THE INCIDENCE OF SRLVs INFECTION IN EUROPEAN COUNTRIES OVER THE 10 YEAR PERIOD, 2006 TO 2015

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Abstract

Maedi-Visna and Caprine Arthritis Encephalitis are specific small ruminants' diseases caused by viruses belonging to family Retroviridae. Romania also reported these diseases, epidemiological investigation notifying a peak of prevalence between 2009 and 2011. In Romania, these diseases have been reported in few counties – 14 out of 42. The SRLVs have a high genetic variability and to discriminate them they must be used serological tests directed to their structural proteins. The need for surveillance of these diseases remains a long term issue, knowing their epidemiological dynamics. The present paper underline the epidemiological pattern of SRLVs in Europe, to point the SRLVs incidence between 2006 and 2015 and to identify the European's SRLVs hot spots.

Key words*: small ruminants, retroviridae, maedi-visna, caprine arthritis encephalitis, epidemiology*

1. INTRODUCTION

Maedi-Visna (MV) and Caprine Arthritis Encephalitis (CAE) are specific small ruminant's diseases caused by small ruminant lentiviruses (SRLVs), a genetic continuum of lentiviral species in sheep and goats, belonging to family *Retroviridae* (Leroux, Cruz & Mornex 2010). The SRLVs have a high genetic variability and, to discriminate them, it must be used various immunological and molecular methods (Brinkhof & van Maanen 2007; Herrmann-Hoesing 2010).

SRLVs and/or their nucleic acid were detected in many different small ruminant species, including wild species, as *Capra ibex* (Erhouma et al. 2008) and *Ovis orientalis* (Guiguen et al. 2000). These species seem to be susceptible and the virus can spread between domestic and wild species. Also, Maedi-Visna virus (MVV) can be experimentally transmitted to goats and Caprine Arthritis Encephalitis virus (CAEV) can also be transmitted to sheep. In addition, some phylogenetic studies on different SRLVs genes suggest that there is a natural way of transmission of the sheep viruses to goats and the natural transmission of the goats' virus to sheep (Shah et al. 2004).

The relation between the breed, the MVV susceptibility and the infection seem to be strengthen. Some breeds are relatively susceptible: Texel, Border Leicester, Finnish landrace. Other breeds are relatively resistant: Columbia, Rambouillet and Suffolk. Awassi, Finnish and Border Leicester breeds were identified as having a high rate of infection, while Roumbouillet and Iceland x Border Leicester had low levels of infection (Muz et al. 2013). The understanding of the influence of the genetic evolution on the biological properties of the SRLVs may lead to adaptive changes influencing the pathogenesis and the viral transmission of the SRLVs (Minardi da Cruz et al. 2013).

The SRLVs can be transmitted from infected animals with or without clinical signs, using different ways, including long term cohabitation with infected animals and consuming of infected colostrum/milk (McNeilly et al. 2007; Patton et al. 2012). Close contact is common among sheep during winter housing conditions and this could have provided an easy means of spread of virus by nose-to-nose contact. This way of contamination is active because the free-virus and the cell with the associated virus are present in the alveolar-bronchial fluid of the infected sheep (McNeilly et al. 2007). In addition, since the SRLVs were detected in the colostrum and milk, the maternal transmission from mother to offspring and the non-maternal transmission by ingestion are important sources of infection. Also, lactating sheep and goats are highly susceptible to lentivirus-induced mastitis and it is already known that the mammary gland is a target structure for SRLVs (Kennedy-Stoskopf, Narayan & Strandberg 1985). After the ingestion of colostrum, the lambs are exposed to the virus when they are

commingled with the adult infected animals. The route of transmission is horizontal and however accepted as being the possibility of viral spread between different geographic regions by programs which involve the commercial trade (Peterhans et al. 2004). The intrauterine transmission is considered neglected or minor, even if the presence of virions in the male's infected semen suggests that this way of transmission can occur (Houwers & Nauta 1989; Brodie et al. 1995). The presence of CAEV-infected epithelial cells in the genital tract tissues could have a major impact on the epidemiology of the disease. Infected epithelial cells could maintain latent infection with no accompanying inflammatory reaction; the embryo or foetus could therefore come into contact with CAEV during pregnancy and therefore could be infected at different stages of development (Ali Al Ahmad et al. 2012).

In contaminated herds, SRLVs are endemic but with variable frequency of clinical occurrence, correlated with the particularities of control programs used from a country to another. Therefore, it is expected that the incidence of disease outbreaks and the number of new cases, vary from one state to another and from one year to another.

The aim of the present paper is to underline the epidemiological pattern of SRLVs in Europe, to point the SRLVs incidence between 2006 and 2015 and to identify the European's SRLVs hot spots.

2. MATERIALS AND METHOD

2.1. Samples collection

Data concerning population of sheep and goats by countries and years were collected from Eurostat Database (Eurostat 2015).

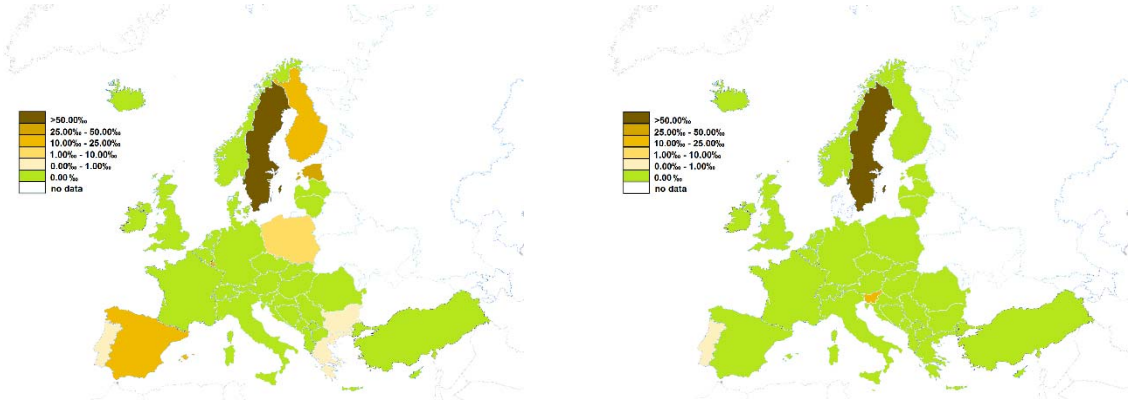
Data concerning the number of cases and outbreaks of CAEV and MVV infections by countries and years were collected from World Animal Health Information Database (WAHIS) Interface (The World Organisation for Animal Health (OIE) 2015).

2.2. Retrospective study

The incidence (new cases/1000 animals) and new outbreaks of CAEV and MVV infections between 2005 and 2015 in European countries was determined and compared by countries and years.

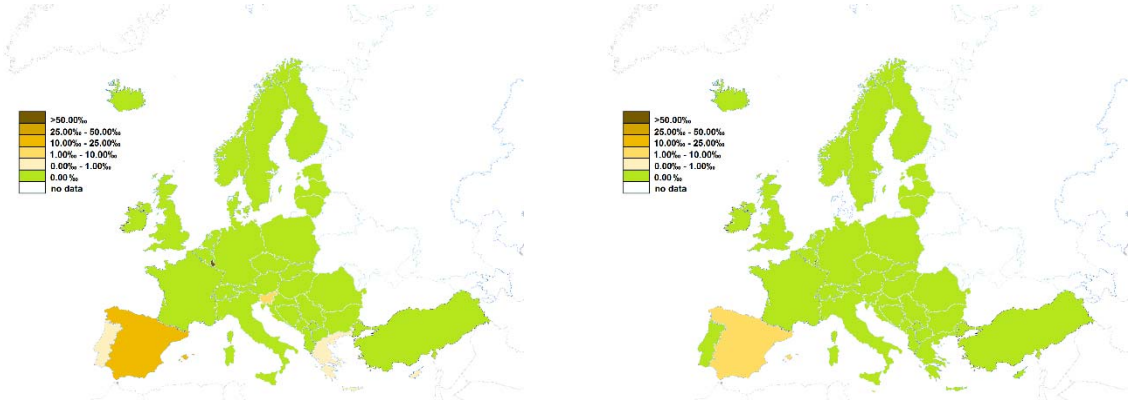
3. RESULTS

The results are synthetically presented in the following figures ant tables.



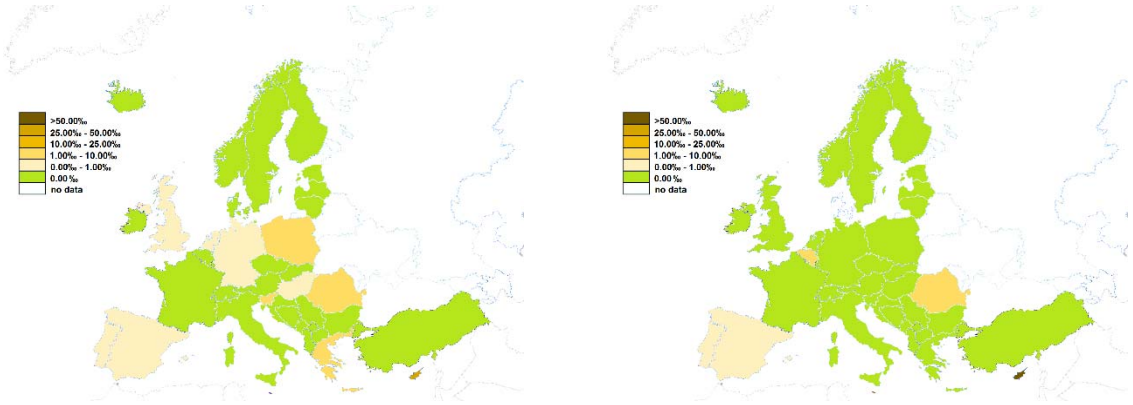
(a) (b)

Figure 1: Prevalence of MVV (a) and CAEV (b) infections in 2006, in European countries.



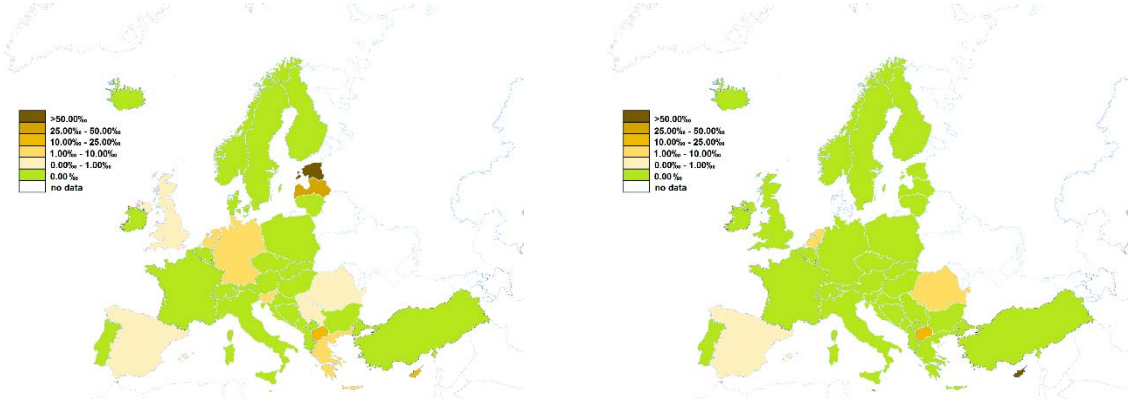
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Figure 2: Prevalence of MVV (a) and CAEV (b) infections in 2007, in European countries.



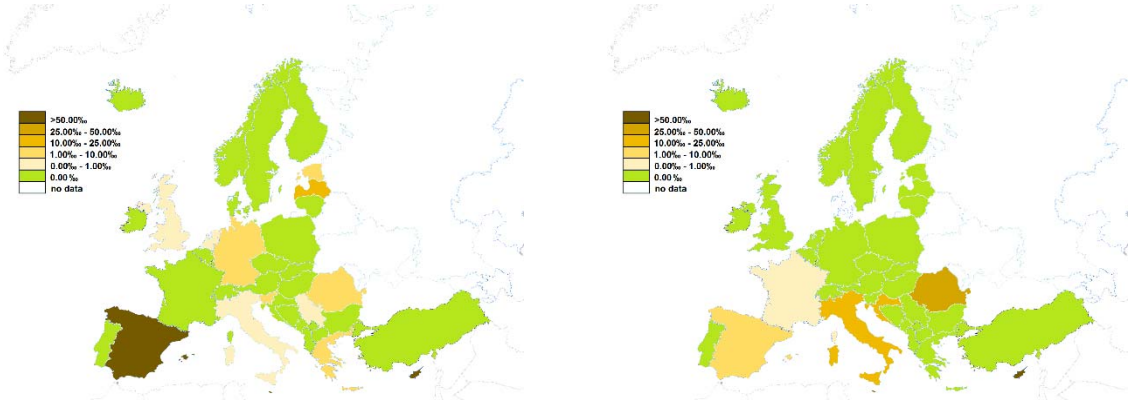
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Figure 3: Prevalence of MVV (a) and CAEV (b) infections in 2008, in European countries.



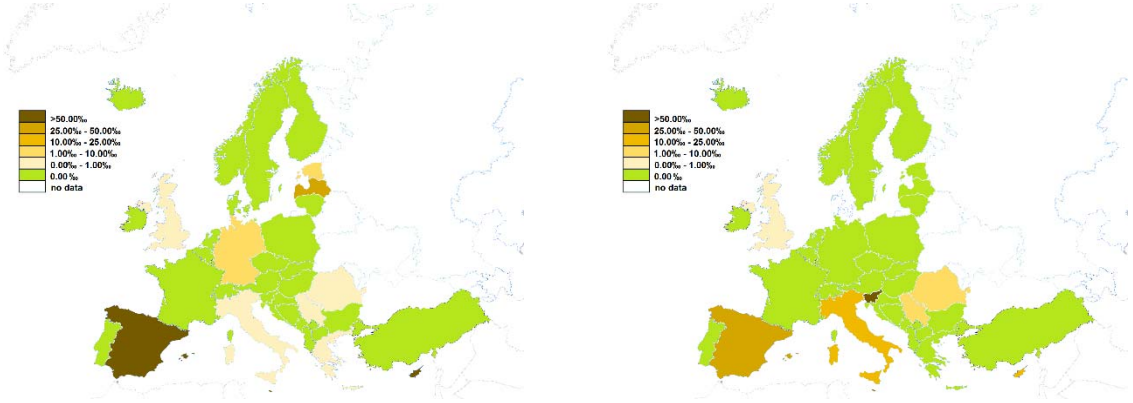
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Figure 4: Prevalence of MVV (a) and CAEV (b) infections in 2009, in European countries.



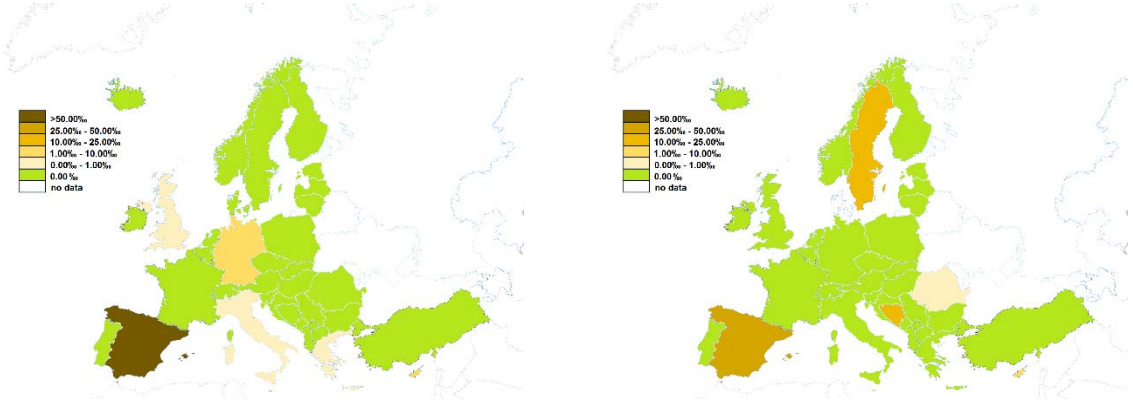
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Figure 5: Prevalence of MVV (a) and CAEV (b) infections in 2010, in European countries.



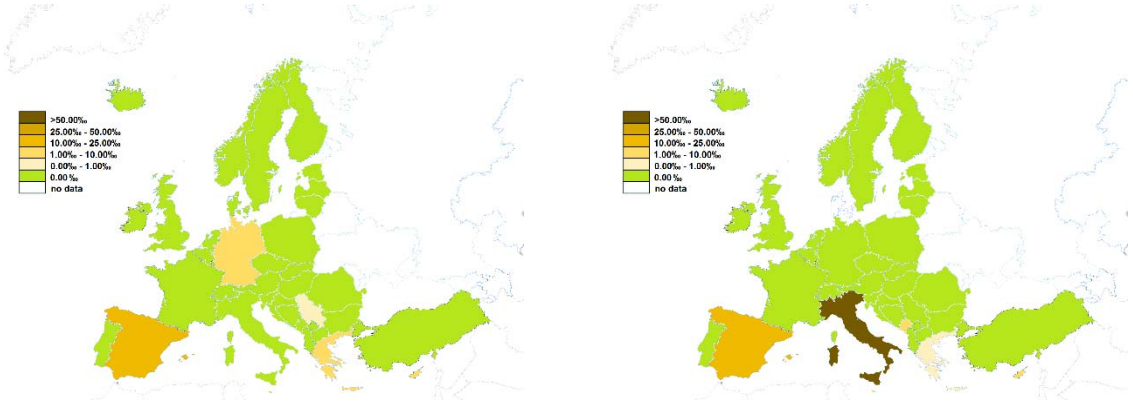
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Figure 6: Prevalence of MVV (a) and CAEV (b) infections in 2011, in European countries.



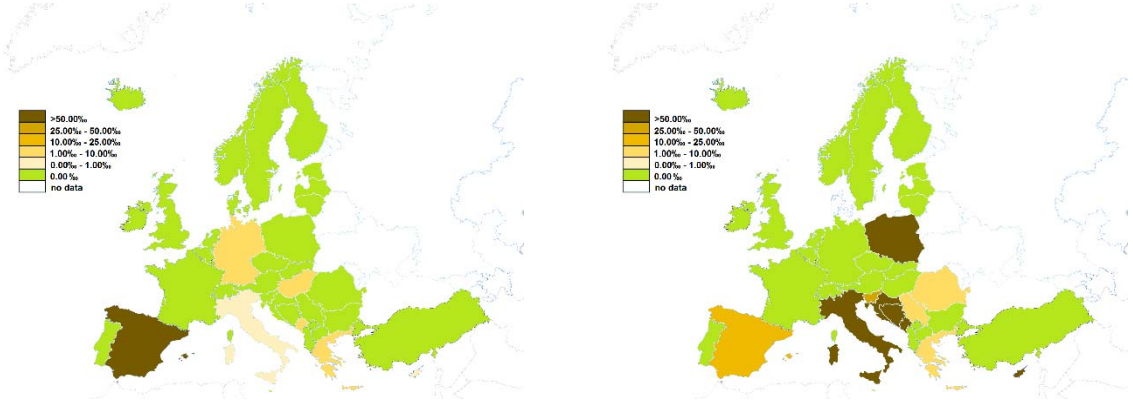
(a) (b)

Figure 7: Prevalence of MVV (a) and CAEV (b) infections in 2012, in European countries.



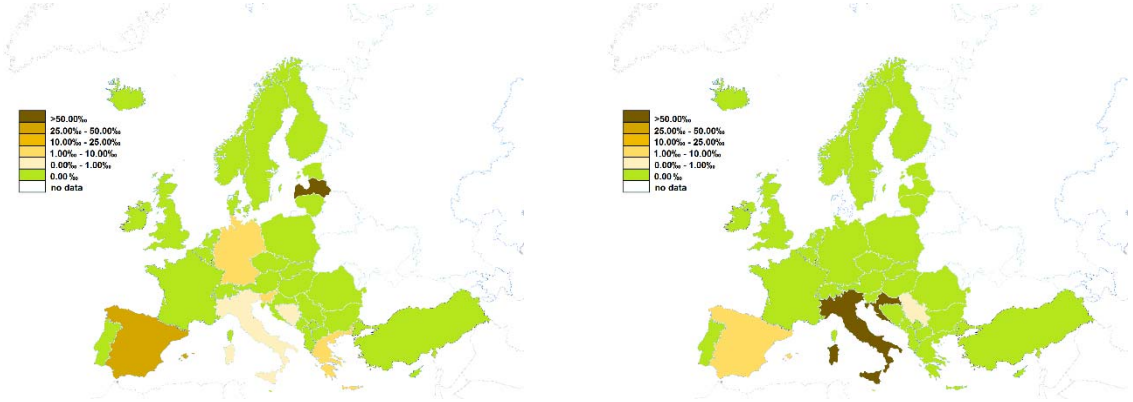
(a) (b)

Figure 8: Prevalence of MVV (a) and CAEV (b) infections in 2013, in European countries.



(a) (b)

Figure 9: Prevalence of MVV (a) and CAEV (b) infections in 2014, in European countries.



(a) (b)

Figure 10: Prevalence of MVV (a) and CAEV (b) infections in 2015, in European countries.

Table 1. Outbreaks of MVV infection between 2006 and 2015 in European countries

	2006	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**Total**
Spain	47	87	1	7	178	46	220	158	18	12	**774**
Germany	21	14	25	44	24	47	39	21	31	47	**313**
Romania	0	0	24	2	225	1	0	0	0	0	**252**
Greece	15	5	8	11	34	12	17	8	17	78	**205**
Malta	0	0	7	0	8	65	0	0	0	0	**80**
Luxembourg	2	42	0	0	0	0	0	0	0	0	**44**
Hungary	0	0	6	0	0	0	0	25	12	0	**43**
Cyprus	0	1	10	6	5	5	11	3	1	0	**42**
United Kingdom	0	0	1	3	11	9	9	7	0	0	**40**
Latvia	0	0	0	7	2	2	0	0	0	15	**26**
Netherlands	0	0	10	11	4	0	0	0	0	0	**25**
Estonia	5	1	1	1	1	2	1	3	2	0	**17**
Italy	0	0	0	0	2	3	2	0	2	7	**16**
Slovenia	0	1	3	5	1	0	0	0	0	3	**13**
Serbia	0	0	3	1	2	1	0	1	0	0	**8**
Poland	6	0	2	0	0	0	0	0	0	0	**8**
Montenegro	0	0	0	0	0	0	0	0	2	0	**2**
Macedonia	0	0	0	2	0	0	0	0	0	0	**2**
Sweden	2	0	0	0	0	0	0	0	0	0	**2**
Finland	2	0	0	0	0	0	0	0	0	0	**2**
Bulgaria	2	0	0	0	0	0	0	0	0	0	**2**
Bosnia	0	0	0	0	0	0	0	0	0	1	**1**

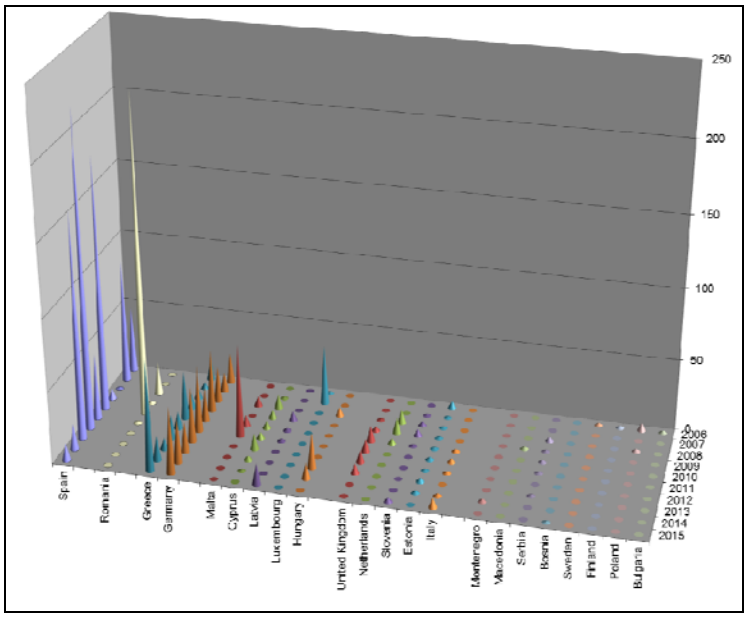


Figure 11: Distribution of MVV infection outbreaks between 2006 and 2015 in European countries.

Table 2. Outbreaks of CAEV infection between 2006 and 2015 in European countries

	2006	**2007**	**2008**	**2009**	**2010**	**2011**	**2012**	**2013**	**2014**	**2015**	**Total**
Romania	0	0	23	12	140	4	1	0	1	0	**181**
Spain	0	5	7	7	34	21	32	14	7	1	**128**
Cyprus	0	0	17	34	6	11	5	3	4	0	**80**
Malta	0	0	6	1	9	50	0	0	0	0	**66**
Croatia	0	0	0	0	2	0	0	0	21	33	**56**
Italy	0	0	0	0	4	2	0	22	14	8	**50**
Sweden	30	0	0	0	0	0	1	0	0	0	**31**
Netherlands	0	0	0	10	0	0	0	0	0	0	**10**
Montenegro	0	0	0	0	0	0	0	1	6	0	**7**
Hungary	0	0	0	0	0	3	0	3	0	0	**6**
Slovenia	2	0	0	0	0	1	0	0	1	0	**4**
Greece	0	0	0	0	0	0	0	1	2	0	**3**
United Kingdom	0	0	0	0	0	1	1	1	0	0	**3**
Serbia	0	0	0	0	0	1	0	0	1	1	**3**
Germany	1	0	1	0	0	0	0	0	0	0	**2**
France	0	0	0	0	2	0	0	0	0	0	**2**
Bosnia	0	0	0	0	0	0	1	0	1	0	**2**
Belgium	0	0	1	0	0	0	0	0	0	0	**1**
Poland	0	0	0	0	0	0	0	0	1	0	**1**
Macedonia	0	0	0	1	0	0	0	0	0	0	**1**

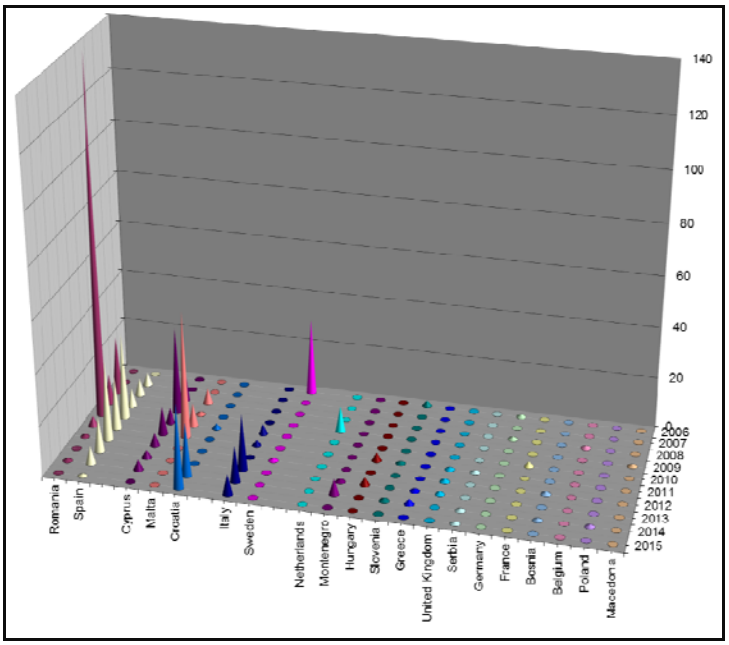


Figure 12: Distribution of CAEV infection outbreaks between 2006 and 2015 in European countries.

4. DISCUSSION

During 2006-2015, Belgium, Czech Republic, Denmark, Ireland, France, Croatia, Lithuania, Austria, Portugal, Slovakia, Iceland, Albania, and Turkey did not report any MVV infection outbreak on their territories. The retrospective data provided by these countries could suggest the absence of virus circulation both in domestic and wild ruminants, but this must be supported by screening and general surveillance policy, applied on a regular basis. Unfortunately, not all countries without MVV infection outbreaks applied general surveillance policy and the infection may be unreported. Therefore, Terrestrial Animal Health Code recommendations for the importation of sheep and goats for breeding need to be applied even if the country does not have active outbreaks of MV; hereby *"(1) the animals showed no clinical sign of maedi-visna on the day of shipment; (2) maedi-visna was neither clinically nor serologically diagnosed in the sheep and goats present in the flocks of origin during the past three years, and also that no sheep or goat from a flock of inferior health status was introduced into these flocks during that period; (3) animals over one year of age were subjected to a diagnostic test for maedi-visna with negative results during the 30 days prior to shipment"* (The World Organisation for Animal Health (OIE) 2011).

Based on the reported number of the outbreaks, we classify the European countries in 6 categories: (1) Countries with 1-10 outbreaks: Bulgaria, Poland, Finland, Sweden, Bosnia, Serbia, Macedonia, Montenegro; (2) Countries with 10-20 outbreaks: Italy, Estonia, Slovenia; (3) countries with 20-50 outbreaks: Netherlands, Latvia, United Kingdom, Cyprus, Hungary, Luxembourg; (4) Countries with 50-100 outbreaks: Malta; (5) countries with 100-400 outbreaks: Greece, Romania, Germany; (6) Countries with 400-800 outbreaks: Spain.

The descriptive statistics of MVV infection outbreaks along European countries revealed the following pattern of relative frequency and relative cumulative frequency (table 3, figure 13).

Table 3. Frequency table of the MVV infection outbreak categories in 35 European countries

Grouped interval of outbreaks	**Frequency***	**Relative frequency (%)**	**Cumulative frequency****	**Relative cumulative frequency (%)**
0	13	37.14	(13)	37.14
1-10	8	22.86	(21)	60.00
10-20	3	8.57	(24)	68.57
20-50	6	17.14	(30)	85.71
50-100	1	2.86	(31)	88.57
100-400	3	8.57	(34)	97.14
400-800	1	2.86	(35)	100.00

*number of countries included in each interval

**cumulative number of countries up to the end of a particular interval

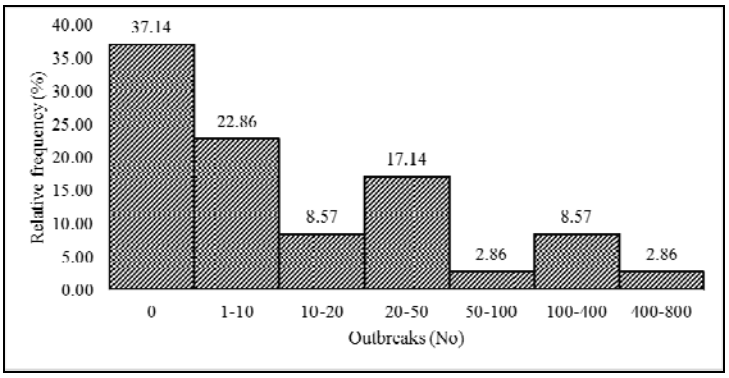


Figure 13. Histogram of the relative frequency distribution of European MVV infection outbreaks

Relative frequency of European countries without reported outbreaks of MVV infection was the highest, followed by countries with 1-10 outbreaks and 20-50 outbreaks. Relative cumulative frequencies analyses revealed that 68.57% of European countries reported less than 20 outbreaks and 11.43% reported over 100 outbreaks.

Our study revealed a high variation of reported outbreaks by European countries and, in some countries, from a year to another. If true (meaning "based on an active surveillance program “of whole population !), this variation can have different causes. The countries were the prevalence was between 1-10 outbreaks (2006-2015), it can be correlated with the consistency of “test and cull” actions. In countries with 10-20 outbreaks for the whole period of the study, it can be put into discussion a testing protocol by the random sampling or by the infected animals introductions based on the number of the reported outbreaks in successive years. In countries with prevalence (20-50 outbreaks), like Luxembourg, Netherlands and United Kingdom In countries with prevalence (20-50 outbreaks), like Luxembourg, Netherlands and United Kingdom could be supposed the introduction of susceptible animals and, in countries like Cyprus, Latvia and Hungary, there must be taken into consideration the surveillance and the implementation of “test and cull” program. In countries like Greece and Germany can be different causes of prevalence by annual new outbreaks distribution: for Germany, a natural wild reservoir of virus, and for Greece an inconsistent policy or both. Particularly, for Romania, it seems to be about the introduction of the disease, and, in case of Spain, it can be a natural source of infection or a lack of screening policies.

During 2006-2015, the following countries did not report any CAEV infection outbreak on their territories: Bulgaria, Czech Republic, Denmark, Estonia, Ireland, Latvia, Lithuania, Luxembourg, Austria, Portugal, Slovakia, Finland, Iceland, Albania and Turkey. Based on the reported number of the outbreaks, we classify the countries of Europe in 6 categories, as follow: (1) Countries with 1-10 outbreaks: Macedonia, Poland, Belgium, Bosnia, France, Germany, Serbia, United Kingdom, Greece, Slovenia, Hungary, Montenegro and Netherlands; (2) Countries with 10-20 outbreaks: none; 3) countries with 20-50 outbreaks: Sweden and Italy; (4) Countries with 50-100 outbreaks: Croatia, Malta and Cyprus; (5) countries with 100-400 outbreaks: Spain and Romania; (6) Countries with 400-800 outbreaks: none.

The descriptive statistics of CAEV infection outbreaks along European countries revealed the following pattern of relative frequency and relative cumulative frequency (table 4, figure 14).

Table 4. Frequency table of the CAEV infection outbreak categories in 35 European countries

Grouped interval of outbreaks	**Frequency***	**Relative frequency (%)**	**Cumulative frequency****	**Relative cumulative frequency (%)**
0	15	42.86	15	42.86
1-10	13	37.14	28	80.00
10-20	0	0.00	28	80.00
20-50	2	5.71	30	85.71
50-100	3	8.57	33	94.29
100-400	2	5.71	35	100.00
400-800	0	0.00	35	100.00

*number of countries included in each interval

**cumulative number of countries up to the end of a particular interval

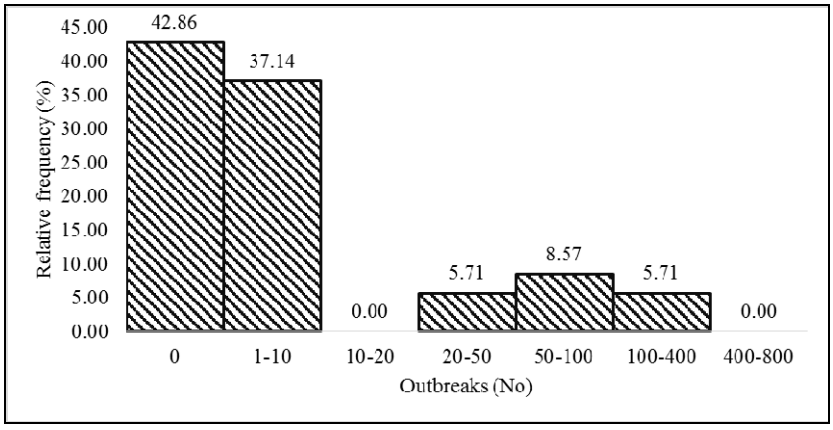


Figure 14. Histogram of the relative frequency distribution of European CAEV infection outbreaks

Like in MVV infection, the highest relative frequency was in the group of European countries without reported outbreaks of CAEV infection, followed by the group of countries with 1-10 outbreaks. Relative cumulative frequencies analyses revealed that 80% of European countries reported less than 20 outbreaks and 5.71% reported at least 100 outbreaks.

The countries were the prevalence of CAEV infection was between 1-10 outbreaks (2006-2015), it can be correlated with the consistency of "test and cull" actions. In countries with prevalence (20-50 outbreaks), like Sweden, seem to be caused by the introduction of susceptible animals. In other countries like Italy, there must be taken into consideration the active surveillance policy and application of the "test and cull" program. In countries like Romania and Spain can be different causes of prevalence by annual new outbreaks distribution: a natural reservoir of virus, inconsistent policies or the introduction of new animals without to perform serological test in order to identify the possible seropositive animals.

The descriptive statistics of MVV and CAEV infection outbreaks revealed broadly similar results that suppose the possibility of ovine-caprine interspecies infections and/or the existence of wild small ruminant's reservoir. Also, Minardi da Cruz et al. (2013) concluded that the "*evolution and the variability of SRLVs can facilitate the interspecies infections and small ruminants can transmit the viruses to other species*".

5. CONCLUSION

The control programs were initiated in many countries and in some of them, the disease was eradicated by slaughtering and the replacement with other animals from free areas/seronegative sheep/by the gradual slaughtering of the infected animals.

Beyond the high prevalence of the infection in many countries, another major obstacle in the eradication of SRLVs is the ability of these viruses to cross the species barrier. The recombination of the different strains and subtypes significantly contribute to the viral diversity and to the evolution of animals and populations.

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