical and temporal outbreak dynamics. The platform supports a syndromic surveillance framework enabling targeted monitoring of zoonotic disease trends. Social Sciences and Humanities (SSH) contributions address social and health inequities, stakeholder engagement, public trust, policy alignment, and effective dissemination. Within PAIR, the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) leads Work Package 4 (WP4), focused on the validation of PANPOC in veterinary settings for wild and farmed target species, reinforcing the One Health dimension. In support of assay development activities in WP2 (coordinated by DTU), IZSVe provided multiple sequence alignments (MSAs) of betacoronaviruses and avian influenza viruses to support RT-LAMP primer design, and supplied inactivated isolates of AIV and IAV-S for preliminary performance testing of PANPOC. The development of RT-LAMP assays proved technically complex, particularly due to difficulties in identifying conserved genomic regions across bCoVs. This led to a partial adjustment of WP2 objectives, recognizing SARS-CoV-2 as the only prototypical RT-LAMP target within bCoVs for PANPOC. As a consequence, the start of WP4 validation activities, originally planned for June 2025, has been postponed to March 2026, and the WP4 validation scope has been refocused on AIV and swine influenza virus (SIV/IAV-S). In parallel, IZSVe has initiated the in silico development of qRT-PCR protocols to support subtype and lineage characterization of swine influenza viruses, using MSAs representative of viruses detected in Italy between 2020 and 2024. Four assays have been designed for simplex or competitive formats to identify pan-H1, avH1, H1pdm, swH1, huH3, and swH3 targets. Additional assays for N1 and N2 genes and the in vitro validation of all protocols are planned for 2026. These molecular tools will complement PANPOC by enabling detailed characterization of detected viruses and supporting integration with PANRISK models. Furthermore, IZSVe recently published a study on swine influenza in Italy (2013–2022), which revealed high genetic diversity and the emergence of new genotypes. These findings provide a solid scientific basis for the design and validation of novel diagnostic assays, strengthening the PANPOC system and enhancing Europe’s capacity for surveillance, early detection of zoonotic influenza threats, and overall pandemic preparedness.

Epidemiology, surveillance, risk assessment, (true)	Characterization of West Nile Viruses Analyzed in Veneto in 2024–2025	West Nile virus (WNV) is a mosquito-borne Flavivirus endemic in north-eastern Italy, where early detection through effective surveillance is essential to protect vulnerable populations. In this context, genomic characterization of circulating WNV strains was conducted to support surveillance and understand viral introduction and spread dynamics. Between November 2024 and December 2025, 69 WNV-positive samples collected in Veneto and Friuli Venezia Giulia were sequenced using whole-genome targeted PCR followed by Next Generation Sequencing. The dataset included 43 lineage I (WNV1) and 26 lineage II (WNV2) viruses obtained from mosquitoes, birds, and humans. Most samples were collected in Veneto in 2024. Phylogenetic analysis showed that all WNV1 sequences clustered within a single monophyletic group together with strains previously detected in north-eastern Italy (2021–2023), indicating continued local circulation. WNV2 sequences were distributed into four distinct clusters, reflecting multiple co-circulating viral lineages linked to strains previously identified in Italy. Phylogeographic analyses, performed using both discrete and continuous approaches, revealed multiple introductions of WNV1 into Italy from sub-Saharan Africa between 2005 and 2019, followed by regional spread from Veneto to neighbouring regions. In contrast, WNV2 likely entered Italy from Eastern Europe around 2008, initially through Lombardy and subsequently spreading to Veneto and Piedmont. Overall, these findings confirm the sustained endemic circulation of both WNV lineages in north-eastern Italy and highlight the value of genomic surveillance in tracking viral evolution, introduction events, and spatial dissemination.
Zoonoses (true)	INF-ACT Project	The IZSVe contributed to the activties focused on emerging infectious diseases, aimed at monitoring the emergence of novel viruses at the human–animal interface and rapidly identifying potential spillover events from wildlife to humans. Between February and May 2025, tissue sampling was conducted on 30 martens (Martes foina/Martes martes) and 65 badgers (Meles meles) received through passive rabies surveillance. Animals were selected based on prior prevalence of ε-CoV (2.7% in badgers, 16.9% in martens). Samples collected included lung, spleen, intestine, central nervous system, trachea, and oronasal and rectal swabs. Overall prevalence was higher than previously observed: MelesCoV in 10.8% of badgers (7/65) and MartesCoV in 36.6% of martens (11/30), likely due to selection of well-preserved carcasses. Tissue tropism was primarily respiratory: 17/18 infected individuals were positive in the lungs. Spleen was positive in 2 martens and 1 badger, while intestine and CNS were negative in all tested animals. Only one marten showed positivity solely in the spleen. Non-invasive samples showed limited detection: no fecal positives, but 3 tracheal swabs and 1 nasal swab reflected lung positivity. Genetic analysis was also performed. Partial RdRp sequences (120 amino

		acids) of 39 MartesCoV and 15 MelesCoV isolates revealed two host-specific subgroups with high intra-group identity (89.2–100% and 89.9–100%) and 60.7–68.5% inter-group divergence, supporting their classification as distinct species. Viral isolation attempts on MDCK, BHK-21, and Vero cells were unsuccessful: no cytopathic effects observed, and all culture supernatants were negative by nested RT-PCR after six blind passages. Near-complete genomes were obtained by next-generation sequencing from one MartesCoV and two MelesCoV samples. In conclusion, both viruses display respiratory tropism and can be detected via nasal or tracheal swabs. No macroscopic lung lesions were observed, and due to carcass preservation limitations, histological assessment or clinical symptom evaluation was not possible. Consequently, no conclusions can be drawn regarding pathogenicity, and viral isolation attempts did not allow phenotypic characterization.
Wildlife (true)	OneBat Project	The IZSVe leads the OneBAT consortium, which comprises 13 partners from seven countries, exemplifying an interdisciplinary, integrative, and international One Health approach. Project activities have been extensively described in last year's report. In 2025, targeted studies continued to investigate coronavirus and filovirus circulation in the common bent-winged bat (Miniopterus schreibersii). Between June and September, five samplings were conducted at two roosting sites (urban and wild), collecting biological samples from 215 individuals, including 215 oral swabs, 99 faecal samples, and 204 blood clots; all clots tested negative for Lloviu virus (LLOV). Samples from June and August (167 total: 66 faecal, 125 clots) were analysed using pancoronavirus nested RT-PCR and compared with 2024 data. Overall, 220 bats (45.17%) tested positive in at least one sample type: 166 oral swabs (34.08%), 91 fecal samples (45.73%), and 9 clots (1.97%). All positive samples were sequenced, and phylogenetic analysis provided putative taxonomy and insights into viral diversity. Three coronavirus species were detected—HKU7 (18.28%), HKU8 (7.60%), and Miniopterus coronavirus 1 (MinioCoV1, 27.31%), all within the subgenus Minunacovirus. MinioCoV1 and HKU7 were present in all samplings, whereas HKU8 was detected only in September 2024 and late August 2025. Co-circulation was observed, with peak viral shedding occurring after pup birth. The results further clarified coronavirus tropism in this species. Consistent with 2024, MinioCoV1 was predominantly associated with oral swabs (25.26% vs. 5.53% in feces), while HKU7 was mostly found in feces (33.17% vs. 3.70% in swabs). HKU8 prevalence increased in 2025, appearing in 7.04% of fecal samples, 5.13% of oral swabs, and in two blood clots, suggesting a viremic phase similar to HKU7 in 2024. These findings indicate that relying solely on fecal sampling may underestimate viruses with predominantly respiratory tropism, such as MinioCoV1. Air sample collection from the studied

		colonies was standardised according to University of Barcelona protocols (OneBAT partner). These samples will be analysed using virus-specific PCRs, and metagenomic analyses will be conducted with a viral enrichment panel developed within the project. Water samples were also collected and will be analysed following standardisation of the concentration method.
Diagnosis, biotechnology and laboratory (true)	Biobank – EVAg and ISIDORe projects	Since 2019, the IZSVe has actively participated in the European Virus Archive (EVAg) network, an EU-funded initiative aimed at creating a global reference infrastructure for the collection, preservation, and distribution of viruses and related biological materials. In 2024, EVAg evolved into the legal entity EVAg AISBL (Belgium), ensuring long-term operational and scientific continuity. Within this network, the IZSVe contributes cryopreserved animal tissue explants and other biological materials, supporting the international scientific community in developing predictive in vitro and ex vivo models for studying viruses with zoonotic potential. Through EVAg, IZSVe is also involved in the Integrated Services for Infectious Disease Outbreak Research (ISIDORe) project, an EU-funded, three-year initiative launched in 2022 with over 150 partners. IZSVe provides high-translational in vitro models for research on SARS-CoV-2 and Influenza and in vivo model for Sars-Cov-2. Between late 2024 and early 2025, the IZSVe was reconfirmed as a research support entity, supplying reference materials and expertise for antiviral studies. Overall, IZSVe contributions to EVAg and ISIDORe strengthen its role in international infectious disease research, facilitating access to high-quality viral resources and translational models that support the development of antiviral strategies and the study of zoonotic pathogens.
Diagnosis, biotechnology and laboratory (true)	Comparison of panfilovirus methods	Bats are known for their association with a wide variety of viruses with zoonotic potential. For several years, the IZSVe has developed specific expertise in surveillance within this animal reservoir, including broad-spectrum methods capable of identifying even unknown viral species of public health relevance. In addition to lyssaviruses and coronaviruses, for which the CdR has long-standing experience, bats are associated with several species belonging to the family Filoviridae, which includes the epidemic human viruses Marburg and Ebola. Although most filoviruses have been identified in Africa, the Lloviu filovirus (LLOV) is associated with a European bat species, the common bent-wing bat (Miniopterus schreibersii), and has also been detected in Italy. In 2025, we compared several panfilovirus methods available in the literature in order to identify one with high sensitivity and broad spectrum to be introduced into the routine active and passive health surveillance carried out by IZSVe. The activity, conducted within the INTERREG ITA-AUT CABLES project, included an in silico evaluation of five protocols, primarily assessing the

		complementarity between 14 primers and 925 reference sequences of mammalian filoviruses using Geneious Prime software. The three protocols whose primers showed the lowest number of mismatches were selected for in vitro evaluation. The protocols were compared using serial dilutions of total LLOV RNA, testing different reagents and protocols in triplicate. A LLOV-specific qPCR method, characterized by high sensitivity for this virus, was used as the gold standard. Two of the three tested protocols showed sensitivity for LLOV up to 10^{-4}, comparable to the reference test. Evaluation of sensitivity against other filoviruses of relevance is currently ongoing, using an RNA panel provided by the Pasteur Institute in Paris within the Horizon EU One BAT project.
Epidemiology, surveillance, risk assessment, (true)	Characterization of Toscana Viruses analysed in Veneto in 2025	Toscana virus (TOSV) is a sandfly-borne Phlebovirus circulating in the Mediterranean basin and responsible for human neuroinvasive diseases, including meningitis and meningoencephalitis. Increasing sandfly density and geographic expansion heighten the risk of human exposure, underscoring the importance of molecular surveillance. Between November 2024 and December 2025, four TOSV samples collected in Baone (Padua province, Veneto) were sequenced, including three from 2025 and one from 2023. Whole-genome segment analysis (L, M, and S) showed very high genetic similarity among the samples, with nucleotide identity values above 99.5%. Phylogenetic analyses demonstrated that all sequences clustered with Italian strains, particularly those collected in 2023 and 2024, and belonged to lineage A (TOSV-A). Limited genetic divergence was observed, indicating continued local circulation of closely related viral strains. Overall, these results confirm the persistence of TOSV lineage A in Veneto and highlight the value of genomic surveillance in monitoring viral circulation and supporting public health risk assessment.
Epidemiology, surveillance, risk assessment (true)	Characterization of SARS-CoV-2 strains Identified in Veneto between 1 November 2024 to 30 November 2025	Since November 2020, IZSVe has conducted regional surveillance of the genetic variability of SARS-CoV-2 circulating in Veneto. During the reporting period, a total of 569 SARS-CoV-2 sequences were analyzed, including 117 generated directly by the IZSVe, using data from the regional sequencing network, the GISAID database, and the national ISS ICoGen platform. During this period, Omicron was the only variant detected in Veneto, with all sequences belonging to the BA.2.86* lineage and its sublineages. Monthly analysis revealed dynamic changes in circulating sublineages, including several variants classified by the WHO as Variants under Monitoring (VUMs) or Variants of Interest (VOIs). In the early months (November 2024–February 2025), co-circulation of XEC*, KP.3.1.1*, and JN.1* was observed. XEC* was initially predominant but progressively declined and disappeared by July 2025, while KP.3.1.1* and JN.1* also showed fluctuating frequencies before decreasing to low levels. During the same period, two additional VUMs, LP.8.1* and

		NB.1.8.1*, emerged and temporarily increased in frequency before declining. A major shift occurred following the introduction of the recombinant sublineage XFG* in May 2025. This lineage rapidly increased in prevalence, replacing previously circulating variants and reaching nearly 90% of sequenced cases by September 2025. A similar trend was observed at the national level. According to the WHO, XFG* poses a low public health risk, with only marginal additional immune escape compared to LP.8.1*. Recombinant viruses belonging to various lineages were also detected, with monthly frequencies ranging from 0% to 15%. Overall, genomic surveillance confirmed rapid lineage turnover within the Omicron variant in Veneto, highlighting the importance of continuous sequencing efforts to promptly detect emerging variants and support public health risk assessment.
Wildlife (true)	INTERREG CABLES Project	Many bat species are experiencing significant declines due to habitat loss, fragmentation, and disturbance, as well as chemical and light pollution. Emerging threats, such as infectious diseases and climate change—including heat waves, droughts, and rising winter temperatures—further exacerbate these declines. Effective bat conservation requires identifying local and large-scale risk factors and implementing monitoring systems capable of assessing the health of bat populations, integrating environmental and individual-level surveillance in line with One Health principles. The CABLES project (INTERREG ITA-AUS), coordinated by IZSVe in collaboration with the University for Health Sciences, Medical Informatics and Technology (Tirol – UMIT), the University of Padua, and Ecotone, aims to develop an innovative monitoring system for subterranean bats to detect early warning signals of climatic, ecological, and health-related threats. In 2025, presence maps were generated for Myotis myotis and M. blythii, a mixed colony with Miniopterus schreibersii was confirmed in Vittorio Veneto, and 182 individuals were marked with subcutaneous PIT tags and 39 with VHF transmitters to track movements and identify previously unknown hibernation sites. Data indicate high roost fidelity, with periodic movements between sites. Four maternity colonies of Myotis in South Tyrol underwent health surveillance, including collection of oral, skin, and fecal swabs, environmental guano and air samples, and ectoparasites. Coronaviruses, the primary initial target, were detected in five oral swabs and no fecal samples, suggesting that CoVs alone are insufficient indicators for population-level surveillance. Further metagenomic analyses will target additional viral and bacterial agents. Standardized protocols for environmental guano and air sampling were established, and ectoparasites will serve as proxies for blood sampling and to investigate potential cross-species transmission pathways. Diagnostic protocols for bat mortality were also implemented. Seventeen deceased Nyctalus noctula in the province of Udine tested

		negative for lyssaviruses, filoviruses, coronaviruses, and hantaviruses. Histopathology revealed no signs of infectious disease, and the mortalities were attributed to a heatwave, with temperatures exceeding 30 °C prior to the event
Diagnosis, biotechnology and laboratory (true)	RC IZSVe 8/23 – Use of environmental matrices to quantify occupational exposure to antibiotic resistance genes and swine influenza viruses	The project aims to quantify occupational exposure to antibiotic resistance genes (ARGs) and swine influenza A virus (IAV-S) among workers in intensive pig farming systems through an integrated surveillance approach combining biomolecular analyses of animal, human, and environmental samples with Bayesian exposure models. The innovative aspect of the project lies in the environmental surveillance component, which required optimization of sampling and analytical protocols for ARG and IAV-S detection in shared animal–worker environments. Following the optimization of molecular methods for IAV-S detection in 2024, activities in 2025 focused on improving nucleic acid extraction from complex matrices. Four RNA/DNA extraction protocols were compared using artificially contaminated oral fluids and livestock wastewater. Based on qRT-PCR and PCR performance, the ZymoBIOMICS MagBead DNA/RNA system was selected and applied to field samples collected during confirmed IAV-S outbreaks. A total of 122 biological and environmental samples were analyzed across seven IAV-S outbreaks (one in 2024 and six in 2025). Traces of IAV-S RNA were detected in 22 samples from four outbreaks, with consistently low viral loads ($\leq 10^2$ RNA copies/μL). Of the samples showing genomic contamination (n = 6), 22.73% originated from workers, predominantly from hand skin swabs.. DNA extracted from all samples was further analyzed using shotgun metagenomic sequencing to characterize antibiotic resistance determinants. Sequencing was performed on an Illumina NextSeq 550 platform, and resulting data will be used to assess resistome diversity across matrices. In parallel, 16S rRNA gene sequencing will be employed to characterize associated microbial communities and to investigate the relationship between microbiota composition and the resistome, with particular attention to potentially pathogenic taxa.
		Within the One Health framework, the health surveillance of stranded marine mammals and their environment is of critical importance, both in terms of animal and public health—given their potential role as reservoirs or carriers of zoonotic pathogens—and in terms of environmental protection, as these species represent valuable sentinels of marine ecosystem health. Particular attention is warranted for infectious diseases of viral origin, especially those associated with host susceptibility and the expansion of host range, including cross-species transmission (spillover) events involving phylogenetically distant hosts. In this context, the National Reference Centre for Diagnostic Investigations on Stranded Marine Mammals (C.Re.Di.Ma.), based at the Istituto

Zoonoses (true)	The Role of Stranded Marine Mammals at the Human–Animal Interface	Zooprofilattico Sperimentale del Piemonte, Liguria e Valle d'Aosta, proposed a Current Research Project for 2024, supported through joint funding by the Ministry of Health and the Ministry of the Environment and Energy Security. The project, entitled "Strengthening the National Health Surveillance for Influenza A Virus in Stranded Marine Mammals", involves all stranding focal points within the network of Italian Experimental Zooprophylactic Institutes (IIZZSS). Within this framework, the Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe) contributed by conducting virological and serological analyses aimed at detecting influenza virus antigens and/or specific antibodies in selected samples. Furthermore, in 2025, C.Re.Di.Ma. proposed an additional Current Research Project entitled "Determination of Microplastics in Marine and Terrestrial Habitats: Investigation of Different Routes of Uptake and Accumulation in Sentinel Organisms", which requires the participation of the entire national network of IIZZSS. This project has been formally approved, and the planned activities are scheduled to commence in 2026
Epidemiology, surveillance, risk assessment (true)	Entomological surveillance for West Nile and Usutu viruses in Italy	In 2025 (May-October), 87 CDC-CO2 mosquito traps were placed in selected areas (plans areas of Veneto and Friuli Venezia Giulia regions) and a total 117,546 mosquitoes of 18 different species were collected. The main mosquito species caught during the entomological surveillance was Culex pipiens, which is well known to be the primary vector of WNV. Virus detection was done in 2,600 pooled specimens. West Nile virus was detected in 71 tested pools (twenty pools with single infection of WNV-lineage 1, thirty-six pools with single infection of WNV-lineage 2, six pools with double infection of WNV-lineage 1 and lineage 2; four pools with double infection of WNV-lineage 2 and USUV and five pools with double infection of WNV-lineage 1 and USUV). Moreover, 27 other pools tested positive for USUV in single infections. The positive pools belonged to Culex pipiens, but 3 pools of Aedes albopictus tested positive for WNV or USUV, and 2 pools of Aedes caspius tested positive for WNV.
Epidemiology, surveillance, risk assessment (true)	Entomological surveillance in locally-acquired Aedes-borne viral diseases	During the summer of 2025, an autochthonous outbreak of chikungunya was recorded in the province of Verona, involving 14 several municipalities. These were local infections, i.e., caused by the bite of the mosquito species Aedes albopictus (tiger mosquito), which became infected after acquiring the virus from an unidentified imported case. A total of 63 confirmed human cases and 5 suspected cases have been recorded to date. During the epidemiological investigation carried out by the competent authorities, BG-sentinel traps were set up and the trapped mosquitoes were sent to the laboratory for Chikungunya virus investigation. A total of 259 mosquitoes were captured in seven different locations; all mosquitoes tested negative for the Chikungunya virus.
		Monitoring of the entry and spread of invasive

Epidemiology, surveillance, risk assessment (true)	Surveillance of Invasive mosquitoes in “Points of entry"	species of mosquitoes of the genus Aedes in Italy, through the surveillance of selected "Points of entry" (POE) in Veneto and Friuli Venezia Giulia regions, such as the ports of Marghera, Trieste and Monfalcone and the airports of Venice, Verona, Treviso and Triste. Surveillance activities were carried out by the means of ovitraps as well as traps for adult mosquitoes (BG-sentinel traps). A total of 43,401 eggs and 4,127 adult mosquitoes were collected Aedes albopictus species has been collected in all sites, while Ae. koreicus have been found at the port of Monfalcone and Trieste airports. Notably, the average number of Aedes eggs per ovitrap and or adults trapped was generally above the threshold value at all monitored sites, indicating high mosquito densities and difficulties in controlling populations through pest control. Aedes aegypti was not recorded in any selected POEs.
Epidemiology, surveillance, risk assessment (true)	Surveillance of Aedes japonicus japonicus and Aedes koreicus in Italy	The invasive mosquito species, Aedes koreicus, and Ae. 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 at all possible breeding sites by collecting larvae in 50 selected municipalities of the Veneto region (Provinces of Belluno, Verona, Vicenza, and Treviso). The mosquitoes were collected mainly from artificial containers in small villages and rural areas. The mosquitoes were identified by means of morphological identification and biomolecular analysis. Briefly, in 2025 Ae. j. japonicus was found in 28 out of 50 municipalities monitored (56%) and Ae. koreicus in 32 out of 50 (64%), respectively.
Epidemiology, surveillance, risk assessment (true)	Surveillance of sand flies Phlebotomine for Leishmania infantum and Toscana virus	In 2021, the first circulation of Toscana virus (TOSV) (Phlebovirus) was recorded in northeastern Italy, with three human cases and one pool of positive vectors to TOSV found in the same area. In 2025, four sites in the Veneto region (Provinces of Padova and Vicenza) were monitored biweekly, collecting sand flies with CDC-CO2 light traps. Sand flies were tested for TOSV and Leishmania investigation via biomolecular techniques. In total, 1,563 sand flies were collected, and 112 pools were tested; eight pools resulted positive for Toscana Virus (7,1%), confirming the circulation of this pathogen in Phlebotomus perniciosus in the four sites of selected provinces. Then, Leishmania infantum was detected in one pool of P. perniciosus in the province of Padova
Epidemiology, surveillance, risk assessment (true)		Culex pipiens and Aedes albopictus mosquitoes have been collected in three Regions of Italy (Veneto, Friuli Venezia Giulia and Trentino Alto Adige) and tested by molecular techniques to evaluate the insecticide resistance to adulticide pyrethroids. To date, 475 adult Culex pipiens and 502 Aedes albopictus specimens have been individually investigated for genetic markers of insecticide resistance. Overall, the frequency of mutated alleles in Culex pipiens was higher in Veneto (49.3%) than in other regions (Friuli-

	Monitoring of insecticide resistance in mosquitoes	Venezia Giulia: 34.1%; Trentino-Alto Adige: 27.3%), with higher values recorded in the provinces of Padua (58.3%) and Rovigo (65%), where the resistant genotype was prevalent. On the contrary, for Aedes albopictus, frequencies of mutations related to pyrethroid resistance were generally low, below 10% (Veneto: 7.3%, Friuli Venezia Giulia: 2.5%, Trentino Alto Adige: 2.3%), with higher values recorded in the province of Rovigo (20%).
Epidemiology, surveillance, risk assessment (true)	EcoSurv Ecological Surveillance for Zoonotic Threats	The EcoSurv project develops an integrated, comprehensive surveillance system based on a One Health approach for selected emerging, re-emerging, or at-risk zoonoses. Surveillance considers the entire ecosystem (host animals, vectors, and the environment) and applies innovative diagnostic and monitoring approaches. The aim is to collect data useful for defining early warning indicators and supporting the assessment of the risk of introduction or reemergence of zoonotic agents in Italy. Although activities are concentrated in specific areas of Italy (with the exception of sampling for RVF in Libya and Mauritania), the results are relevant for many countries in the EU's Mediterranean region. The project strengthens the capacity for early detection of the introduction and spread of zoonoses, particularly those transmitted by vectors, and promotes closer collaboration between public health, animal health, and environmental protection. Within the project, IZSVe analysed samples for Echinococcus, Borrelia, and Tick-borne encephalitis virus (TBEV). In 2025, 123 Echinococcus samples were analysed. Regarding tick-borne pathogens (Borrelia and TBEV), 200 samples (pools of larvae and nymphs, and individual adults) were analysed up to October 2025. Within WP3, H5N1 surveillance was conducted on environmental samples from five wetlands in Veneto and Friuli Venezia Giulia frequented by overwintering high-risk avian species. A total of 1,909 samples were tested by real-time RT-PCR, of which 328 collected between January and March and September and December were positive. In WP5, metagenomic analyses were performed on 13 samples (tissues, faeces, and oral swabs) from four bat species to identify potential emerging pathogens (pathogen Y). Coronavirus sequences were detected in 10 samples. Additional viral reads (80–90% identity) were related to viruses within the orders Herpesvirales (Betaherpesvirinae, Gammaherpesvirinae), Reovirales (Orbivirus, Rotavirus), and the family Astroviridae (Mamastrovirus). Finally, H5N1 screening was carried out on organs from carnivores collected through rabies surveillance (1 marten, 6 wolves, 25 badgers, and 81 red foxes) during the same seasonal periods. One red fox sampled in October tested positive.
Diagnosis, biotechnology and laboratory (true)	Diagnostic activity for Coxiella burnetii	We tested 4667 ruminant sera, and 551 samples (i.e. aborted foetuses, tank milk) with real-time PCR. We organized a national Proficiency testing for the diagnosis of Q fever by ELISA, CFT and Real Time

		PCR.
Diagnosis, biotechnology and laboratory (true)	Diagnostic activity for Leptospirosis	In 2025, 1360 farm animals' sera, 635 companion animals' Sera with MAT, and 543 samples (i.e. urine, organs, blood, culture) with real-time PCR were tested. We share the strains and the nucleic acids with the National Reference Centre for Leptospirosis (c/o IZLER) for genotyping activities.
Diagnosis, biotechnology and laboratory (true)	EVA AISBL	Since 2025, IZSVe has been part of the Consortium EVA AISBL (Association Internationale Sans But Lucratif), a non-profit organisation that mobilises a global network of experts in virology to collect, amplify, characterise, standardise, authenticate, distribute, and track viruses and derived products. The Consortium is the natural follow-up of EVA Global (H2020)
Diagnosis, biotechnology and laboratory (true)	Partner in: "The WOAH Virtual Biobank: a Web-based Catalogue of Biological Resources"	The scope of the project is to provide a web-based catalogue of biological resources held in Biobanks hosted by OIE's Reference Centres. However, once the OIE Virtual Biobank is operative and functional, other organisations, such as National Reference Laboratories and research institutions, will be able to join the OIE Virtual Biobank's network and expose information on their own biobank materials. This would expand and facilitate the search for and availability of high-value biologicals to the scientific community.
Diagnosis, biotechnology and laboratory (true)	Assessment of in-house libraries for Phlebotomine identification via MALDI-TOF MS	Sand flies (larvae and adults) collected during field activities or in an insectary were collected and manipulated for a preliminary assessment and validation of species identification using MALDI-TOF MS. This approach offers rapid, accurate, and cost-effective species differentiation of these vectors. In 2025, a total of 4,672 analyses were carried out working with P. perniciosus, P. perfiliewi, P. neglectus and Sergentomia minuta.
Zoonoses (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.
Zoonoses (true)	Mammalian Orthoreovirus in companion animals (dogs and cats)	This project arises from the detection of MRVs in pets. To date, the distribution and related health impacts of MRVs in pets remain unclear and need to be elucidated. So far, the pet's role in the transmission of MRVs to other species, including humans, has not been investigated. The project aims to evaluate the circulation of MRV in dogs and cats by screening samples using molecular techniques and cellular isolation, followed by genetic characterisation, sequencing, and phylogenetic analysis of positives. Any possible reassortant strains identified will be compared with human isolates already present in the shared databases, highlighting any potential MRV zoonotic risk. The results will be issued to the scientific community. The dissemination activity will be addressed to physicians' experts in infectious diseases, with a One

		Health perspective, to involve them in early warning and reporting cases of human infection of potential zoonotic origin.
Zoonoses (true)	Partner in: "The global Capnocytophaga consortium: Understanding pathogen evolution and virulence at highest resolution across humans and animals"	Research Project Name: The global Capnocytophaga consortium: Understanding pathogen evolution and virulence at the highest resolution across humans and animals The project is endorsed by four ESCMID study groups: ESGMD, ESGVM, ESGBIES, and ESGICH. This project aims to: (a) build an unprecedentedly large and diverse global strain collection of C. canimorsus, C. canis, C. cynodegmi, and other Capnocytophaga species from different geographical regions and origins (dogs/cats and humans), addressing the one-health nature of this zoonotic disease; (b) to explore pathogen evolution at a global scale by studying spatiotemporal diversity across different clinical settings, such as infection vs. colonisation. (c) To merge geno- and phenotypic data to determine the most critical virulence factors and translate our key findings towards novel diagnostic targets with risk profiling of hyper-virulent strains and the potential identification of therapeutic and vaccine targets for humans and animals. (d) To form a global network to study a neglected infectious disease.
Diagnosis, biotechnology and laboratory (true)	Detection of Trichinella spp. in domestic animals	Swine, equine and wild boars regularly slaughtered (n=5857) have been controlled for the presence of Trichinella spp. larvae in muscle samples. All samples were negative.
Diagnosis, biotechnology and laboratory (true)	Collection and molecular characterization of zoonotic dermatophytes, yeasts and other filamentous fungi of medical interest for animals and humans	Skin specimens from pet and domestic animals(n=648) have been tested for the presence of dermatophytes. Trichophyton mentagrophytes (n=2), Microsporum canis (n=8) and Nannizia gypsea (n=5) were isolated and identified from companion animals (cats n=6; dogs n=2. A total of 319 strains of filamentous fungi (genus Aspergillus, Penicillium, Fusarium, etc.) and yeasts (genus Candida species including C. auris, Debaryomyces, Yarrowia, Cryptococcus spp, Bullera spp., etc.) were molecularly identified at the species level and stored in the fungal collection at the IZSVe.
Diagnosis, biotechnology and laboratory (true)	Development of monoclonal antibodies against Zika virus	Within the framework of the PNRR CN3 Spoke 5 project and in collaboration with the Toscana Life Sciences research center (Siena), ten mice were immunized using different strains of inactivated Zika virus, following a prime–boost immunization protocol. After assessing the antibody titers in immunized animals, bone marrow and spleen were collected for plasma cell isolation. From isolated plasma cells, selected using a purified viral antigen, supernatants containing monoclonal antibodies were obtained and tested using a focus reduction neutralisation test (FRNT) to evaluate their neutralising capacity. Based on the results obtained, the two most promising candidates were selected for purification and further development as potential therapeutic agents for Zika virus infection.

Diagnosis, biotechnology and laboratory (true)	Development of methodologies and antiviral testing	During the year, a methodology for the assessment of influenza virus mutations conferring resistance to neuraminidase inhibitors was validated. Based on genetic analyses, viruses carrying mutations potentially involved in antiviral resistance mechanisms were selected. With regard to neuraminidase inhibitors, the methodology is based on the use of substrates that emit fluorescence upon cleavage by viral neuraminidases. Control viruses provided by the CDC were used for method validation and as references for experimental sessions. In addition, a methodology for the evaluation of viruses potentially resistant to Baloxavir, a viral replication inhibitor, was implemented. The assay (IRINA, Influenza Replication Inhibition Neuraminidase-based Assay) relies on the same principle as neuraminidase activity inhibition assays for the quantification of viral particles and offers the advantage of high-throughput applicability compared with the more labour-intensive classical plaque reduction assays commonly used for this class of compounds.
Epidemiology, surveillance, risk assessment (true)	MONZEC project	The MONZEC project, funded under the INTERREG VI Italy–Austria CLLD Dolomiti Live Programme, aims to monitor tick vectors of pathogens in East Tyrol, the Puster Valley, and the Province of Belluno, involving the hunting community as a territorial network for information, prevention activities, and the study of the impact of climate change on vector-borne infections. ULSS n.1 Dolomiti participates as a project partner together with the Dr. Walder Gernot GmbH Laboratory (lead partner) and the Südtiroler Jagdverband, with scientific support from the Istituto Zooprofilattico Sperimentale delle Venezie in the Belluno area, where structured baseline data were previously lacking. Activities included both passive surveillance (ticks collected from wildlife, animals submitted for necropsy, and domestic animals) and active environmental surveillance through dragging/flagging. All analyzed ticks belonged to the species Ixodes ricinus. Several zoonotic pathogens were investigated, including Borrelia spp., tick-borne encephalitis virus (TBEV), Babesia spp., Rickettsia spp., Anaplasma phagocytophilum, and Francisella tularensis. The results showed the circulation of different Borrelia genospecies, while no samples tested positive for Francisella tularensis. Overall, the project provides the first structured epidemiological overview of tick-borne pathogens in the Belluno area, integrating data from the environment, wildlife, and domestic animals, and laying the groundwork for future assessments of health risks related to climate change.
		The WildArt project aims to evaluate the role of wildlife as an indicator of environmental antimicrobial resistance (AMR). The study focuses on the analysis of the fecal microbiota of resident wild species with different feeding habits, in relation to their use of areas affected by human wastewater discharge. The objective is to contribute to

Epidemiology, surveillance, risk assessment (true)	WildArt project	understanding the relationship between AMR in wildlife and the environmental context in which these animals live. The study includes four sampling sessions over one year to assess possible seasonal variations in AMR levels in areas with different degrees of human impact. Samples consist of wastewater collected at the outlet of treatment plants by the Provincial Department of Belluno of ARPAV, and fecal samples from rodents, foxes, and roe deer collected in surrounding areas by IZSVe. In 2025, a total of 88 fecal samples (41 in summer and 48 in autumn) and 6 water samples were collected. So far, 85 fecal samples and all water samples have been processed on selective media, leading to the isolation of 194 bacterial strains. Samples have been aliquoted and frozen pending further analyses, including determination of minimal inhibitory concentrations (MICs) to confirm resistance profiles. Subsequently, once the main resistance genes have been identified, their quantification will be performed using digital PCR.
Diagnosis, biotechnology and laboratory (true)	Validation of a multiplex Real-Time PCR method for the detection of Echinococcus multilocularis and Echinococcus granulosu	In 2025 was validated a multiplex Real-Time PCR method for the detection of Echinococcus multilocularis and Echinococcus granulosus in feces, intestinal content of carnivores, organs of intermediate hosts, and adult helminths. The method supports monitoring and surveillance of these zoonoses in domestic and wild animal populations and contributes to assessing human exposure risk. The protocol was applied to wildlife surveillance in the Autonomous Province of Bolzano, an area where previous studies had already reported the presence of E. multilocularis. During the study period, 359 fox fecal samples were analyzed, with 8% (28 samples) testing positive for E. multilocularis.
Wildlife (true)	The Role of Small Rodents in the Local Distribution and Epidemiology of Emerging Zoonoses: Echinococcus multilocularis and Hantavirus	The project investigates the role of small rodents in the local distribution of two emerging zoonoses, Echinococcus multilocularis and Hantavirus, by analyzing the relationships between micromammal communities and pathogen presence in Alpine environments. The study is conducted in two main areas: South Tyrol for E. multilocularis and Friuli Venezia Giulia (province of Udine) for Hantavirus. In 2025, a total of 107 small mammals were sampled using live traps: 51 in South Tyrol (Apodemus flavicollis, Myodes glareolus, Microtus lavernedii/arvalis, Apodemus sylvaticus) and 56 in Friuli Venezia Giulia (Apodemus flavicollis, Apodemus sylvaticus). Regarding Echinococcus, all analyzed samples tested negative for E. multilocularis and E. granulosus. In some Arvicola amphibius individuals, liver cysts were observed and later identified as Taenia taeniaeformis. For Hantavirus, 102 samples were analyzed (51 from South Tyrol and 51 from Friuli Venezia Giulia), and all tested negative. Overall, during the study period, neither E. multilocularis nor Hantavirus was detected in the examined rodents, while the presence of non-zoonotic cestodes (Taenia taeniaeformis) was

		documented in some individuals.

TOR 3: 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
CABLES Project Consortium (CAve Bats Linked Ecopatological Surveillance)	Austria Italy	Europa	Interregional Italy–Austria network dedicated to the ecopathological monitoring of cave-dwelling bats, with the aim of studying and preventing ecological, climatic, and health threats. https://interreg.net/en/events-italy-austria/bat-protection-in-the-spotlight/
Istituto Zooprofilattico Sperimentale del Lazio e della Toscana “M. Aleandri	Italy	Europa	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 pathogens: database and bioinformatic analysis/ FAO Reference Centre for Zoonotic Coronaviruses, in collaboration with IZSVe) https://www.fao.org/animal-health/fao-reference-centres/en	Italy	Europa	Serological characterisation of animal sera for the detection of SARS-CoV-2 antibodies in wild mammals
Fondazione Biotecnopolo di Siena			Among the many objectives of the collaboration: i) setting up working groups to draft national and international research projects and related

https://www.biotecnopolo.it/en/	Italy		activities; ii) consultancy and advisory group on different issues and according to the needs; iii) implementing activities of common interest and production of literature
H2020 “OneBAT” Project Consortium : A One Health approach to the study and prevention of bat-borne viral emergencies HORIZON-HLTH-2022-DISEASE-07 https://onebat.eu/	Belgium Cyprus France Hungary Italy Spain Ukraine UK USA	América Europa	Project aim: to explore the complex interaction between host, pathogens, and environment with a view to identifying factors that can trigger viral spillover from European bats to humans or domestic animals
INF-ACT Project Consortium https://www.inf-act.i	Italy	Europa	The INF-ACT research program addresses pressing unmet needs of human emerging infectious diseases in both fundamental as well as translational aspects, taking into consideration human health in a wider context, including domestic and wild animals as potential disease reservoirs and environmental factors enhancing the possibility for spillover (One Health approach).
FAO and IAEA Centre of Nuclear Techniques in Food and Agriculture	Italy Austria	Europa	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
ConVErgence Project consortium: Assessing swine as potential hosts for emerging Coronaviruses - Era-Net ICRAD https://www.icrad.eu/portfolio-items/assessing-swine-as-potential-hosts-for-emerging-coronaviruses/	Italy, The Netherlands, United Kingdom	Europa	Investigating the process of the emergence of coronaviruses in the pig industry, focusing on bats and humans as the most likely sources of infection
H2020 “VERDI” Project Consortium SARS-coV2 variants Evaluation in pRegnancy and paeDIatrics cohorts https://verdiproject.org/the-project/	Belgium, Italy, Israel, France, Switzerland, United Kingdom, South Africa, Thailand, Haiti, USA	África América Asia y el Pacífico Europa Oriente Medio	Improving the understanding of the epidemiology, transmission, disease progression and treatment of variants of SARS-CoV-2 among children and pregnant women
			EVA-AISBL is currently the only research infrastructure in the world dedicated to the collection, characterization, production, and distribution of

EVAg AISBL Project Consortium https://www.european-virus-archive.com/	Worldwide	África América Asia y el Pacífico Europa Oriente Medio	viral resources. It manages unique virus collections and aims to provide researchers in the public and private healthcare sectors with equitable access to high-quality viral resources such as strains, diagnostic tools, and other materials, in full compliance with international regulations.
ISIDORe Project Consortium - Integrated Services for Infectious Disease Outbreak Research European research and innovation programme, H2020 Project https://isidore-project.eu/services/	Worldwide	África América Asia y el Pacífico Europa Oriente Medio	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.
Region of Friuli Venezia Giulia	Italy	Europa	Epidemiological Surveillance Programs in Veterinary Public Health
Province of Bolzano – Hunting and Fishing Office	Italy	Europa	Epidemiological surveillance in veterinary public health
National Centre for Foreign Animal Disease of the Canadian Food Inspection Agency (NCFAD)	Canada	América	Scientific collaboration for the development of projects related to avian influenza and zoonotic diseases
Institute of Microbiology and Immunology – Medical Faculty of Ljubljana	Slovenia	Europa	Scientific cooperation and research activities in microbiology and immunology
European Union Reference Laboratory for Public Health on Vector-borne Viral Pathogens (EURL-PH-VBV)	Italy	Europa	Research collaboration for diagnostic and scientific purposes on arboviruses
			To strengthen the One Health strategy through the development of innovative point-of-care (POC) diagnostic tools and epidemiological modelling Based on past pandemics, PAIR identified respiratory RNA target viruses to be detected: human and animal Influenza A (InfA, AIV and SIV), Influenza B and beta-

PAIR Project Consortium- Pandemic Information to support rapid Response (Horizon EU) https://pairproject.eu/	Denmark Italy France Estonia Spain Turkey Poland Latvia Austria	América Europa Oriente Medio	CoV (SARS-CoV-2 variants and emerging beta-coronaviruses) PAIR develops 2 technologies: PANPOC and PANRISK: PANPOC is a Point-of-Care (POC) instrument for rapid detection of respiratory RNA viruses with pandemic potential in human, animal, and environmental samples. The pioneering technology rests on a new fluorescence-based optical system for target virus detection and includes a touchscreen for fast and straightforward use. PANRISK is a spatio-temporal epidemiologic model that processes field data from freely accessible online resources and proprietary partner results. Based on existing predictive methods, PANRISK monitors, evaluates and gives an alarm in case of pandemic risk
Q-NET-Assess https://www.icrad.eu/portfolio-items/qnetassess/	Europe	Europa	Molecular Surveillance of Coxiella burnetii: funded by ERA-NET ICRAD (International Coordination of Research on Infectious Animal Diseases)
Q-FIG https://qfig.au	Worldwide	África América Asia y el Pacífico Europa Oriente Medio	To Improve Understanding and Outcomes of Q fever QFIG (Q Fever Interest Group) is an international collaboration of Q fever experts from diverse disciplines. This website is a platform for networking and information helpful for managing Q fever
Ospedale Sacro Cuore Don Calabria (IRCCS - Scientific Institute for Research, Hospitalization and Healthcare)	Italy	Europa	Research collaboration for diagnostic and scientific purposes

TOR 4 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
			Project led by IZSLER (Istituto

Istituto Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna for the WOAH Virtual Biobank (WOAH-VB)	Italy	Europe	Zooprofilattico Sperimentale della Lombardia e dell'Emilia Romagna) and supported by WOAH (World Organisation for Animal Health). The WOAH-VB aims to create a digital network of biobanks that enables the secure, transparent, and efficient sharing of high-quality biological materials for research, diagnostics, and test validation.
WOAH Reference Laboratory for Brucellosis, IZSAM	Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
National Reference Centre for Leptospirosis, IZSLER	Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
National Reference Centre for Antrax (Centro di Referenza Nazionale per l'Antrace (Ce.R.N.A.) IZSPB	Italy	Europe	Diagnosis confirmation, proficiency testing
WOAH Reference Laboratory For Foot-And-Mouth Disease, IZSLER	Italy	Europe	Diagnosis confirmation, proficiency testing
National Reference Centre for Leishmaniosis (C.RE.NA.L) IZSSi	Italy	Europe	Diagnosis confirmation, proficiency testing
National Reference Centre for Exotic Diseases (CESME) IZSAM	Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
Woah Reference Laboratory for Avian Influenza and Newcastle Disease	Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
Woah Reference Laboratory for Salmonellosis	Italy	Europe	Diagnosis confirmation, research projects, proficiency testing
Woah Reference Laboratory for Rabies	Italy	Europe	Diagnosis confirmation, research projects, proficiency

			testing
Woah Collaborating Centre for Epidemiology, Training and Control of Emerging Avian Diseases	Italy	Europe	Research projects, data analysis and modelling
Namur Research Institute for Life Sciences, University of Namur	Belgium	Europe	Research collaboration for diagnostic and scientific purposes
Institute of Medical Microbiology, University of Zurich	Switzerland	Europe	Research collaboration for diagnostic and scientific purposes

TOR 6: EXPERT CONSULTANTS

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

No

TOR 7: 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 : 3

b) Seminars : 1

c) Hands-on training courses: 3

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
A	Two representatives from the Istituto Zooprofilattico of Piemonte, Liguria and Valle d'Aosta visited the Animal Models Research Laboratory	Italy	2
A	Activities envisaged under the Agreement for training and research internships between our Institute and the Abdus Salam International Centre for Theoretical Physics, within the framework of the International Atomic Energy Agency (IAEA) "Fellowship Programme and Scientific Visits Programme"	Algeria	1
C	Training on VBDs surveillance, vectors identification and pathogen investigation	Italy	1

C	Training on VBDs surveillance, vectors identification and pathogen investigation	Romania	1
C	Laboratory training for the diagnosis of fungal disease in domestic and wild animals	Italy	1
B	Diseases at the animal-human-environment interface	Italy	55

TOR 8: 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?

No

TOR 9: 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

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EU-EFSA The European Union One Health 2024 Zoonoses Report
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Invited speakers at national training courses (n° 3)
Cavicchio, L. (2025). Research activities at IZSVe on noroviruses detected in pig farms in Veneto and their genetic characterization. Presentation at the event Norovirus in the swine population: is it a real threat to humans, IZSVe. 30 June 2025, Legnaro, Italy.
Leopardi, S. (2025). Ecology of viral agents in bats. Seminar at the University of Padua, Department of Animal Medicine, Production and Health. 15 April 2025, Legnaro, Italy.
Leopardi, S. (2025). Epidemiological surveillance and scientific research with wildlife: The example of bats. ECM Webinar Course Epidemiological surveillance and scientific research with wildlife – Bioethical, managerial and environmental aspects, IZSVe. 28 & 31 October 2025, Legnaro, Italy.

National training courses organized by IZSVe (n° 1)
Norovirus in the swine population: is it a real threat to humans?
https://www.izsvenezie.it/corso-ecm-webinar-norovirus-suini/

Links from IZSVe's site
NRL and WHOA Collaborating Centre for diseases at the Animal/Human Interface (IZSVE)
http://www.izsvenezie.com/reference-laboratories/diseases-at-the-animalhuman-interface/
IZSVe's section on bats (Italian)
https://www.izsvenezie.it/temi/animali/pipistrelli/
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:
08/04/2025 https://www.izsvenezie.it/appunti-scienza-malattie-trasmesse-vettori/
08/04/2025 https://www.izsvenezie.it/corso-ecm-online-vettori-patogeni-flebotomi/
08/04/2025 https://www.izsvenezie.it/corso-ecm-fad-artropodi-vettori-patogeni-zanzare/
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17/06/2025 https://www.izsvenezie.it/west-nile-sorveglianza-integrata-one-health-efficace/
25/07/2025 https://www.izsvenezie.it/west-nile-zanzare-circolazione-veneto/

Research and news on animal reservoir and infectious diseases
28/01/2025 https://www.izsvenezie.it/rischio-zoonosi-canili-colonie-oasi-feline/
11/02/2025 https://www.izsvenezie.it/mammalian-orthoreovirus-mrv-cani-gatti-collabora-ricerca/
20/02/2025 https://www.izsvenezie.com/webinar-long-term-urban-bat-monitoring/ [ENG]
21/02/2025 https://www.izsvenezie.it/webinar-long-term-urban-bat-monitoring/
24/03/2025 https://www.izsvenezie.it/corso-ecm-zoonosi-gravidanza-eta-pediatrica/
27/03/2025 https://www.izsvenezie.it/progetto-cables/
31/03/2025 https://www.izsvenezie.it/febbre-q-video-webinar/
26/05/2025 https://www.izsvenezie.com/european-vaccines-hub-launch/
09/06/2025 https://www.izsvenezie.it/corso-ecm-webinar-norovirus-suini/
27/06/2025 https://www.izsvenezie.com/european-virus-archive-international-association/
23/07/2025 https://www.izsvenezie.it/progetto-rabtool/
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16/10/2025 https://www.izsvenezie.it/studio-one-health-pipistrelli-suini-virus/

03/12/2025 https://www.izsvenezie.it/corso-ecm-webinar-animal-mycosis/
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Press releases (Italian)
https://www.izsvenezie.it/comunicazione/relazioni-media/comunicati/
07/04/2025 Arrivano le zanzare, un decalogo per difendersi dalle punture e dalle malattie (PDF)
23/05/2025 Lanciato l'European Vaccines Hub (EVH) for Pandemic Readiness (PDF)
26/06/2025 Nasce l'associazione internazionale European Virus Archive. L'IZSVe tra i partner (PDF)
24/07/2025 West Nile nelle zanzare, circolazione moderata in Veneto (PDF)

Facebook/Instagram/LinkedIn (Italian)

28/01/2025 - Rischio zoonosi in canili, colonie e oasi feline. Puntare su monitoraggio, formazione e comunicazione
Facebook:https://www.facebook.com/izsvenezie/posts/pfbid0eUjUHoWpCWiwRDBEFSdNe5wHDVakYHwvN6JKy7tyF4cDu6qrVyhBb1qaHP7jhshil
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11/02/2025 - Mammalian Orthoreovirus (MRV) in cani e gatti di proprietà, collabora alla ricerca
Instagram: https://www.instagram.com/p/DF-cPWFCs-m/?img_index=1

21/02/2025 - Webinar "Long-term urban bat monitoring and notes on the effects of full-scale war on urban wildlife" [ENG]
Facebook:https://www.facebook.com/izsvenezie/posts/pfbid0Y6HwFb6P1N51vada59eyiK4vQVwRVZLtZG43ofqfBENRRVgPyKQz92pUqoNunXRGl
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08/04/2025 - Arrivano le zanzare, decalogo per difendersi dalle malattie e ciclo di eventi in provincia di Padova
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Instagram: https://www.instagram.com/p/DILnHvPt8VD/?img_index=1
Linkedin:https://www.linkedin.com/posts/izsvenezie_zanzare-malattie-prevenzione-activity-7315311701535424512-aESZ

26/05/2025 - European Vaccines Hub (EVH) for Pandemic Readiness, una nuova partnership europea per lo sviluppo di vaccini
Facebook:https://www.facebook.com/izsvenezie/posts/pfbid02KA1zUoXRqWvyB5SMqgHD9chJX25ScNk8Ynek3iEb7DCYH5aLytEXpveiLbzt5bsAl
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17/06/2025 - West Nile Virus, la sorveglianza integrata One Health è efficace nelle regioni endemiche
Facebook:https://www.facebook.com/izsvenezie/posts/pfbid0dxUuFfTF37ewdHoZ9P5qRCAF82wpgmRACsvVrAjruz3rBFMxUCLc8aV63ssPR7Zml
Instagram: https://www.instagram.com/p/DLAm7JCyrrH/?img_index=1
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11. What have you done in the past year to advance your area of focus, e.g. updated technology?
- Host-pathogen interactions: Isolation and characterisation of primary cells derived from bats (Myotis myotis and Miniopterus schreibersii). Such cells will be used to compare the susceptibility of different hosts to emerging viral pathogens;

- As part of the collaboration with the University of Zurich and the University of Namur, we have been implementing advanced molecular screening methods and MALDI-TOF–based characterization approaches to improve the identification of pathogenic Capnocytophaga species;

12. Additional comments regarding your report: