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Establishment of a surveillance system on selected (re)emergent and at-risk of introduction zoonoses based on a ecologic approach

WOAH Regional Seminar

Vector-Borne Diseases in the European Region

25 - 27 June 2025

Teramo (Italy)

Paolo Calistri

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2021-2027
EU4Health Programme

- European Union's key initiative to strengthen health systems and improve health outcomes across member states
- With a budget of €5.3 billion, it aims to address health challenges, enhance crisis preparedness, and foster a more resilient and accessible European Health Union
- CP-g-22-04.01 Direct grants to Member States' authorities: setting up a coordinated surveillance system under the One Health approach for cross-border pathogens that threaten the Union

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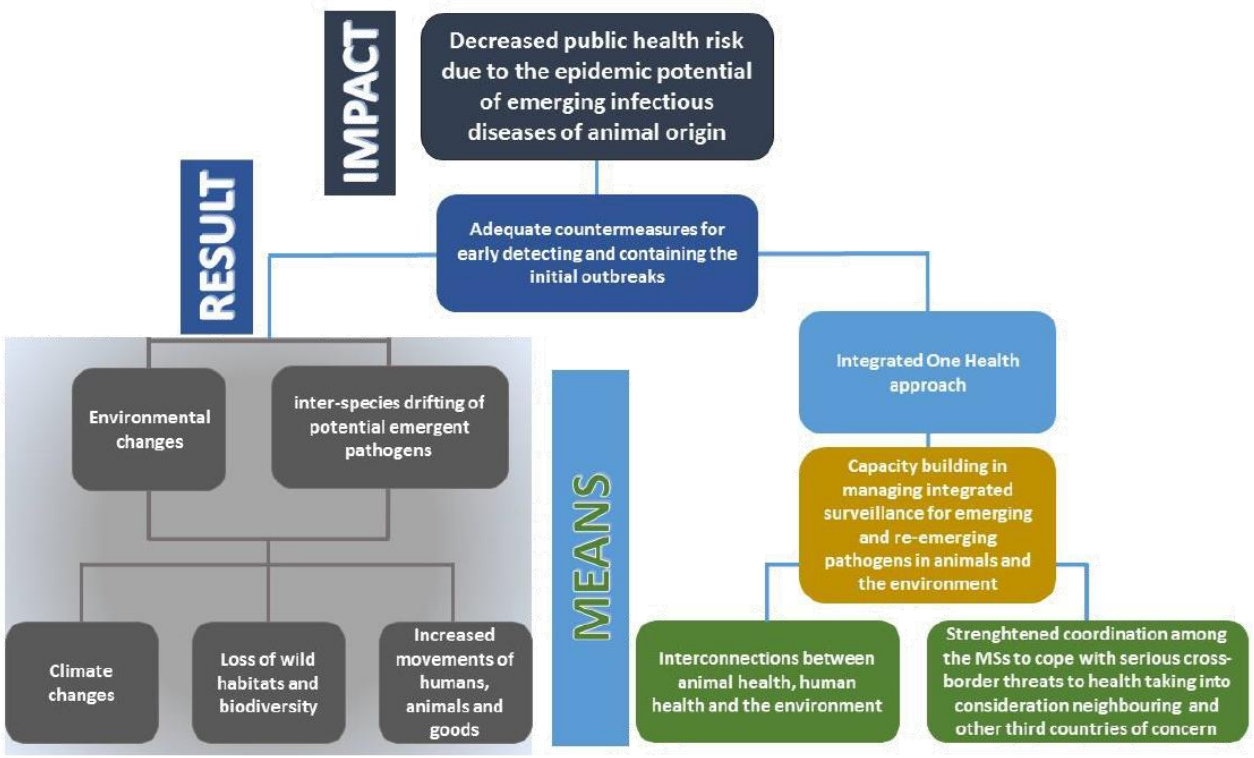
EcoSurv Partners

Istituto Zooprofilattico Sperimentale dell'Abruzzo e del Molise "G. Caporale" (IZS – Teramo) -> Nominated as Competent Authority

Affiliated Entities

- Italian Ministry of Health
- Istituto Superiore di Sanità (ISS)
- Istituto Zooprofilattico Sperimentale delle Venezie (IZSVe)

Objective



EcoSurv will aim to provide the Italian health system with a coordinated surveillance that innovates the current traditional siloes health approaches through the setting of a risk assessment based One Health surveillance for emerging and re-emerging pathogens, representing serious cross-border threats to health in the country and potentially in Europe

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Specific objectives

- To define innovative sample collection protocols and samples testing
- To organise the national data collection, collation and national data sharing
- To carry out national assessments (across animal and public health and the environment in a One Health approach) to identify national risks and future priorities
- To address residual capacity building needs not fully addressed, including awareness campaigns/events

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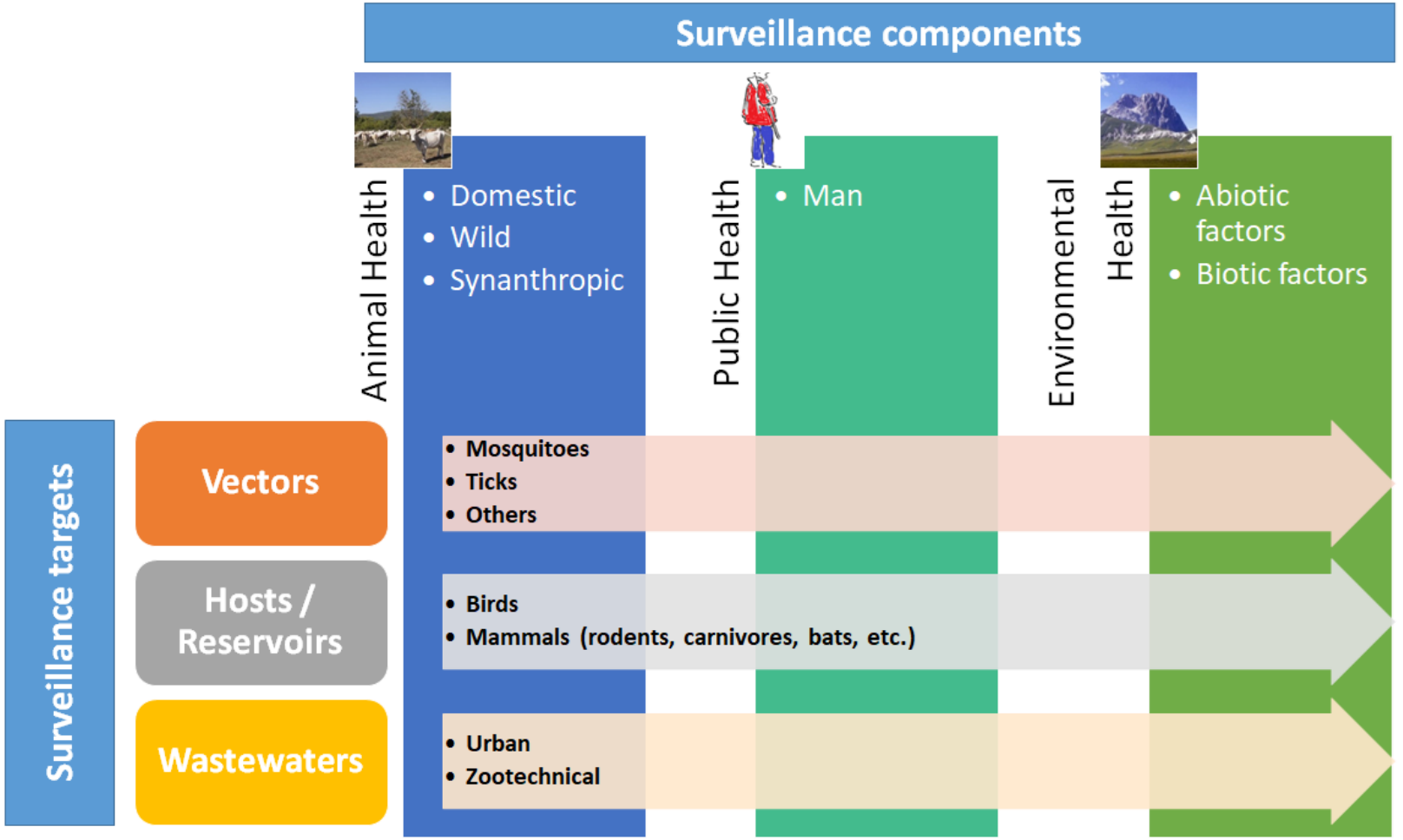
Approach



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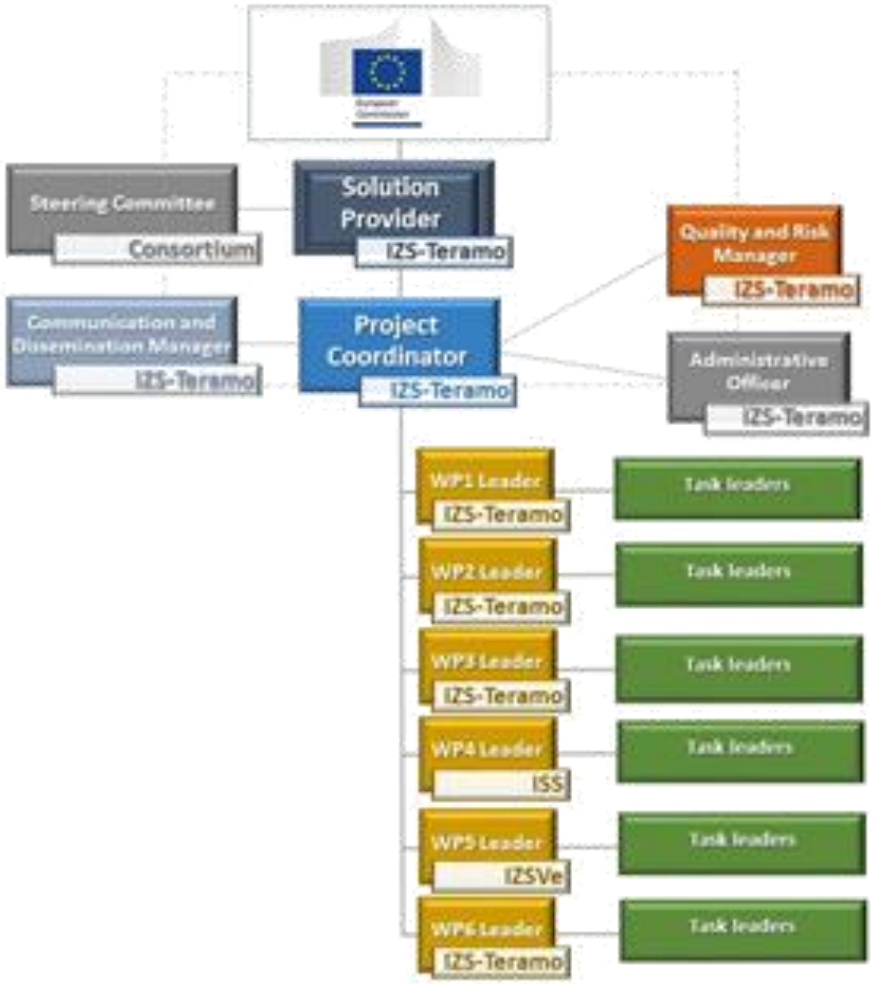
Organization

- WP1 project coordination
- WP2 Surveillance activities on Domestic Ruminants and related VBD [RVF, CCHF, Q fever]
- WP3 Surveillance activities on migratory birds and their environment [CCHF, WNF, HPAI]
- WP4 Surveillance activities in pig farms and wild boars [HEV, SIV]
- WP5 Surveillance activities on wild and synanthropic mammals [HPAI, *Echinococcus*, Lyme, Disease Y]
- WP6 Data Management



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Objectives WP2

- To early detect the presence and circulation of RVF in infected neighbouring countries, assess the risk of introduction of this zoonotic disease into Italy and plan possible preventive measures
- To early detect the presence in Italy of CCHF in ticks over domestic ruminants
- To estimate the zoonotic risk linked to *Coxiella burnetii* strains infecting ruminants, based on genome characterization of isolates from ruminants and subsequent comparison with those from human cases

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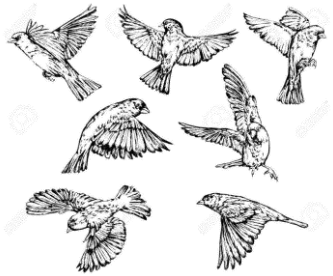
WP2 activities

Pathogen	Target species	Geographical area covered	Sampling strategy	Sampling matrix	Diagnostic tests
RVF	Cattle, sheep, goats, and dromedaries	At-risk locations (markets, slaughterhouses, oases) in Libya (at least 2 locations each year)	Random sampling	Serum and EDTA blood samples. In case of suspected RVF cases: organs and aborted foetuses	RT-PCR, IgM and IgG ELISA, SN
RVF	Aedes spp and Culex spp.	Libya and Mauritania in vector breeding sites in identified at-risk and infected areas.	Targeted sampling	Mosquitoes	Species identification, RT-PCR
CCHF	Ticks collected from domestic ruminants (Hyalomma spp.)	Abruzzo, Puglia, other Southern Regions, Islands (Sicily and Sardinia)	About 300 animals (400-500 ticks) sampled per year	Adult Hyalomma spp.	Ticks identification, PCR. CCHFV characterization (NGS)
Coxiella burnetii	Cows, ewes, goats and their miscarriage products	Year 1 Abruzzo, Triveneto Year 2 and 3 involvement of other areas too	Passive. about 300 samples annually	Abortion products: foetuses, abomasal fluids, foetal organs, placentas. Vaginal swabs	PCR, Genotyping by MLVA
Coxiella burnetii	Hard tick (Genus Ixodes).	High cattle density areas (Abruzzo, Veneto)	Environmental samples collected on and in the vicinity of goat and sheep farms	Whole ticks	quantitative PCR

Objectives WP3



To early detect:

- the introduction of CCHF virus into Italy through migratory birds carrying infected ticks
- novel strains of WNF viruses in migratory birds
- new viral incursions and/or new genotypes/subtypes of HPAI in the sites under observation/surveillance and at the wild birds/poultry interface

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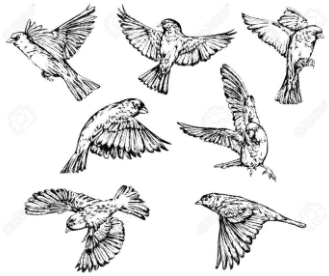
WP3 activities



Pathogen	Target species	Geographical area covered	Sampling strategy	Sampling matrix	Diagnostic tests
CCHF	Ticks (Hyalomma spp.) collected from migratory birds	Abruzzo, Islands, Southern Italy	Ticks collected from migratory birds caught for ringing. Ringing stations already in place in Italy will be used	Adult/Immature Hyalomma spp. on migratory birds	Ticks identification, PCR. CCHFV characterization (NGS)
WNF	Migratory birds (Passeriform, Charadriiformes, and other Orders)	Ringing stations in North and South Italy, covering the main fly routes	Ringing stations	Birds' feathers	RT-PCR
HPAI	Environmental samples from wild bird habitats	Veneto	Target sampling. Selection of sites (n = 4) in the proximity of DPPA (densely populated poultry area)	Surface waters, sediments, molluscs, and fresh faecal samples collected from the banks	RT-PCR, molecular characterization by sequencing

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Objectives WP4

- To detect the presence and circulation of HEV in pig farms
- To map the main and new emerging genotypes of HEV in pig and wild boar populations
- To detect the emergence of new relevant genotypes/subtypes of SIV in the pig population

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WP4 activities

Pathogen	Target species	Geographical area covered	Sampling strategy	Sampling matrix	Diagnostic tests
HEV	Farmed pigs	Year 1 Abruzzo, Triveneto Year 2 and 3 involvement of other areas too	Fattening farms, sampling on the basis of the expected within-farm prevalence.	Pooled faecal samples or boot socks, randomly collected from different barns and pens.	Real-time reverse transcription PCR, sequencing
HEV	Wild boars	Abruzzo, Veneto	Convenient sampling. At least 100 animals will be tested annually.	Liver	Nucleic acid extraction from liver and HEV-RNA detection by Real-time qRT-PCR. Sequencing and genomic characterization
SIV	Symptomatic pigs	Abruzzo, Veneto	Target sampling	Nasal swabs collected from subjects with acute respiratory symptoms.	Screening by Real-time rt PCR. Isolation in cell culture. Genome sequencing (NGS)
HEV	Farmed pigs	Abruzzo and Veneto / Friuli Venezia Giulia regions.	First year on selected pig farms (n=3 per Region). The following years also sampling at pig slaughterhouses (n=1)	Pigs slurries in farms and wash water from slaughterhouses.	RT-PCR, molecular characterization by sequencing

Objectives WP5

- To early detect HPAI H5N1 spillover events in wild carnivores
- To detect the introduction of *Echinococcus* into new geographic areas and populations of wild canids and investigating the trends over time
- To early detect possible changes in the geographic distribution and spread to new areas of Lyme Disease (LD) and Tick-Borne Encephalitis (TBE)
- To collect information and genomic data on the circulation of untargeted viruses (disease Y) in selected animal species

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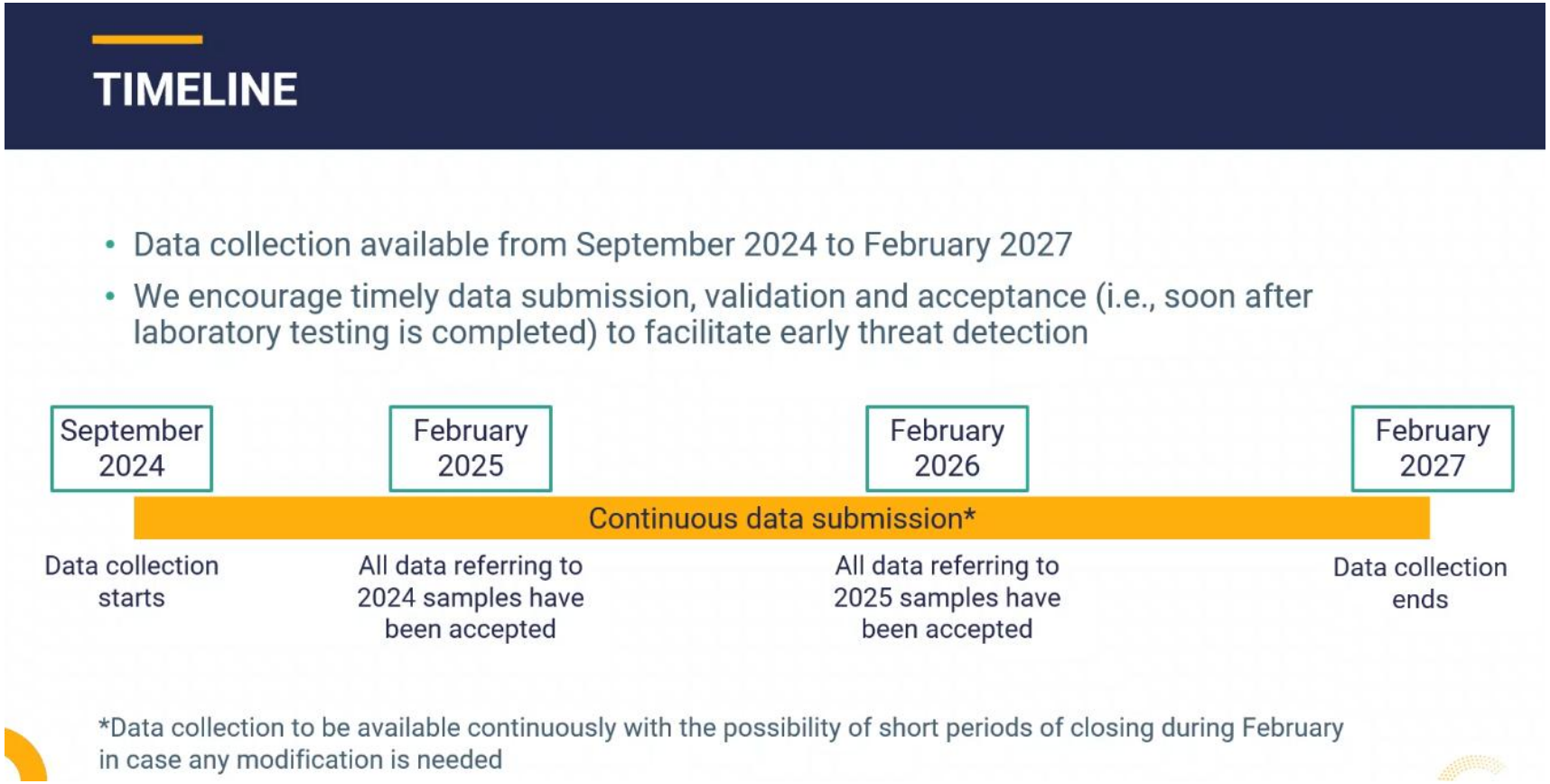
WP5 activities

Pathogen	Target species	Geographical area covered	Sampling strategy	Sampling matrix	Diagnostic tests
HPAI	Wild carnivores	In the avian–carnivores interfaces. Selected wetlands	Convenient sampling. Carcasses from hunting/culling, found dead	Central nervous system and lung.	RT-PCR, sequencing
Echinococcus	Free-ranging wild canids	Selected areas. At least two areas each year (on the basis of previous infestation records)	Convenience sampling of hunted, trapped, road-killed and found dead wild canids	Carcasses	Sedimentation and Counting Technique (SCT), PCR , genotyping
Borrelia burgdorferi s.l. TBE virus	Hard ticks – Genus Ixodes	Areas with high-risk of disease prevalence; areas where Lyme dis. and TBE have been previously diagnosed	Target sampling	Ticks collected from the environment	Tick species identification with subsequent detection of the pathogen by polymerase chain reaction (PCR)
Pathogen Y – RNA and DNA viruses of different families	Rats, Bats and Hedgehogs.	Central and Northern Italy	Convenient sampling	Faeces, lungs, intestine, oral or rectal swabs and other internal organs.	NGS analysis: metagenomics

Detailed data on the results submitted to EFSA



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