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INDEX

EDITORIAL

The BENV as a tool for disseminating information

Dear readers,

in this first issue of 2018, the BENV is presenting a lot of interesting articles regarding both human and animal topics, in the view of the one health perspective.

In the section **In recent months**, you can find an article on the recent outbreaks of Chikungunya virus (CHIKV) in Italy. In 2017 a total of 359 (184 confirmed and 175 probable) autochthonous cases were reported in Lazio and 61 (50 confirmed and 11 probable) in Calabria. Other probable and confirmed cases have also been reported by other Italian regions. All were epidemiologically linked to the cases reported in Lazio region. CHIKV occurred for the first time in Italy in 2007: the presence of the vector in the national territory, combined with other factors, such as climate changes and increase in the travel to / from endemic countries, determined an epidemic of autochthonous cases in Emilia-Romagna with 281 confirmed cases.

In the same section, a review on Tuberculosis in wildlife is presented. Tuberculosis caused by *M. bovis* is a zoonosis: at global level, an high number of human cases are caused by *M. bovis* and bovines represent the main reservoir of the infection. Also, a wide range of domestic and wild animals can be infected by *M. bovis*. Even though livestock is considered the principal host, among wild animals some species are recognized as reservoir, reducing the efficacy of eradication programs in livestock. An appendix presents the main outcomes of the test results related to a monitoring protocol applied during necropsy in wild ungulates and established from 2010 in Abruzzo region.

Whereas extensive efforts in developed countries have largely contributed to control rabies in non-flying mammals, dog rabies remains enzootic in much of the developing world. Eliminating dog-mediated human rabies by 2030 is one of the one-health global challenges. An interesting article in the section Around us shows epidemiological situation of rabies in dogs in Latin America, Asia and Africa and the Tools available to reach the "Zero by 30" goal.

Another article in the same section regards the last published Global animal disease inteligence report (GADIR), which regulary updates on the main disease threats monitored and analysed by the FAO/AGAH/GLEWS worldwide. This intelligence report contains relevant analysis of disease information collected by FAO GLEWS from official and informal sources to enhance global early warning and surveillance for animal diseases.

The maps show the outbreaks 'distribution of the main animal diseases occurred in Italy in 2017 and reported to the national information system SIMAN.

Regarding the data on outbreaks, in the Hand on data section, you can consult and download the tables with the data on outbreaks reported to SIMAN in 2017, the health status of the territories and the animal species involved in the outbreaks. Also, the tables and maps of the Officially free territories have been updated: the Standing Committee for Plants, Animals, Food and Feed has approved the Implementing Decision 2017/1910/EU recognizing the officially free status for enzootic bovine leucosis in Italy. Following this recognition, the whole Italian territory is now completely free from the disease. The enzootic bovine leucosis can lead to significant economic losses attributable in particular to the blocking of national and international animal trade and to the costs of the eradication and surveillance plans. Since 1996, an Eradication Plan (Legislative Decree No. 358 of 2 May 1996) is compulsory throughout Italy.

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We wish you all to enjoy a happy new year together with the BENV.

Simona Iannetti
COVEPI

IN THESE MONTHS

The main events of epidemiological interest in the last months in Italy and in the European Union

Outbreaks of Chikungunya virus in Italy: history of the disease and infection in the country

Introduction

The Chikungunya virus (CHIKV) is an RNA virus that belongs to the Togaviridae family, the Alphavirus genus. CHIKV is transmitted by the mosquitoes bite that become infected if they sting a person during the viremic phase. The duration of viremia in humans is not well defined; it is thought to last from 3 to 10 days, starting immediately before the onset and ending 5-7 days after the onset of symptoms (1). Infected mosquitoes can then transmit the virus to other people by bite. The infection can be transmitted from person to person only through blood or transplantation of infected organs and tissues or from mother to child (2). The most typical symptoms of Chikungunya are fever and joint pains with an acute onset. Joint swelling, rash, and other non-specific symptoms such as weakness, chills, headache, nausea, vomiting may also be present. The clinical presentation may affect both young adults and children more prevalently (3). The disease is usually self-limited, cases with a severe course are reported, but usually in individuals with underlying conditions with clinical pictures involving the central nervous system (meningo-encephalitis) hit defunct individuals; deaths are attributable to complications from concomitant diseases (4). The infection may be asymptomatic and sero-prevalence studies have shown that up to 10-15% of people with specific circulating antibodies did not remember having the disease (5).

The presence of the vector combined with other factors, such as climate changes and increase in the travel to / from endemic countries, in 2007 determined an epidemic of autochthonous cases of CHIKV in Emilia-Romagna, in the Municipalities of Cervia, Cesena , Ravenna, Rimini and Bologna, about 334 total cases have been identified, of which 281 confirmed with laboratory investigations. The indigenous transmission was also confirmed by the isolation of the Chikungunya virus (CHIKV) in tiger mosquitoes collected in the affected area (6-8). Since 2011, the CHIKV is reported by the Regions and Autonomous Provinces through a special surveillance system set up by the Ministry of Health and the National Institute of Health, for CHIKV cases during the period of vector activity (June-November) and of the cases imported all year round (9).

In 2016, the Regional Office of the Americas for the World Health Organization notified nearly 350,000 suspected cases of chikungunya, of which 146,000 were confirmed in the laboratory. Brazil (265 thousand suspected cases), Bolivia and Colombia (in both 19 thousand suspected cases) the most affected countries. In 2016, in the African Region, Kenya has notified a Chikungunya outbreak with over 1,700 suspected cases and in Pakistan an outbreak is still ongoing (10).

In early August 2017, France in the department of Var (Southern France) reported the presence of an outbreak of CHIKV with 6 autochthonous confirmed cases and a probable case, all residing in the same district of Cannet-des-Maures (11).

In the beginning of September 2017, an outbreak of autochthonous cases has been identified in Italy in Anzio (province of Rome, Lazio region) which gave rise to several outbreaks occurring in Rome, Latina (both in Lazio region) and in in the municipality of Guardavalle marina (Calabria region) (12). In this paper, we report preliminary results on the epidemiological investigation conduct during the CHIKV epidemic that occurred from August to October 2017 in Italy

The surveillance system of authoctonous and imported cases in Italy

The surveillance of human cases of Chikungunya is throughout the year, however, during the period of vector activity (June-October) the surveillance system is enhanced in mosquito-infested areas to allow the identification of cases, for the purposes of immediate adoption of the necessary control measures (in relation to entomological surveillance), to reduce the risk of transmission. In the vector activity period, the surveillance system provides for the timely identification of suspected cases (symptomatic persons returning from an endemic country) and the potential identification of people with clinical symptoms, according to the case definition reported in Table 1, with no history of travel to endemic countries, in order to recognize autochthonous cases and outbreaks (two or more cases occurring within a 30-day time frame in a restricted territorial area). From 2008 to 2016, 85 confirmed CHIKV cases have been reported to the surveillance System

Table 1. Chikungunya case definition, Ministry of Health 2017

Clinical criteria	Fever and severe polyartralgia (limiting daily activities), in absence of other causes
Laboratory criteria[1]	Probable case: - Detection of chikungunya specific IgM antibodies in a single serum sample. Confirmed case (At least one of the following four): - Isolation of chikungunya virus from a clinical specimen; - Detection of chikungunya viral nucleic acid from a clinical specimen; - Detection of chikungunya specific IgM antibodies in a single serum sample AND confirmation by neutralisation; - Seroconversion or four-fold antibody titre increase of chikungunya specific antibodies in paired serum samples.
Epidemiological criteria	History of travel to, or residence in an area with documented on-going transmission of chikungunya, within the two-week period prior to the onset of symptoms
Classification	
Probable case	Any person meeting the clinical criteria and the laboratory criteria for a probable case
Confirmed case	Any person meeting the laboratory criteria for a confirmed case.

[1] Serological results should be interpreted according to previous exposure to other alphaviral infections

Autochthonous cases in Italy, 2017

On 6 and 7 September 2017, the National reference Laboratory for arboviral infections based at the National Institute of Health, Italy, received serum and urine samples from three patients with a history of high fever (>38°C), severe joint pain and an itching skin rash. Symptoms had started while they were on holiday near the coastal town of Anzio, in the province of Rome, Lazio region (ca 58 km from Rome). Later we talk about epidemiology on the territory of Anzio, confirmed cases of CHIKV have been reported in the municipality of Rome and Latina (13).

After the autochthonous cases of Chikungunya reported by the Lazio region, a secondary outbreak has been identified in Calabria in the municipality of Guardavalle marina (CZ). It all started from four confirmed cases reported between 19 and 25 September 2017 to the national surveillance system from two regions (one in Lazio and three from Emilia-Romagna), in persons resident in both regions that showed suggestive symptoms of CHIKV infection in August while they were staying in Guardavalle Marina for summer holidays.

In total, 359 probable and confirmed autochthonous cases of Chikungunya were reported in the Lazio region in the municipalities of Anzio, Rome and Latina (184 confirmed and 175 probable) and 61 probable and confirmed autochthonous cases in the Calabria region in the municipality of Guardavalle marina (50 confirmed and 11 probable). Several probable and confirmed cases have also been reported by other Italian regions (for example Emilia-Romagna, Marche) and in other Member States (France and Germany). All were epidemiologically connected to Anzio, Rome or to Guardavalle Marina. In total, 428 probable and confirmed CHIKV cases were reported in Italy (Figure 1).

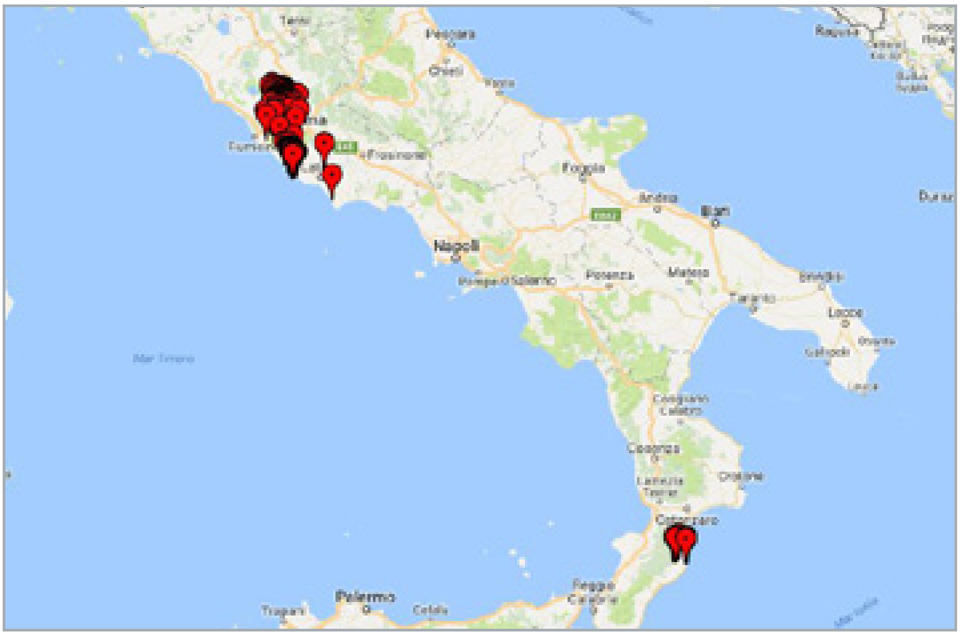


Figure 1.
Maps of the autochthonous cases by site of exposure, Italy, August-September 2017

Sequences of the PCR amplicons of the virus envelope (E)1 gene from patients (GenBank numbers: LT908477 and LT908478) and from the mosquitoes were identical (GenBank number: LT908476), and also showed a 100% similarity with the sequence of a chikungunya East Central South African (ECSA) strain involved in an ongoing epidemic in Pakistan (12), which does not carry the A226V mutation, responsible of the 2007 Emilia – Romagna outbreak in Italy (7).

Most of the cases had onset between August and September and the last date of onset is registered on the 17th of October 2017 (Figure 2 and 3).

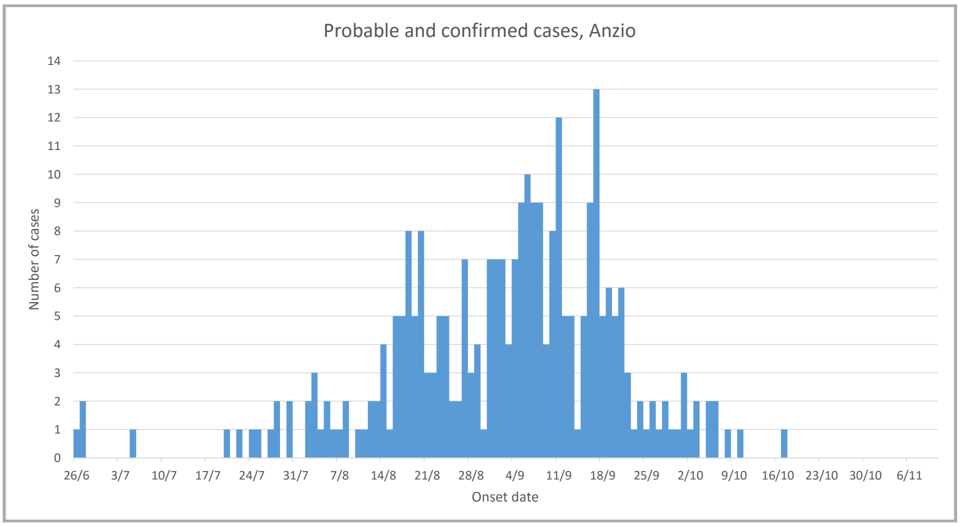


Figure 2.
Epidemic curve of cases reported or linked to the Lazio region outbreak. August – October, 2017

Panel A: Anzio; Panel B: Roma

Epidemic curve of cases reported or linked to the Lazio region outbreak. August – October, 2017

Panel B: Roma

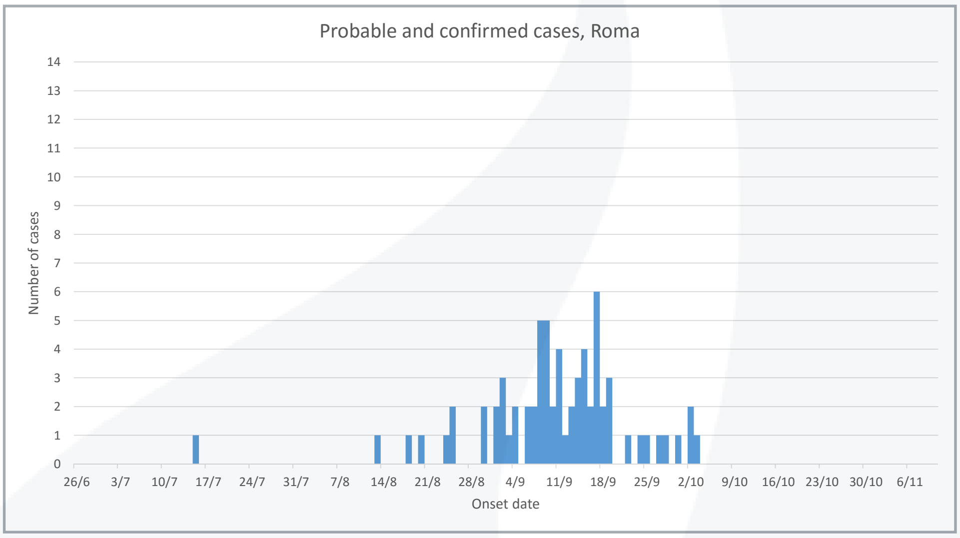
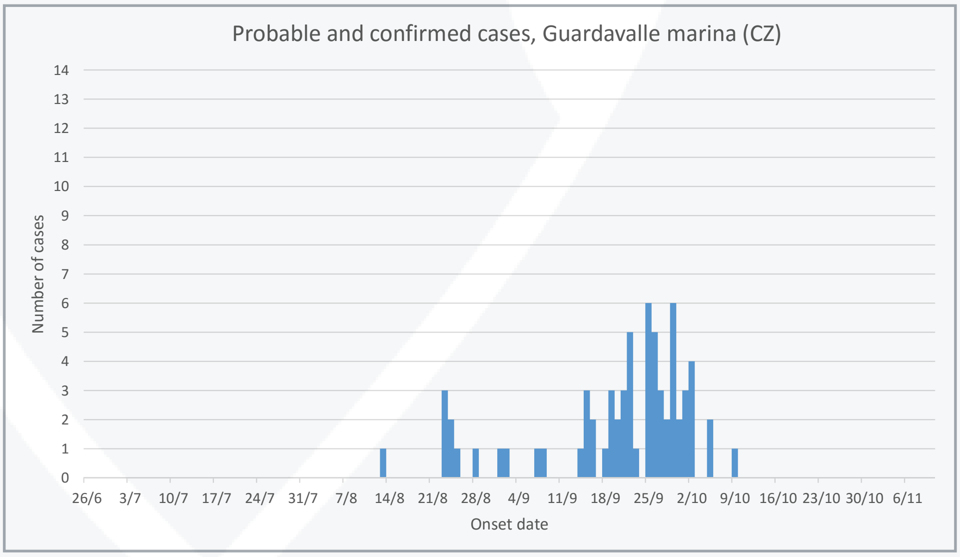


Figure 3. Epidemic curve of cases reported or linked to the Calabria region outbreak, August – October, 2017



Prevention and control measures adopted

FIn the areas with the highest concentration of cases both in the Lazio region and in Guardavalle marina (CZ), an epidemiological investigation was immediately set up with an enhanced epidemiological surveillance of cases, a retrospective investigation to identify the real burden, and an entomological surveillance to describe the vector present in the area and its density.

Furthermore, all the measures for the prevention of the disease have been activated in relation to the donations of blood, tissues and organs for the reduction of the risk of transmission from blood products, according to the indications of the National Blood Center and the National Transplant Center (14). The control measures adopted were also related to the disinfestation of the areas involved, to reduce the density of the vector and the relative transmission risk. A communication campaign was also activated to alert people to protect themselves from mosquito bites.

The suspension of donations concerned only the municipality of Anzio, the Local Health Autority n 2 of the municipality of Rome, the municipality of Latina and the municipality of Guardavalle marina. In all other areas of the regions of Lazio and Calabria, based on the assumption of a lower level of risk of infection, the ‘quarantine’ of 5 days was applied to the blood collected if the donor stayed in the endemic areas on the Italian territory. At national level, donors who stayed in the affected municipalities were suspended for 28 days (14).

During entomological surveillance samples of eggs, larvae and adult mosquitoes of species Aedes albopictus were collected. Agreements were also made with the municipal authorities to activate entomological monitoring with ovitraps, and to map the larval presence in the area. Furthermore, vector control interventions have been carried out, both with adulticides and larvicides, following the procedures indicated in Annex IV of the Ministry of Health's National Plan for Surveillance and Control of aroviral infections published on 10th July 2017 (9). Disinfection / disinfestation services in the affected regions have carried out at least 3 larvicidal and adulticidal interventions to control the outbreaks in areas affected by autochthonous transmission.

Conclusions

Vector borne diseases are a priority for public health in the coming years. The Italian model, which includes integrated and multidisciplinary surveillance and response plans, is considered one of the most advanced in Europe and internationally. However, despite the preparednessactivities, the question concerning the identification of these cases by physicians, still remains open.

The 2017 epidemic in Italy also shows how difficult it is to think of CHIKV infection, if the first case imported from an affected area is not identified, as was the case in 2007 in Emilia-Romagna. On the other hand, the identification of imported cases is not always easy, because the symptoms are neither specific nor serious. From now until next spring it will be important to improve the knowledge on this infection both among health workers and the population.

In order to rapidly respond in the case of a new autochthonous transmission, close coordination between different figures is essential, so that: a) pediatricians and family doctors also consider CHIKV among the causes of acute febrile illness, if coupled with joint and muscular pains, and if the onset in the months of vector activity; and b) adequate laboratory capacity is available to confirm the diagnosis. At the moment, a national reference laboratory has been identified at the Istituto Superiore di Sanità; c) the suspected and confirmed cases are rapidly reported to the local health authorities; d) the notified case activate a prompt epidemiological investigation and appropriate actions for vector control.

The presence of this mosquito in other European countries is a serious cause for concern also in the rest of Europe, and ECDC stands for this by closely monitoring the situation given the outbreaks already reported in France and Italy in 2017.

Furthermore, research in this sector plays a fundamental role and should be strengthened. Other areas to be further developed are the harmonization of procedures among the different Italian regions, training and information and evaluation of control meaures.

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Mycobacterium bovis in Wildlife

Introduction

Tuberculosis (TBC) is a disease caused by microorganisms of the *Mycobacterium Tuberculosis complex* (Figure 1) including *Mycobacterium tuberculosis* and *Mycobacterium bovis*, etiological agent apiece of human and animal tuberculosis.

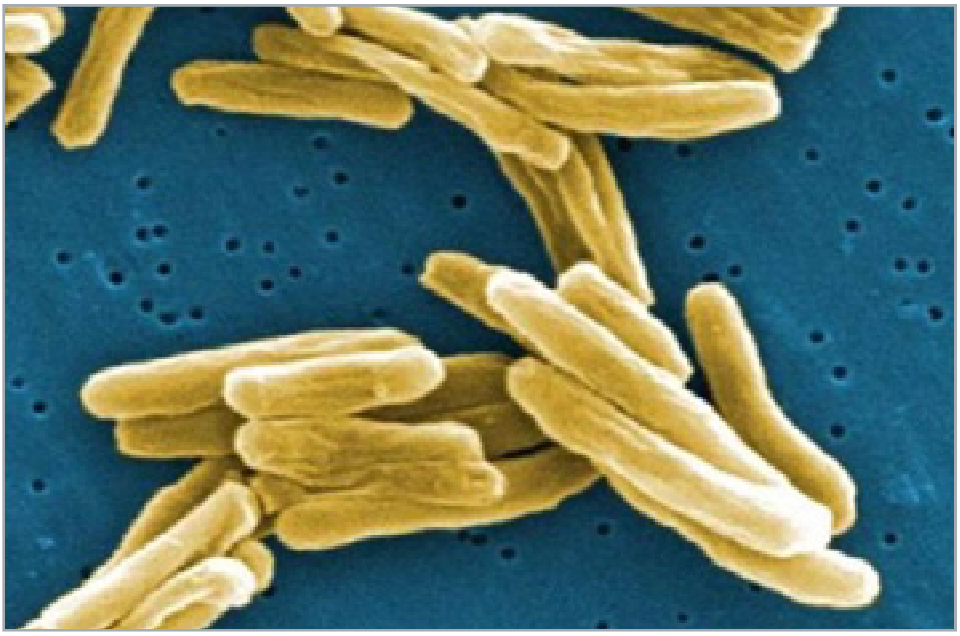

Figure 1.
M. tuberculosis

About 8,8 million of new human TBC cases are diagnosed each year worldwide, equal to 122 cases each 100.000 inhabitants, with 1,5 million of deaths in 2010 (WHO,2011). The 58% of TBC cases is reported in Asia, specifically in India and China where the highest number of diagnosis is performed, equal to 26% and 12% of total cases respectively.

Despite significant progresses have been made in the control and/or eradication of tuberculosis in industrialized countries, the disease remain one of the most important infectious disease in humans and livestock in different countries of the world (WHO 2010).

The Mycobacterium genus includes more than 190 species, some of which are pathogenic both to humans and animals. Pathogenic Mycobacteria which can infect humans and/or animals (domestic and wild) are: *M. tuberculosis*, *M. leprae* (responsible for human leprosy), *M. bovis*, *M africanum*, *M pinnipedii*, *M. bovis subsp caprae* e *M. microti*.

Tuberculosis caused by *M. bovis* is a zoonosis (Perez-Lago et al., 2014), humans can be infected through the inhalation of infected aerosols, the contact with infected animals, or through the ingestion of contaminated foods and drinks. Raw milk produced by infected animals represents an important source of infection for humans. At global level, an high number of TBC cases are caused by *M. bovis* and bovines represents the main reservoir of the infection (Müller *et al.*, 2013)

In animals as well the main routes of infection are inhalation of infected aerosols and ingestion of contaminated tissues (Palmer, 2013). A specific example of oral route infection has been recorded in some areas of Spain where wild boars have been infected by feeding on infected deer carcasses (Gortazar *et al.*, 2012). Mycobacterium bovis can be eliminated also through secretion and excretion, such as urine and feces (Barasona *et al.*, 2015).

It is suspected that characteristics like soil type and ph might play a role in the persistence of *M. bovis* in the environment, but further studies are needed to clarify this relationship (Barbier *et al*., 2017). Experimental studies on different substrates have demonstrated that *M. bovis* can survive in the environment also for a long time: until 12 months in sterilized soils incubated in controlled laboratory conditions (Ghodbane *et al*., 2014). In Michigan (USA) it has been demonstrated the persistence of the bacteria until 88 days under meteorological natural conditions (Fine *et al*., 2011) at low temperatures (4 °C) (Barbier *et al*., 2017) protected from solar radiations (ultraviolet), as for example in feces (Tanner *et al*., 1999), corn, hay, water or in fresh and humid soil during winter and spring (Fine *et al*., 2011; Jackson *et al*., 1995; Barbier *et al*., 2017).

A wide range of domestic and wild animals can be infected by *M. bovis* (Biet *et al*., 2005), and even though livestock is considered the principal host, among wild animals some species are recognized as reservoir, including: European badger (Meles meles) in Great Britain and Ireland, red deer (*Cervus elaphus*) and brushtail possum (*Trichosurus vulpecula*) in New Zeland, African buffalo (*Syncerus caffer*) in South Africa, wild boar (*Sus scrofa*) in the Iberian Peninsula and white-tailed deer (*Odocoileus virginianus*) in Michigan, USA (Palmer, 2013; Naranjo *et al*., 2008).

The presence of a wildlife reservoir may reduce the efficacy of eradication programs in livestock, especially where the infection has been reduced or eradicated in domestic animals (Aranaz *et al*., 2004; Gortázar *et al*., 2007).

It must be taken into account that the endemization of the infection in wild populations is a complex phenomenon which requires the interaction between many factors such as density and social behaviors of wild animals, frequency of contact with domestic animals, availability of trophic resources and the alteration of habitats, for example through the use of fences or through the land abandonment.

The complexity of this mechanism is well described in some areas of Spain, where wild boars and red deer are responsible of the maintenance of the infection in the environment and act as spill-over to domestic cattle. (Gortázar *et al*., 2012).

Transmission between wild and domestic animals may occur at common foraging and watering areas (Kaneene *et al*., 2002). In the Iberian Peninsula, for example, the highest prevalence of tuberculosis in deer and wild boars has been reported in the south-western area, where protected natural areas are present.

Conditions which are believed to influence the transmission and persistence of TBC at local level are: (1) the high density of wild animals (2) the concentration of animals around foraging and watering points, and (3) a Mediterranean weather, with hot and dry summer, which improve the aggregation of animals around watering points (Palmer, 2013).

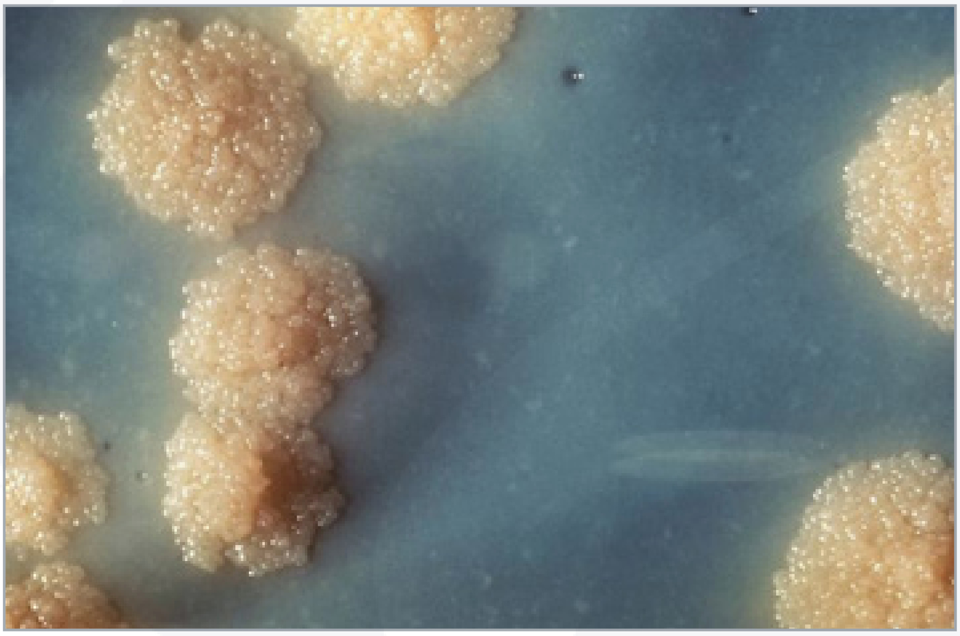

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Figure 2.
Colture in vitro of *Mycobacterium tuberculosis* showing the morphology of the colony

It’s important therefore to understand that tuberculosis must be monitored in all the animal species potentially involved in the epidemiological cycle, both domestic and wild, including in the monitoring process all the stakeholders: administrators, farmers, hunters, environmentalists and academics.

In Spain tuberculosis is present especially where there is an overlapping of pastures used by domestic (bovine and caprine, ovine and suidae also at a local level) and wild animals (wild boar, deer and fallow deer, badgers).

Badger is also strongly suspected to have an important role in transmission of TBC in the North of Spain (Gortázar *et al*., 2012). The infection has been reported in France in wild boars, where a possible association between the presence of badgers and bovine herds with TBC has been suspected (Payne *et al*., 2012).

Eurasiatic wild boar (*Sus scrofa*) with steady increase is considered to have an important role in the epidemiology of tuberculosis.

In Spain, the eurasiatic wild boar is reported as the main reservoir, responsible of the persistence of TBC into the wild. Prevalence rates of infection in this species are over the 50% (Vicente *et al*., 2013), with one third of the piglets at risk to get infected in the first 6 months of life (Che’ Amat *et al*., 2015).

Monitoring tuberculosis in these species, therefore, is of fundamental importance to better understand possible mechanisms of persistence of the infection in certain territories.

In France, with the purpose of estimating the exposition of wild boar to the *M. tuberculosis* complex (MTC), 2.080 serum samples of hunted wild boars were collected in 58 France “departments”.

The samples were tested using ELISA as first method of detection. From the results it was possible to deduce that the exposition of wild boars to the MTC was related with outbreaks of TBC in cattle: the average distance from infected wild boars to livestock outbreak was 13 Km, coherent with the home-range of a wild boar (a male can cover until 38 Km) (Richomme *et al*., 2013).

The diagnosis intra-vitam in wild animals is limited due to the difficulty of capturing and manipulating animals on a regular base. Surveillance, therefore, is based mainly on post mortem examination of hunted (Santos *et al*., 2010) or found death animals.

Cultural exam of M.bovis led to a definitive diagnosis of tuberculosis. It can be made on frozen tissues at -20 °C and on live animals from bronchial suction, urine or tampons (for example feces, abscess, wounds).

On death animals, the collection of 2 gr of tissue gathered from organs with lesions and from interested lymph nodes can be adequate for bacteriological culture and molecular characterization.

It is necessary underline, as already stated, that conditions and mechanisms responsible of infection maintenance in wild animals can be different, according to the geographic areas and species involved. Consequently, control measures should be adapted to local circumstances. Otherwise, in many European areas, wild boars and deer populations are growing rapidly both geographically than demographically.

One of the control methods widely used in the past was depopulation. Depopulation was realized through an intense hunting activities with the aim of reducing the density of wild animals up to a level which unable the maintenance of the transmission in the population.

This approach was used in the United Kingdom in badgers with contrasting results. If in some areas a decrease of incidence of TBC in cattle was reported, on the other hand in peripheral areas an increasing rate of infection was noticed.

This can be explained by the pressure that hunting has on the social structure of badgers with an enlargement of animals home range and therefore of the likelihood of contacts between infected and healthy individuals (Palmer, 2013).

Additional measures of control are based on prevention of contact between wild and domestic animals avoiding situations of promiscuity such as the sharing of watering and foraging points.

Nevertheless the most promising measure of control is the use of vaccines in wild population.

Studies on wild boar using oral vaccination through the distribution of baits two times per summer (Buddle *et al*., 2003), have reported a strong protective response against field strain of M. bovis (Gortazar *et al*. 2014). Other experimental studies using oral vaccination have been performed on badgers in which high levels of protection against infection were confirmed (Gormley *et al*., 2017).

An experiment completed in United Kingdom demonstrated the absence of interference with tubercoline test in the case of accidental ingestion by cattle of oral bait, containing inactivated vaccines, distributed for wild animals (Jones *et al*., 2016).

Appendix. Results of exams from 2010 at IZSAM laboratories

In Abruzzo, as in other Italian regions, in the last 10 years the density and geographical distribution of certain wild species have increased resulting in an enlargement of the overlapping with human activities.

In order to understand the potential involvement of wild ungulates in the transmission cycle of the bovine tuberculosis, in those provinces still not officially free of infection a monitoring protocol has been developed to be applied during necropsy procedures. For each sample a set of metadata is collected through a specific form.

From 2010 to August 2017 815 wild ungulates were tested for *Mycobacterium spp*., of which 413 were wild board, 253 roe deer, 111 deer and 20 Apennine chamois. Around 80% of examined animals came from the province of L'Aquila.

Isolated mycobacteria were identified by PCR and PCR-RFLP. Only two animals, both wild boars, tested positive, one of them to *Mycobacterium avium* (2017) and the other one to *Mycobacterium kumamotonense* (2015).

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HAND ON DATA

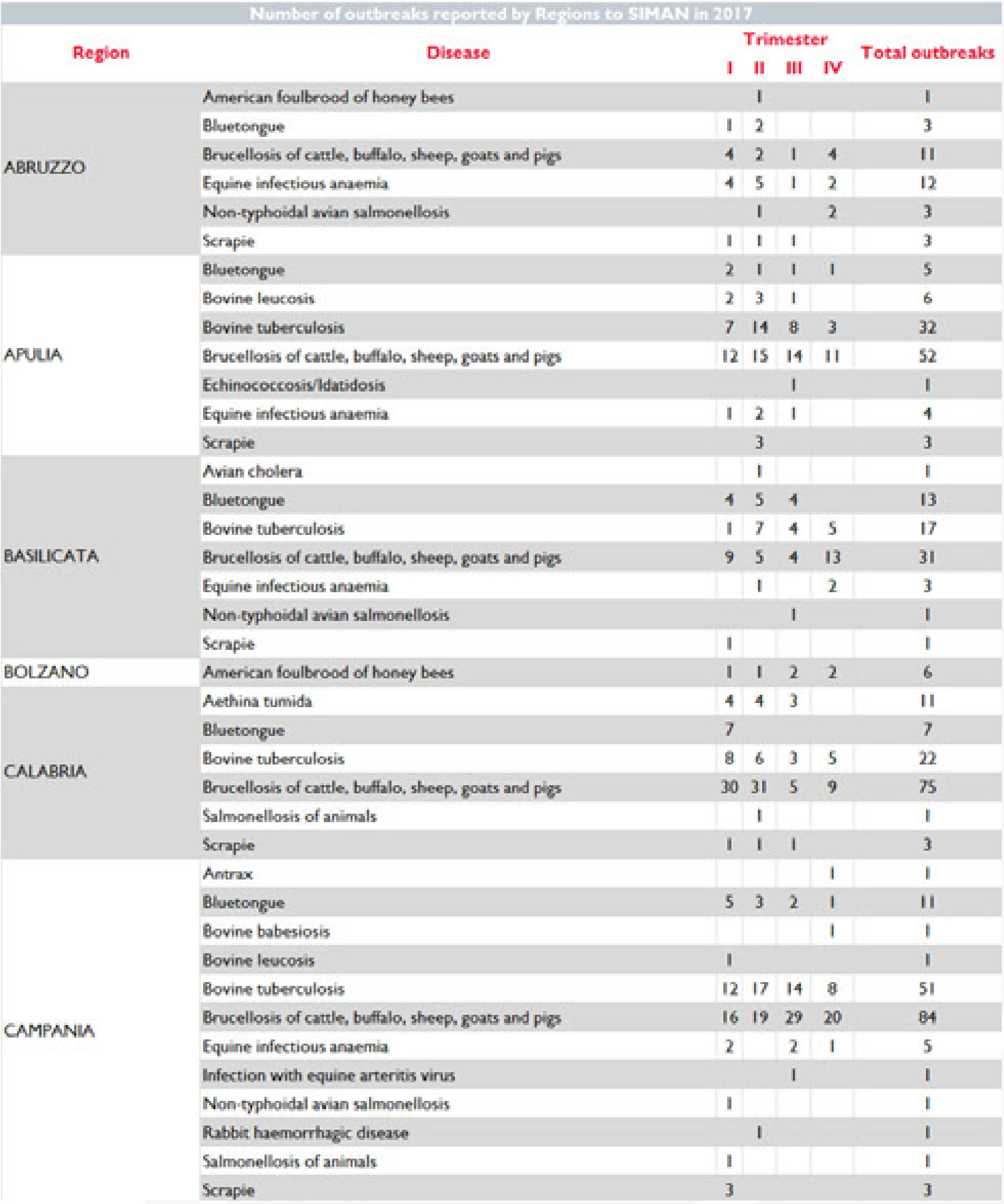
Processing date: 9h January 2018

Number of outbreaks reported to SIMAN in 2017

Number of outbreaks reported to SIMAN in 2017

Disease	Jan	Feb	Mar	Apr	May	Jun	Jul	Aug	Sept	Oct	Nov	Dec	Total outbreaks
Aethina tumida			4	1	2	1	2		1				11
African swine fever	28	1	6	1	4	2	1			1	48	20	112
American foulbrood of honey bees		1	5	2	2	8	12	3		2			35
Antrax								1		1			2
Avian cholera						1							1
Bluetongue	42	14	20	15	10	10	6	122	667	934	710	23	2573
Bovine babesiosis										1			1
Bovine leucosis	1	1	1	3		1	2	1					10
Bovine tuberculosis	20	26	34	27	49	44	28	20	21	19	16	11	315
Brucellosis of cattle, buffalo, sheep, goats and pigs	31	42	78	44	85	64	54	35	57	60	48	26	624
Caprine arthritis/encephalitis					1								1
Chlamydophila abortus infection (Enzootic abortion of ewes, ovine chlamydiosis)						1		1					2
Contagious agalactia	5	3	8	4	8	8	7	3	4		1		51
Contagious bovine mastitis					1								1
Crayfish plague (Aphanomyces astaci)							1						1
Echinococcosis/Idatidosis							1						1
Equine infectious anaemia	6	4	7	4	1	6	1	2	2	4	3	1	41
Equine rhinopneumonitis						1							1
Erysipelas	4	2	3	1						2	1	1	14
European foulbrood of honey bees				2	3	2	1						8
High patogenicity Avian influenza in poultry	3	6	4	2	1		6	13	6	23	18	1	83
High patogenicity Avian influenza in wild birds	3			1	1			2	1	4			12
Infection with equine arteritis virus							1						1
Koi herpes virus disease (KHV)							3						3
Leptospirosis	2	3	4			1	2	1	1	3	4		21
Low patogenicity Avian influenza in poultry										1	3	2	6
Mange of equidae, bovines, buffaloes, ovine and caprine			1										1
Mixomatosis				1					1				2
Non-typhoidal avian salmonellosis	1	1	3	3	4	2	2	2	4	4	2	4	32
Nosemiasis	1												1
Paratuberculosis					1					1			2
Pasteurellosis of cattle, buffalo, sheep, goats and pigs				1									1
Porcine respiratory reproductive syndrome (PRRS)							1						1
Q fever	1							1					2
Rabbit haemorrhagic disease	1		3	3	1	2	3	1	1	4	7	2	28
Salmonellosis (S. abortusovis)	7	5	1			1				1			15
Salmonellosis of animals	1		1			1	2		2	2		1	10
Schmallengberg disease								1					1
Scrapie	4	7	8	7	1	8	2	3	2	3		1	46
Symptomatic anthrax									1				1
Trichinellosis							1			1			2
Tuberculosis of other mammals			1	1	1	3	1	1		2			10
West Nile Disease	1					1	27	63	28	11	5		136

Number of outbreaks reported by Regions to SIMAN in 2017



Number of outbreaks reported by Regions to SIMAN in 2017

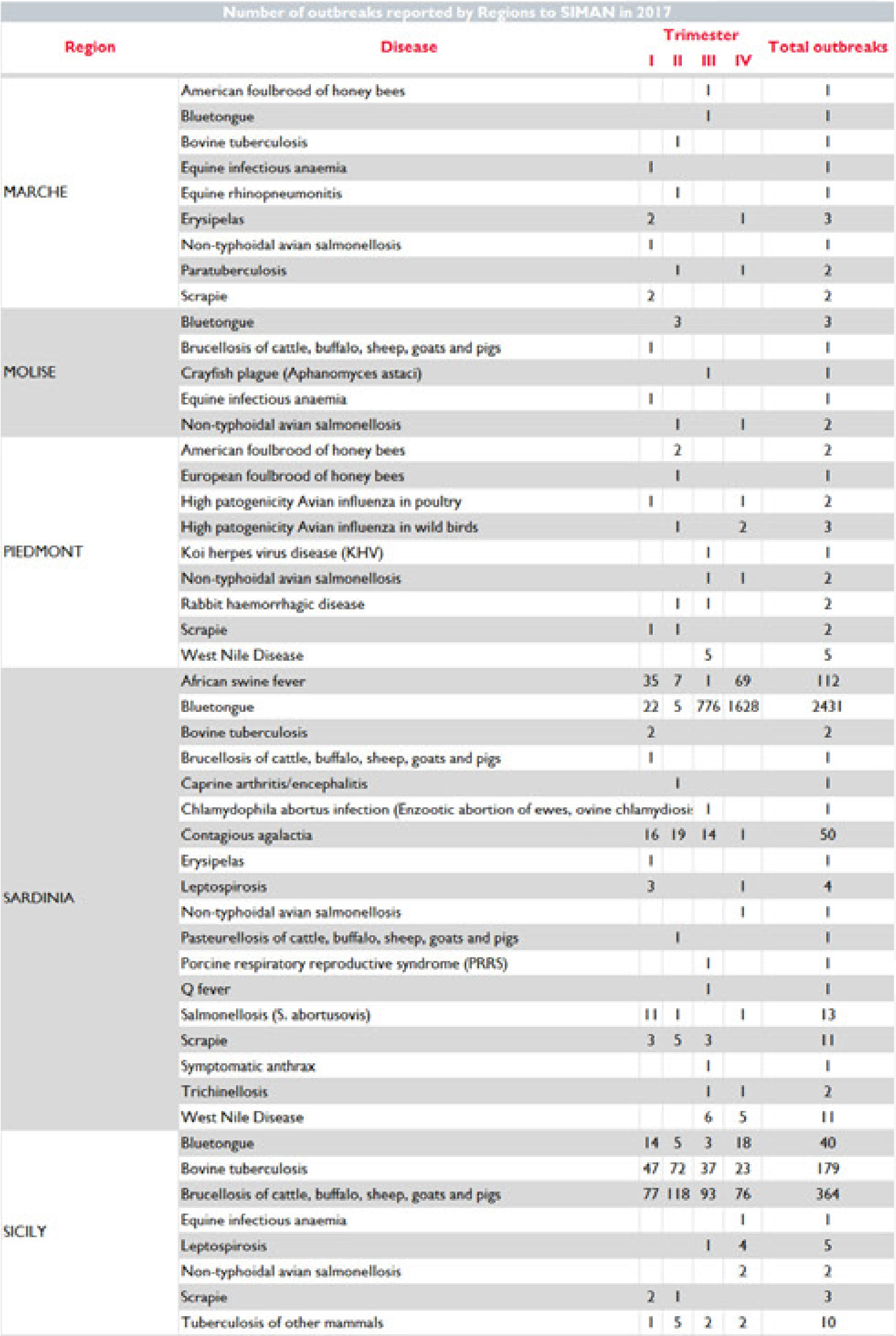
Region	Disease	Trimester				Total outbreaks
		I	II	III	IV	
ABRUZZO	American foulbrood of honey bees		1			1
	Bluetongue	1	2			3
	Brucellosis of cattle, buffalo, sheep, goats and pigs	4	2	1	4	11
	Equine infectious anaemia	4	5	1	2	12
	Non-typhoidal avian salmonellosis		1		2	3
	Scrapie	1	1	1		3
APULIA	Bluetongue	2	1	1	1	5
	Bovine leucosis	2	3	1		6
	Bovine tuberculosis	7	14	8	3	32
	Brucellosis of cattle, buffalo, sheep, goats and pigs	12	15	14	11	52
	Echinococcosis/Idatidosis			1		1
	Equine infectious anaemia	1	2	1		4
	Scrapie		3			3
BASILICATA	Avian cholera		1			1
	Bluetongue	4	5	4		13
	Bovine tuberculosis	1	7	4	5	17
	Brucellosis of cattle, buffalo, sheep, goats and pigs	9	5	4	13	31
	Equine infectious anaemia		1		2	3
	Non-typhoidal avian salmonellosis			1		1
	Scrapie	1				1
BOLZANO	American foulbrood of honey bees	1	1	2	2	6
CALABRIA	Aethina tumida	4	4	3		11
	Bluetongue	7				7
	Bovine tuberculosis	8	6	3	5	22
	Brucellosis of cattle, buffalo, sheep, goats and pigs	30	31	5	9	75
	Salmonellosis of animals		1			1
	Scrapie	1	1	1		3
CAMPANIA	Antrax				1	1
	Bluetongue	5	3	2	1	11
	Bovine babesiosis				1	1
	Bovine leucosis	1				1
	Bovine tuberculosis	12	17	14	8	51
	Brucellosis of cattle, buffalo, sheep, goats and pigs	16	19	29	20	84
	Equine infectious anaemia	2		2	1	5
	Infection with equine arteritis virus			1		1
	Non-typhoidal avian salmonellosis	1				1
	Rabbit haemorrhagic disease		1			1
	Salmonellosis of animals	1				1
	Scrapie	3				3

Number of outbreaks reported by Regions to SIMAN in 2017

Number of outbreaks reported by Regions to SIMAN in 2017

Region	Disease	Trimester				Total outbreaks
		I	II	III	IV	
EMILIA ROMAGNA	American foulbrood of honey bees	5	7	2		14
	Bluetongue	3				3
	Brucellosis of cattle, buffalo, sheep, goats and pigs	1	2		1	4
	Contagious bovine mastitis		1			1
	Equine infectious anaemia	1	1			2
	Erysipelas	3	1		1	5
	European foulbrood of honey bees		2			2
	High patogenicity Avian influenza in poultry	1	1	1	2	5
	High patogenicity Avian influenza in wild birds				2	2
	Low patogenicity Avian influenza in poultry				4	4
	Non-typhoidal avian salmonellosis		1	1		2
	Nosemiasis	1				1
	Scrapie		1		1	2
	West Nile Disease	1	1	41	3	46
FRIULI VENEZIA GIULIA	Bluetongue	6	6			12
	High patogenicity Avian influenza in poultry	1				1
	High patogenicity Avian influenza in wild birds	3				3
	Leptospirosis	2				2
	Non-typhoidal avian salmonellosis			1		1
	Rabbit haemorrhagic disease				3	3
LAZIO	American foulbrood of honey bees		3			3
	Antrax			1		1
	Bluetongue		2	4	9	15
	Bovine leucosis		1	2		3
	Bovine tuberculosis	3	2	3	1	9
	Brucellosis of cattle, buffalo, sheep, goats and pigs		1			1
	Chlamydophila abortus infection (Enzootic abortion of ewes, ovine chlamy		1			1
	Contagious agalactia		1			1
	Equine infectious anaemia	5	2		2	9
	European foulbrood of honey bees		2			2
	High patogenicity Avian influenza in poultry				1	1
	Leptospirosis	2				2
	Non-typhoidal avian salmonellosis			2		2
	Salmonellosis (S. abortusovis)	1				1
	Salmonellosis of animals	1		1		2
	Scrapie	2	1	1	2	6
	West Nile Disease			3		3
LIGURIA	Bluetongue			1		1
	Koi herpes virus disease (KHV)			1		1
	Rabbit haemorrhagic disease				1	1
LOMBARDY	American foulbrood of honey bees		2			2
	Bluetongue	1				1
	Bovine tuberculosis		1			1
	High patogenicity Avian influenza in poultry	2	1	13	31	47
	High patogenicity Avian influenza in wild birds		1	3		4
	Leptospirosis	1	1		1	3
	Low patogenicity Avian influenza in poultry				1	1
	Non-typhoidal avian salmonellosis	2	3	2	1	8
	Rabbit haemorrhagic disease		1	3	1	5
	Salmonellosis of animals			3	3	6
	Scrapie	1			1	2
	West Nile Disease			10		10

Number of outbreaks reported by Regions to SIMAN in 2017



Number of outbreaks reported by Regions to SIMAN in 2017

Region	Disease	Trimester I	II	III	IV	Total outbreaks
MARCHE	American foulbrood of honey bees			1		1
	Bluetongue			1		1
	Bovine tuberculosis		1			1
	Equine infectious anaemia	1				1
	Equine rhinopneumonitis		1			1
	Erysipelas	2			1	3
	Non-typhoidal avian salmonellosis	1				1
	Paratuberculosis		1		1	2
	Scrapie	2				2
MOLISE	Bluetongue		3			3
	Brucellosis of cattle, buffalo, sheep, goats and pigs	1				1
	Crayfish plague (Aphanomyces astaci)			1		1
	Equine infectious anaemia	1				1
	Non-typhoidal avian salmonellosis		1		1	2
PIEDMONT	American foulbrood of honey bees		2			2
	European foulbrood of honey bees		1			1
	High patogenicity Avian influenza in poultry	1			1	2
	High patogenicity Avian influenza in wild birds		1		2	3
	Koi herpes virus disease (KHV)			1		1
	Non-typhoidal avian salmonellosis			1	1	2
	Rabbit haemorrhagic disease		1	1		2
	Scrapie	1	1			2
	West Nile Disease			5		5
SARDINIA	African swine fever	35	7	1	69	112
	Bluetongue	22	5	776	1628	2431
	Bovine tuberculosis	2				2
	Brucellosis of cattle, buffalo, sheep, goats and pigs	1				1
	Caprine arthritis/encephalitis		1			1
	Chlamydophila abortus infection (Enzootic abortion of ewes, ovine chlamydiosi			1		1
	Contagious agalactia	16	19	14	1	50
	Erysipelas	1				1
	Leptospirosis	3			1	4
	Non-typhoidal avian salmonellosis				1	1
	Pasteurellosis of cattle, buffalo, sheep, goats and pigs		1			1
	Porcine respiratory reproductive syndrome (PRRS)			1		1
	Q fever			1		1
	Salmonellosis (S. abortusovis)	11	1		1	13
	Scrapie	3	5	3		11
	Symptomatic anthrax			1		1
	Trichinellosis			1	1	2
	West Nile Disease			6	5	11
SICILY	Bluetongue	14	5	3	18	40
	Bovine tuberculosis	47	72	37	23	179
	Brucellosis of cattle, buffalo, sheep, goats and pigs	77	118	93	76	364
	Equine infectious anaemia				1	1
	Leptospirosis			1	4	5
	Non-typhoidal avian salmonellosis				2	2
	Scrapie	2	1			3
	Tuberculosis of other mammals	1	5	2	2	10

Number of outbreaks reported by Regions to SIMAN in 2017

Number of outbreaks reported by Regions to SIMAN in 2017

Region	Disease	Trimester				Total outbreaks
		I	II	III	IV	
TRENTO	American foulbrood of honey bees		1	11		12
	Mixomatosis		1			1
	Rabbit haemorrhagic disease		1		7	8
	Scrapie		1			1
TUSCANY	American foulbrood of honey bees		4			4
	Bluetongue	2		3	9	14
	Equine infectious anaemia			1		1
	Erysipelas	1			1	2
	European foulbrood of honey bees		5	1		6
	Leptospirosis	1			1	2
	Mixomatosis			1		1
	Non-typhoidal avian salmonellosis		1		2	3
	Rabbit haemorrhagic disease	3	1	1	1	6
	Salmonellosis (S. abortusovis)	1				1
	Scrapie	1	1	1		3
	West Nile Disease			9	6	15
UMBRIA	American foulbrood of honey bees		2	1		3
	Bluetongue	1	2		1	4
	Erysipelas	1				1
	European foulbrood of honey bees		1			1
	Non-typhoidal avian salmonellosis	1				1
	Schmallengberg disease			1		1
VENETO	American foulbrood of honey bees			1		1
	Bluetongue	8	1			9
	Bovine tuberculosis				1	1
	Equine infectious anaemia	2				2
	Erysipelas	1			1	2
	High patogenicity Avian influenza in poultry	8	1	11	7	27
	Koi herpes virus disease (KHV)			1		1
	Leptospirosis			3		3
	Low patogenicity Avian influenza in poultry				1	1
	Mange of equidae, bovines, buffaloes, ovine and caprine	1				1
	Non-typhoidal avian salmonellosis		2			2
	Q fever	1				1
	Rabbit haemorrhagic disease	1	1			2
	Scrapie	1				1
	West Nile Disease			44	2	46

Animals involved in outbreaks reported to SIMAN in 2017

Animals involved in outbreaks reported to SIMAN in 2017

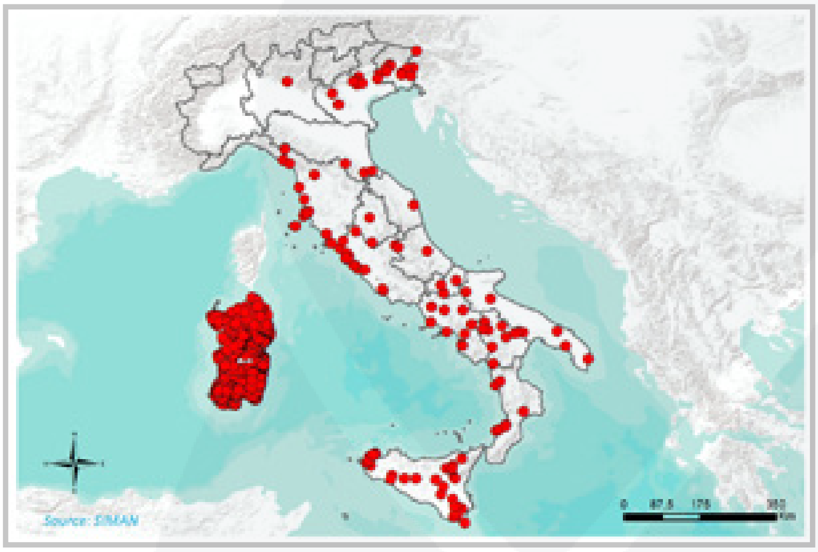
Disease	Animals involved	No. of animal	No. of diseased	No. of died	No. of culled	No. of destroyed
Aethina tumida	Bees	216	43	1	212	213
African swine fever	Suidae	507	323	83	399	474
American foulbrood of honey bees	Bees	699	98	7	82	89
Antrax	Ruminants	233	10	10	0	10
Avian cholera	Poultry	240	150	150	0	2
	Acquatic animals	4	1	0	0	0
Bluetongue	Ruminants	874293	122641	36222	1	36218
Bovine babesiosis	Ruminants	87	1	0	0	0
Bovine leucosis	Ruminants	607	12	0	1	1
Bovine tuberculosis	Ruminants	25410	2260	7	130	69
Brucellosis of cattle, buffalo, sheep, goats and pigs	Ruminants	358547	9365	22	949	559
	Suidae	29	12	0	0	0
Caprine arthritis/encephalitis	Ruminants	236	23	0	0	0
Chlamydophila abortus infection (Enzootic abortion of ewes, ovine chlamydiosis)	Ruminants	1639	6	2	0	2
Contagious agalactia	Ruminants	21140	2667	5	0	5
Contagious bovine mastitis	Ruminants	41	7	0	0	0
Crayfish plague (Aphanomyces astaci)	Acquatic animals		2	2	0	0
Echinococcosis/Idatidosis	Ruminants	98	1	0	0	0
Equine infectious anaemia	Equines	471	101	1	5	5
Equine rhinopneumonitis	Equines	45	1	1	0	0
Erysipelas	Suidae	17220	46	21	3	24
European foulbrood of honey bees	Bees	159	11	1	5	5
High patogenicity Avian influenza in poultry	Birds	101888	7443	4044	84049	88032
	Poultry	2668856	1114465	65698	2559290	2624514
High patogenicity Avian influenza in wild birds	Birds	10020	22	22	0	20
Infection with equine arteritis virus	Equines	7	1	0	0	0
Koi herpes virus disease (KHV)	Acquatic animals		31	22	13	33
Leptospirosis	Domestic carnviores	163	8	6	0	3
	Equines	155	34	0	0	0
	Ruminants	485	55	0	0	0
	Suidae	3015	47	0	1	0
Low patogenicity Avian influenza in poultry	Birds	24773	17990	61	24712	24773
	Poultry	2300	0	0	2300	2300
Mange of equidae, bovines, buffaloes, ovine and caprine	Ruminants	108	100	0	0	0
Mixomatosis	Lagomorphs	12	4	1	3	4
Non-typhoidal avian salmonellosis	Poultry	446962	224449	718	22578	22611
Nosemiasis	Bees	17	17	16	0	16
Paratuberculosis	Ruminants	181	2	0	0	0
Pasteurellosis of cattle, buffalo, sheep, goats and pigs	Ruminants	180	10	8	0	8
Porcine respiratory reproductive syndrome (PRRS)	Suidae	27	2	0	0	0
Q fever	Ruminants	1333	12	0	0	0
Rabbit haemorrhagic disease	Lagomorphs	54250	3844	3818	827	4472
Salmonellosis (S. abortusovis)	Ruminants	8129	196	0	0	0
Salmonellosis of animals	Poultry	12130	4280	0	1080	1080
	Ruminants	1747	394	5	0	4
	Suidae	51	1	0	0	0
Schmallengberg disease	Ruminants	435	8	0	0	0
Scrapie	Ruminants	22340	73	27	384	408
Symptomatic anthrax	Ruminants	38	8	6	0	6
Trichinellosis	Wild animals	2	2	2	0	2
Tuberculosis of other mammals	Suidae	935	18	0	20	20
West Nile Disease	Birds	80	69	32	13	42
	Equines	517	90	2	0	2
	Insects	177	78	1	0	1

A LOOK AT THE MAPS

The geographical distribution of the main animal diseases reported to SIMAN in 2017

Processing date: 9th January 2018

Bluetongue



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Geographical distribution of the outbreaks

High patogenicity Avian influenza in poultry

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Geographical distribution of the outbreaks

Low patogenicity Avian influenza in poultry

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Geographical distribution of the outbreaks

High patogenicity Avian influenza in birds

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Geographical distribution of the outbreaks

African swine fever

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Geographical distribution of the outbreaks

West Nile Disease

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Geographical distribution of the outbreaks

AROUND US

The main events of epidemiological interest in the last months in the European Union and in the neighbour countries

Eliminating dog-mediated human rabies by 2030: a One Health challeng

Whereas extensive efforts in developed countries have largely contributed to control rabies in non-flying mammals, dog rabies remains enzootic in much of the developing world. Although efficient vaccines are available for humans and animals, rabies remains one of the most neglected diseases inequitably affecting the poorest rural communities in developing countries, with an estimated 59,000 deaths per year, almost all transmitted by dogs. In the last decades, health leaders have increased their awareness that this fatal disease could be eliminated as a public health problem cost. Elimination of canine rabies is a priority to the World Health Organisation (WHO), the World Organisation for Animal Health (OIE) and the Food and Agriculture Organization of the United Nations (FAO) tripartite collaboration. "Zero by 30" is a campaign run by The Global Alliance for Rabies Control (GARC) jointly with the three international organizations to eliminate human deaths from canine rabies by 2030. Nevertheless, progress still remains slow. Currently, Latin America is undoubtedly the most successful region and the closest to the goal. South East Asia has engaged itself to reach the goal by 2020 and Africa by 2030. Several initiatives have been undertaken over the last years to move things forward in a relatively short time.

Dog rabies epidemiological situation (Latin America – Asia – Africa)

Latin America and the Caribbean - Countries in this region have made steady progress toward eliminating canine rabies, although four different dates for the elimination of rabies have been set so far (1990, 2000, 2012, and 2015), with the last one fixed at 2022. With substantial help from the Pan American Health Organization, they jointly purchase and share vaccines, use standardized surveillance and coordinate vaccination along borders. The regional elimination program has triggered a reduction of about 90% of dog-transmitted human cases from 1980 to 2017. However, Brazil, Peru and Venezuela still count for sporadic dog-mediated human cases and dog rabies is still endemic in Bolivia, Guatemala and Haiti (Figure 1).

Southeast Asia – In 2017, eight out of ten ASEAN (Association of Southeast Asia Nations) Member States (AMS) are still endemically infected with rabies, namely Cambodia, Indonesia, Lao PDR, Myanmar, the Philippines, Thailand, Vietnam and Malaysia, which unfortunately has recently acquired rabies in areas close to neighboring Thailand and Myanmar. Similarly, in the 2000s certain Indonesian islands, historically dog-rabies free, have experienced an extensive re-emergence of the disease (Bali, 2008, Nias Island, 2010, Larat Island, 2010, Dawera Island, 2012). Those incidents further highlight the transboundary nature of rabies virus and the need for a joint regional control to ensure national disease elimination. The remaining two small countries, namely Singapore and Brunei, historically free of rabies, are not representative but an exception to the general status of South East Asia, very likely due to their small size. Importantly, in 2014 and with the support of the tripartite international organizations and GARC, ASEAN countries have unanimously endorsed the regional Rabies Elimination Strategy (ARES) (Figure 2).

Figure 1. Epidemiological status of dog and human rabies in Latin America and the Caribbean

Figure 2. Epidemiological status of dog and human rabies in South East Asia

Africa – The African continent experienced one of the most successful rabies elimination programs, which was founded by the Bill and Melinda Gates foundation in Kwa-Zulu-Natal (KZN, South Africa). The 2008-2013 program proved to be extremely successful by reducing human deaths in the South African region to almost zero. The elimination program has been extended and is now funded by the SA authorities, demonstrating the feasibility of eliminating dog rabies in Africa. Since then, the KZN actors have become worldwide champions, and have stimulated other African countries to reach a similar accomplishment. Thus, in 2015 the commitment of Africa to eliminate the disease was renewed through the launch of the Pan-African Rabies Control Network (PARACON) with the aim to unify pre-existent networks, such as SEARG, AfroReb, RIWA and RESOLAB Rabies subnetwork. The first PARACON meeting held in South Africa in 2015 considered the elimination of canine-mediated human rabies by 2030 to be a plausible achievement. Since then, several initiatives have been undertaken under the PARACON umbrella, among these regional and sub-regional meetings and consultancies, the development of a regional Rabies Epidemiological Bulletin and guidance to national authorities for planning elimination programs (Figure 3).

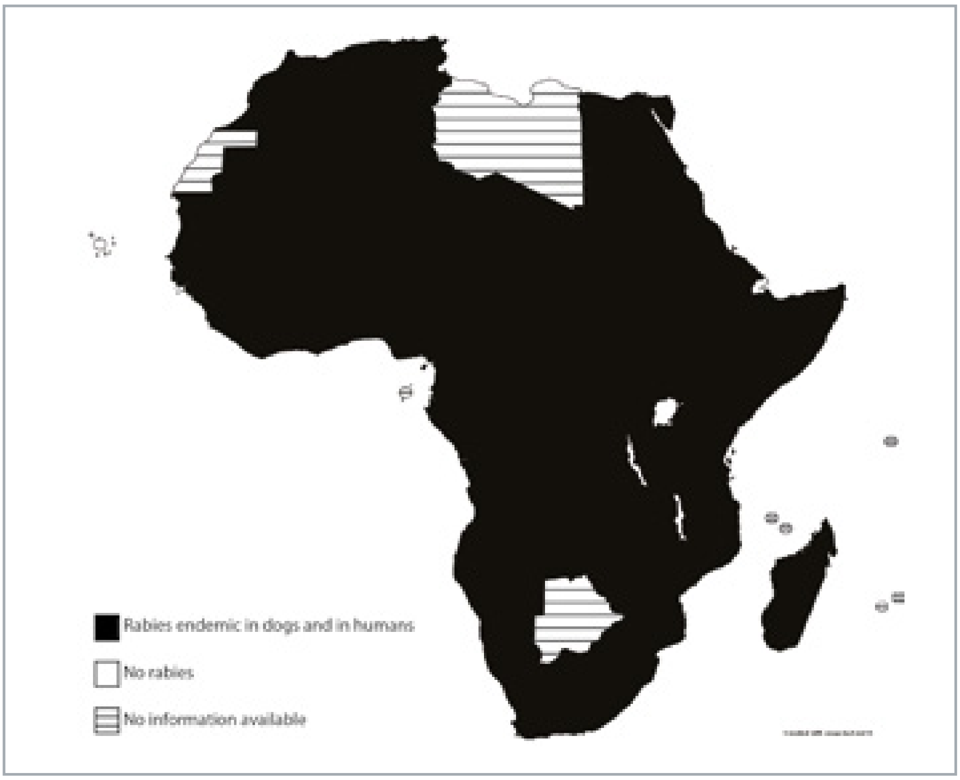

Figure 3.
Epidemiological status of dog and human rabies in Africa

Tools available to reach the "Zero by 30" goal

Several technical guidance tools are now available to national authorities. With the aim of increasing community awareness and of promoting education about the disease, in 2007 GARC launched the **World Rabies Day** (WRD- 28th of September), whose focus is to coordinate and organize local, regional or national events in rabies endemic countries. In 2015, the WRD initiative was backed up by an international campaign named End Rabies Now.

Similarly, global rabies experts (GARC, FAO, and European Commission) have put into place the Blueprint for Canine Rabies Prevention and Control, to assist countries where rabies is still endemic to design, implement and evaluate a large-scale rabies control program. This online resource consists of a single online point of access to all relevant international resources, which offers practical guidance on rabies control. Over time, the rabies blueprint has developed detailed modules on canine rabies, on fox rabies, on rabies surveillance, and particularly, they have included the Stepwise Approach towards Rabies Elimination (SARE) developed by FAO and GARC. The SARE tool is intended to provide detailed guidance to countries to measure the progress towards achieving rabies control and eventually elimination of dog-transmitted human rabies. SARE is not intended to replace existing regional or national rabies control strategies: it is supposed to serve as a self-assessment tool and a practical guide to develop a national rabies program and to successfully implement a long-term elimination strategy. The SARE is divided into 5 stages: countries can progress from stage 0 (no available information on rabies) to stage 5 (continuous monitoring for elimination of human rabies transmitted by dogs). Across the stage key themes such as a) data collection and analysis, b) prevention and control, c) laboratory diagnosis, d) dog population related issues, e) information, education and communication, f) cross cutting issues, g) legislation are considered. Spurred on by a simple idea, the SARE tool was initially conceived as an excel datasheet into which policy makers could enter available information related to their own countries. Nowadays, the SARE assessment gives a complete evaluation of the situation with the attribution of an overall SARE score and then, accordingly, provides programmed activities and well-defined actions ranging from one to five-year plans.

The whole process aims to divide the efforts needed to reach elimination into small steps and to evaluate the progress made. Furthermore, yearly SARE updates allow countries to quantify their journey into the path towards the elimination of human death caused by canine rabies by 2030.

At a global level rabies epidemiological data are scarcely and inconsistently input into the official databases, so that human (and animal cases) are mostly estimated. Official OIE notification of rabies through the WAHIS is patchy and not representative of the real situation. The WHO Rabnet database has even been discontinued until further notice due to its unreliable and irregular data uploading from member states. However, there is a growing trend for feeding regional epidemiological bulletins with regional data, with the final idea that a targeting approach has more potential than a global one. So far, the WHO funded Rabies Bulletin Europe has proven to be extremely successful and has played as an excellent example for new initiatives, such as in Latin America, the Caribbean and in Africa.

International organizations have committed themselves to facilitate the access to vaccines and immunoglobulins in endemic countries. In particular, the development of the OIE animal vaccine bank has been fruitful, uses production on demand to ensure good shelf life, and offers lower prices. Five years after its creation, the bank has delivered 19 million doses over 27 countries worldwide.

From a public health point of view, the Strategic Advisory Group of Experts (SAGE) on Human Immunization from WHO has required the establishment of a background study on whether administration of pre-exposure prophylaxis (PrEP), post-exposure prophylaxis and rabies immunoglobulin (RIG) could be simplified and rendered more cost-effective. Furthermore, as the availability and accessibility to vaccines in endemic countries is problematic, the Global Alliance for Vaccines and Immunization (GAVI) is currently considering including rabies vaccine in their priority list.

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Global Animal Disease Intelligence Report (GADIR)

The "Global animal disease intelligence report" (GADIR) is a regular update on the main disease threats monitored and analysed by the FAO/AGAH/GLEWS worldwide. This intelligence report contains relevant analysis of disease information collected by FAO GLEWS from official and informal sources and prepared with the kind support of donors to enhance global early warning and surveillance for animal diseases.

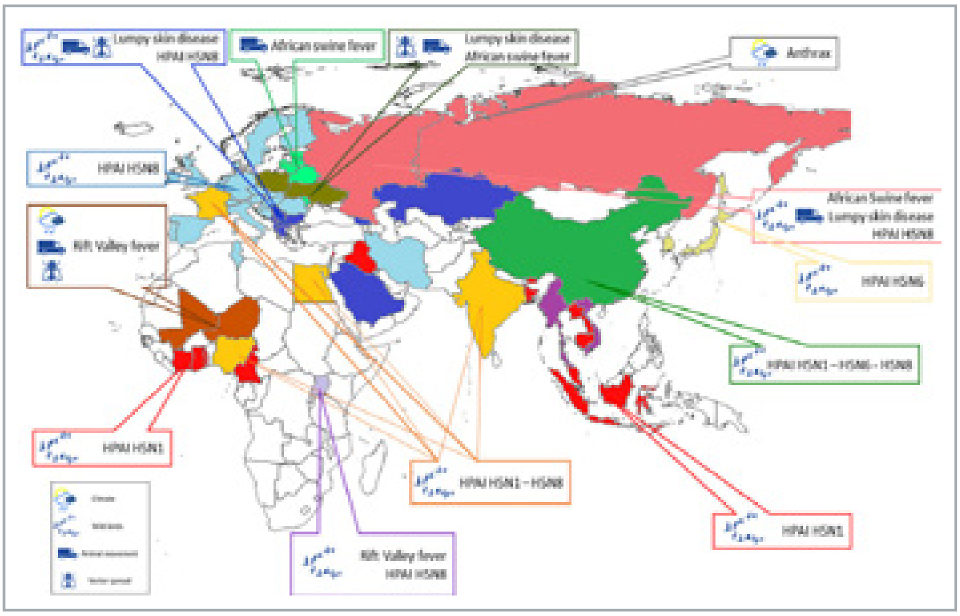

Figure 1.
Main remarkable animal health events occurred during 2016 with the indication of major drivers (reproduced from FAO/AGAH, GADIR 2016).

The Global Early Warning System (GLEWS) became one of the mechanisms used by the OIE, FAO and WHO together for monitoring data from existing event-based surveillance systems and to track and verify relevant animal and zoonotic events. This mechanism has provided a global platform that brought together expertise, data, functional networks, operational systems and stakeholders to improve inter-organizational coordination and support to Member countries for detecting, preventing and controlling threats to health and the food chain.

Animal Disease Overview

As in previous years, a continuous circulation of highly pathogenic avian influenza (HPAI) H5 subtypes was observed in China and other Asian countries. At the same time, however, a notable global spread of subtype H5N8 took place. Starting from migratory birds' summer breeding sites in Asia, and driven by subsequent bird movements, this subtype was able to spread across the whole of Europe and reach sub-Saharan countries in Africa.

Concerning vector-borne infections, lumpy skin disease (LSD) continued to spread across the Balkan countries during 2016 (Bulgaria, Greece, Kosovo, the Former Yugoslav Republic of Macedonia, Serbia and Albania) and in the southwestern zones of the Russian Federation, supported by the presence of vectors and, possibly, uncontrolled movements of infected animals.

Spread of LSD in Greece was mitigated by a vaccination campaign and movement restrictions imposed in the affected areas. A risk assessment issued by the European Food Safety Authority (EFSA) concluded that vaccination had a greater impact in reducing LSD spread than stamping out, despite low vaccination effectiveness (40%). Howev¬er, independently of any stamping-out intervention, vaccination measures were considered most effective in reducing LSDV spread if protection had already been developed at the time of virus entry. The assessment stressed the importance of vaccinating susceptible cattle populations in regions at risk of LSDV introduction prior to any virus incursion (EFSA, 2016).

Climatic conditions, and anomalous higher precipitations in particular, were probably associated with the occurrence in August 2016 of Rift Valley fever (RVF) in Niger, where around 400 human cases with more than 30 deaths were observed. Considering the likelihood of occurrence in the neighbouring countries, the predictions made in October 2016 by a rapid risk assessment performed by FAO were confirmed in January 2017 with the notification of the first RVF outbreak in small ruminants in Mali.

Weather conditions were also associated with an unusual outbreak of anthrax in Siberia (Russian Federation) in July 2016, when reindeer - *Rangifer tarandus* - (Linnaeus, 1758) and humans were affected. Abnormally high temperatures in the spring and early sum¬mer facilitated permafrost melt, disturbing the soil and bringing anthrax spores to upper soil layers. Human cases occurred among people who had been in contact with infected animals or had consumed their meat or blood.

During 2016, African swine fever (ASF) continued to spread in Eastern Europe (Belarus, Estonia, Latvia, Lithuania, Republic of Moldova, Poland the Russian Federation and Ukraine) and in 2017 in Czech Republic, Ukraine, Romania, Russia, Poland, Rep. of Moldova, Lithuania, Latvia, Estonia. Different risk factors have been considered for the disease's massive spread across Eastern Europe: uncontrolled movements of infected animals and contaminated pork meat, swill feeding habits, and the scarce application of biosecurity principles, especially in the backyard sector, which is clearly play¬ing an important role in the maintenance of the infection in some countries. Moreover, wild boar population plays a crucial role in maintaining and spreading the disease, significantly hampering eradication efforts.

Different studies highlighted the extensive geographical distribution of wild boar, wild boar management (hunting systems, winter feeding), local density and size of the infected population, together with direct contact with dead infected wild boar, as the most relevant risks for the spread and the persistence of the virus in wild boar populations (Bellini *et al.*, 2016).

However, wild animals can be also victims of infections introduced by domestic animals. The recent case of Peste des petit ruminants infection in saiga antelopes (Saiga tatarica ssp. mongolica) in Mongolia is just one such spillover events. Mongolian saiga is an extremely rare species, to be found only in the Altai-Sayan ecoregion of Mongolia. Thanks to conservation efforts, the saiga population rose to 14 600 in 2015. However, with the PPR infection, which killed more than 4 000 animals, the survival of this species is being challenged again.

During 2016, 13 outbreaks of Middle East Respiratory syndrome –coronavirus (MERS-CoV) in camels were reported to the OIE- 11 from Saudi Arabia and 2 from Jordan. In 2016 a total of 255 human cases with 96 deaths were reported globally. Dromedaries infected with MERS-CoV and asymptomatic humans were likely to play the main role for human infection. Direct contacts between humans and dromedaries were identified as the major risk factor- far greater than consumption of camel products (meat and milk).

Drivers of animal diseases

Factors/drivers influencing the dynamics of animal and zoonotic diseases globally include changes in land use, animal and food product movements and trade (informal and uncontrolled animal movements and poor biosecurity conditions), changes or intensification of con¬tacts with the wildlife and livestock or human interfaces, migrations due to wars and civil unrest, and the effects of climate and cli¬mate-related phenomena.

El Niño Southern Oscillation (ENSO)

The global climate during the year was influenced by the continuation of strong El Niño conditions in the winter (Jan¬uary–March 2016), its transition into a neutral phase during the summer season (June-September), and the development of La Niña conditions in October–December 2016.

Animal trade

The globalization of trade in live animals and products, together with increased international travel is facilitating disease incursion into free areas. The protection formerly offered by natural barriers is now becoming ineffective. Significant amounts of natural or ag¬riculture-based resources harvested or produced in developing countries are further processed or consumed in economically more advanced countries, providing regular routes for hitchhiking organ¬isms. Similarly, developing countries are often not self-sufficient in various food commodities and, when importing them, the are exposed to the risk of bringing in new pests or pathogens (Richardson *et al.*, 2016). Although not reflected in glob¬al trade data, price differentials across regions and borders are well known to encourage unregulated movements of animals and animal products, thus increasing the risk of the risk of pathogens and disease spreading.

Festival and traditions

In various countries around the world, many traditional feasts and festivals are celebrated every year, often boosting demand for an¬imal products, with consequent increased animal trade and move¬ments, as well as human travel. For example, during the Chinese New Year, mass travel by peo¬ple within China, or returning to their hometowns, from abroad is often seen as one of the main drivers for increased person-to-per¬son infections such as seasonal influenza and respiratory diseas¬es in general.

Wildlife

Many scientific papers dealing with disease control and preven¬tion consider wild animals reservoirs of pathogens and the key actors in the (re)emergence of epidemic threats.

From an ecological perspective, wild animals may play a main¬tenance function, allowing the conservation of pathogens within ecosystems. A maintenance host (or reservoir), is therefore a host population (a single population) or a community/host complex (several populations) in which pathogens may persist even in the absence of transmission from other hosts (Caron *et al.*, 2015). However, wild animal populations, given their capacity to transmit in¬fections to farmed animals and human beings, are monitored by veterinary and public health authorities. From the epidemiological point of view, wild species may act as reservoirs that maintain pathogens in the environment, as bridge species involved only in the transmission of pathogens, or they may play both roles (Caron *et al.*, 2015).
A recent review identified the ten zoonotic diseases most often discussed in scientific papers dealing with the wildlife–livestock interface (Wiethoelter *et al.*, 2015). First among them was avian influenza (both low- and highly pathogenic). That is not surprising, considering the crucial role played globally by wild bird popula¬tions in the emergence of new virus subtypes and in their main¬tenance and spread.

A recent analysis of H5N8 HPAI covering viral sequences, epidemiological data, waterfowl migration, and poultry trade was able to demonstrate that the virus spread along two main long-distance migration routes: one from the Korean peninsula, northward to the Arctic coast of the Eurasian conti¬nent and then west to Europe and the other north from the Korean peninsula, then east across the Bering Strait, and south along the northwest coast of North America.

The results of outbreak investigations on affected poultry farms in North America and Europe show that the likelihood of virus intro¬duction via contaminated water, feed, and poultry was negligible and no links between the outbreaks in one country and those in other countries could be attributed to personnel contacts or trade in live animals, feed, or products of animal origin. In contrast, many affected poultry farms were in areas where wild waterfowl were abundant, and direct contact with infected wild birds or indirect contact with materials (e.g. bedding, boots, and vehicle wheels) contaminated by wild bird faeces were considered the most likely route of introduction (Global Consortium for H5N8 and Related Influenza Viruses, 2016). Recognition of the likely role of wild birds in the spread of HPAI reinforces the need to improve biosecurity on poultry farms and strengthen surveillance over waterfowl at the crossroads of migratory flyways, both in win¬tering and breeding sites

Another disease at the wildlife-domestic animal interface of major concern is African swine fever. Different risk factors have been considered for the disease's massive spread across Eastern Europe: uncontrolled movements of infected animals and pork meat, swill feeding habits, and scarce application of biosecurity principles, especially in the backyard sector, which is clearly play¬ing an important role in the maintenance of the infection in some countries. However, in the Baltic countries and in Poland, it was observed that wild boar habitat suitability and the distance from infected wild boar and domestic pig farms were the main risk factors for the spread of the virus through infected wild boar (Bellini *et al*., 2016).

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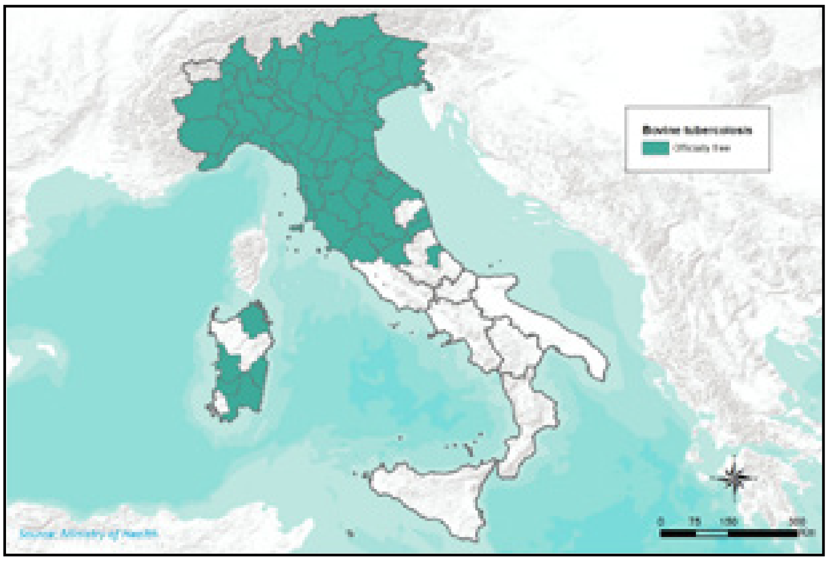
OFFICIALLY FREE TERRITORIES

Bovine tuberculosis: provinces and regions officially free according to the community legislation updated to up to 22th May 2017

Decision	Region	Province
2016/168/UE	Abruzzi	Pescara
	Emilia Romagna	The whole region
	Friuli Venezia Giulia	The whole region
	Lazio	Rieti Viterbo
	Liguria	The whole region
	Lombardy	The whole region
	Marche	Ancona Ascoli Piceno Fermo Pesaro-Urbino
	Piedmont	The whole region
	Sardinia	Cagliari Medio-Campidano Ogliastra Olbia-Tempio Oristano
	Tuscany	The whole region
	Trentino-Alto Adige	Bolzano Trento
	Veneto	The whole region
2017/888/UE	Umbria	The whole region

Bovine tuberculosis



Source: Ministry of Health

Bovine leukosis: Provinces and Regions Officially Free according to the EU legislation updated to 17th October 2017

Decision	Region	Province
2017/1910/EU amending Decision 2003/467/EEC	All regions	All provinces

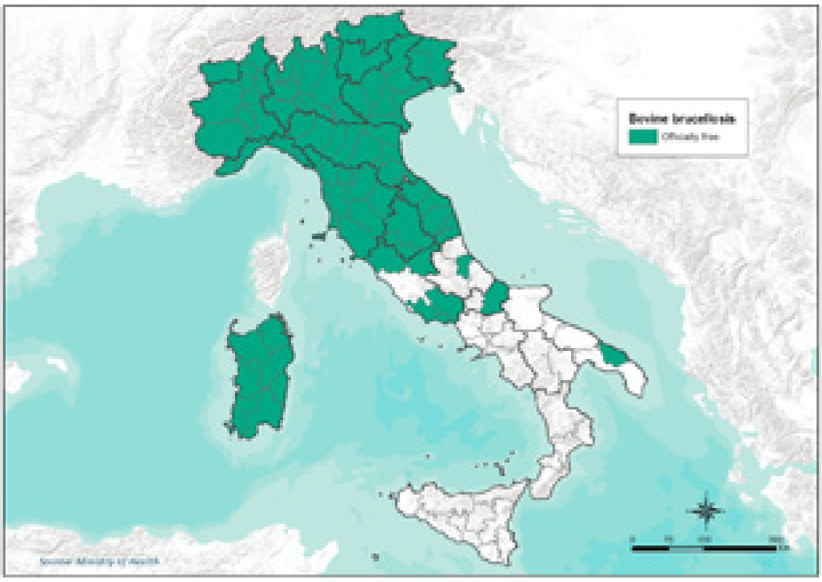
Bovine leukosis

Source: Ministry of Health

Bovine brucellosis: Provinces and Regions Officially Free according to the EU legislation updated to 11th October 2016

Decision	Region	Province
2016/168/UE	Abruzzi	Pescara
	Emilia Romagna	The whole region
	Friuli Venezia Giulia	The whole region
	Lazio	Rieti
		Viterbo
	Liguria	The whole region
	Lombardy	The whole region
	Marche	Ancona
		Ascoli Piceno
		Fermo
		Pesaro-Urbino
	Piedmont	The whole region
	Sardinia	Cagliari
		Medio-Campidano
		Ogliastra
		Olbia-Tempio
		Oristano
	Tuscany	The whole region
	Trentino-Alto Adige	Bolzano
		Trento
	Veneto	The whole region
2017/888/UE	Umbria	The whole region

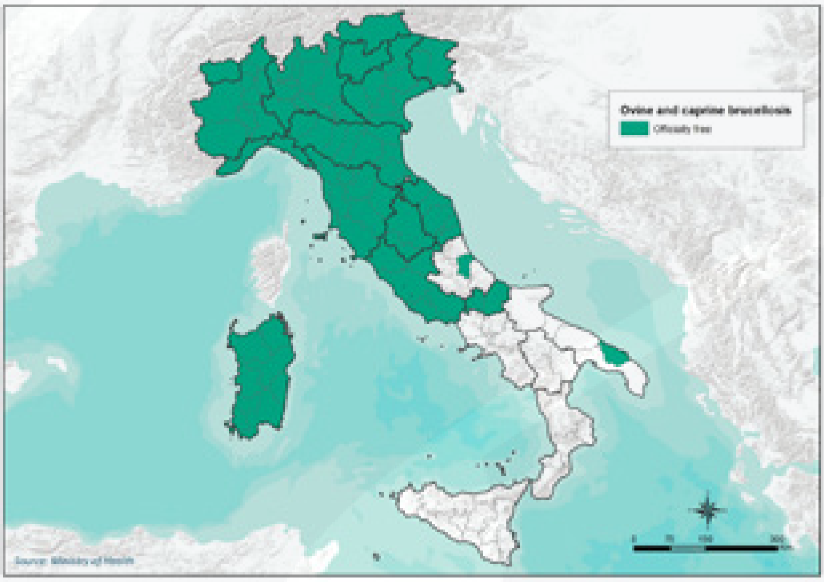
Bovine brucellosis



Ovine and caprine brucellosis: Officially Free according to the EU legislation updated to 11th October 2016

Decision	Region	Province
2014/91/EU amending annex II of Decision 93/52/EEC	Abruzzi	Pescara
	Emilia Romagna	The whole region
	Friuli Venezia Giulia	The whole region
	Lazio	The whole region
	Liguria	The whole region
	Lombardy	The whole region
	Marche	The whole region
	Molise	The whole region
	Piedmont	The whole region
	Sardinia	The whole region
	Tuscany	The whole region
	Trentino Alto Adige	Bolzano Trento
	Umbria	The whole region
	Valle d'Aosta	The whole region
	Veneto	The whole region
2016/1811/EU amending Annex II to Decision 93/52/EEC	Apulia	Brindisi

Ovine and caprine brucellosis



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