The Risk of Introducing Tick-Borne Encephalitis and Crimean-Congo Hemorrhagic Fever into Southwestern Europe (Iberian Peninsula)

Ana M. Palomar, Aránzazu Portillo
Department of Infectious Diseases
Hospital San Pedro-Centre of Biomedical Research of La Rioja, Spain

José M. Eiros
Department of Pathological Anatomy, Microbiology, Preventive Medicine and Public Health
University of Valladolid, Spain

José A. Oteo
Department of Infectious Diseases
Hospital San Pedro-Centre of Biomedical Research of La Rioja, Spain
1 Introduction

Arboviral infections are world-wide distributed viral infections transmitted by arthropods, such as insects and ticks.

Ticks are arthropods (Arachnida belonging to Acari), ectoparasites and blood-sucking of vertebrates (mammals, birds and reptiles). They may act as vectors, intermediate hosts and reservoirs of a wide variety of infectious agents.

There are three families of ticks: Nutalliellidae, Argasidae (soft ticks) and Ixodidae (hard ticks). This last one is the most diverse, with at least 692 described species in the world (Nava et al., 2009), and with great importance in human and animal (veterinary) health (Jongejan & Uilenberg, 2004). The life cycle of a tick comprises three growth stages: larva, nymph and adult (male and female) (Figure 1). In this cycle, animals (wildlife, livestock and/or companion animals) can act as reservoirs or amplifier hosts and humans are accidental hosts. In favourable conditions, it takes from months (i.e. *Rhipicephalus* spp.) to 1-3 years (i.e. *Ixodes ricinus*) for the tick to hatch from the egg, go through all three stages, reproduce, and then die. Ticks normally feed on more than one host. This fact gives them a high potential for pathogens transmission such as bacteria, protozoa or viruses.

![Figure 1. Life cycle of the hard tick *Ixodes ricinus* (courtesy of the authors).](image)

Tick-bites may cause diseases by different pathogenic mechanisms. They may cause anaemia in animals they parasite (in some cases there are hundreds of ticks feeding on a unique animal), preventing them to get fatter and causing important economic losses. Ticks may also cause paralysis by inoculation...
of neurotoxins, allergic reactions and local injury with subsequent risk of super-infection by skin bacteria. Nevertheless, the most important mechanism of disease transmission is through the inoculation of pathogenic microorganisms.

Among factors for a tick-borne disease to be present in a certain area, we should consider: (1) The presence of the tick vector (each tick species is associated to particular microorganisms); (2) the presence of the reservoir (an organism able to maintain and amplify the pathogen without developing disease, and that in some cases may be the tick); (3) the susceptibility of each individual to the inoculated agent.

The Iberian Peninsula has different geographic and climatic zones with great contrasts, from wetlands up to desert areas. This fact coupled with the diversity of the fauna, favours the presence of many species of hard ticks and a broad spectrum of associated diseases (Table 1).

<table>
<thead>
<tr>
<th>Tick (Vector of disease)</th>
<th>Pathogen</th>
<th>Disease</th>
<th>Presence of human TBD in the Iberian Peninsula</th>
<th>Reference of human TBD in the Iberian Peninsula</th>
</tr>
</thead>
<tbody>
<tr>
<td><em>Ixodes ricinus</em></td>
<td><em>B. burgdorferi</em> s.l.</td>
<td>Lyme borreliosis</td>
<td>Yes</td>
<td>Oteo et al., 2000a</td>
</tr>
<tr>
<td></td>
<td><em>A. phagocytophilum</em></td>
<td>Human anaplasmosis</td>
<td>Yes</td>
<td>Oteo et al., 2000b</td>
</tr>
<tr>
<td></td>
<td><em>R. monacensis</em></td>
<td>Rickettsiosis</td>
<td>Yes</td>
<td>Jado et al., 2007</td>
</tr>
<tr>
<td></td>
<td>Babesia spp.</td>
<td>Babesiosis</td>
<td>Yes</td>
<td>Miguelez et al., 1996</td>
</tr>
<tr>
<td></td>
<td></td>
<td>Louping ill virus</td>
<td>TBE-Like</td>
<td>No</td>
</tr>
<tr>
<td><em>Dermacentor marginatus</em></td>
<td><em>R. slovaca</em></td>
<td>DEBONEL/TIBOLA</td>
<td>Yes</td>
<td>Oteo et al., 2004</td>
</tr>
<tr>
<td></td>
<td><em>Candidatus R. rioja</em></td>
<td>DEBONEL/TIBOLA</td>
<td>Yes</td>
<td>Portillo et al., 2009</td>
</tr>
<tr>
<td><em>Hyalomma</em> spp.</td>
<td>CCHFV</td>
<td>CCHF</td>
<td>NC</td>
<td>Filipe et al., 1985</td>
</tr>
<tr>
<td></td>
<td>Dhori virus</td>
<td>Innominated</td>
<td>NC</td>
<td>Filipe et al., 1985</td>
</tr>
<tr>
<td><em>Rhipicephalus sanguineus</em> group</td>
<td><em>R. conorii</em></td>
<td>MSF</td>
<td>Yes</td>
<td>Bacellar et al., 1999</td>
</tr>
<tr>
<td></td>
<td><em>R. massiliae</em></td>
<td>Rickettsiosis</td>
<td>Yes</td>
<td>Garcia-Garcia et al., 2010</td>
</tr>
<tr>
<td></td>
<td>Thogoto virus</td>
<td>Innominated</td>
<td>NC</td>
<td>Filipe et al., 1985</td>
</tr>
<tr>
<td><em>Haemaphysalis punctata</em></td>
<td>Bhanja virus (Palma virus)</td>
<td>Innominated</td>
<td>NC</td>
<td>Filipe et al., 1985</td>
</tr>
</tbody>
</table>


1 Only detected in sheep and goats (Gonzalez et al., 1987; Balseiro et al., 2012).
2 Confirmed in a patient returning to Spain from Argentina.

Table 1. Species of hard ticks with medical importance present in the Iberian Peninsula as well as the main pathogens they transmit and the associated human tick-borne diseases.
The list of tick-borne diseases (TBD) has grown in the last years. There are recent reviews of TBD caused by bacteria (Parola et al., 2005; Stanek et al., 2011; Oteo & Portillo, 2012; Portillo & Oteo; 2012). However, other TBD can be under-diagnosed or misdiagnosed in our environment due to the lack of clinical or diagnostic tools, or because they have not been previously present. This could be the case of human infection with Candidatus Neoehrlichia mikurensis. Only five cases of this bacterial infection have been reported in Europe (Welinder-Olsson et al., 2010; von Loewenich et al., 2010; Fehr et al., 2010; Pekova et al., 2011). Nevertheless, the identification of the causative agent in European I. ricinus ticks suggests that the incidence of this TBD could be higher.

At present, prevalence and geographic distribution of infections caused by tick-borne arboviruses (the arboviruses with greatest importance in human health, after dengue virus) also appear to increase (Ergonul, 2006; Mansfield et al., 2009; Ergonul, 2012; Hubálek & Rudolf, 2012). This may be due to better diagnostic tools and greater knowledge and surveillance on ticks (Donoso Mantke et al., 2011) but there are other factors that may influence this increase. Thus, climate change may favour the increase in populations of vectors and hosts in some regions (Parola et al., 2008; Estrada-Peña et al., 2012a). Cultural, social and economic changes that favour the conservation of natural areas and their enjoyment are associated to an increase in tick populations and greater exposure of humans to tick-bites (Figure 2). Migrations of the hosts favour the circulation of their ectoparasites and consequently of their infectious agents (Waldenström et al., 2007; Palomar et al., 2012). Furthermore, the import of livestock (Chisholm et al., 2012), hunting species or pets such as exotic reptiles that may be parasitized by infected ticks, should also be considered (Pietzsch et al., 2006; Nowak, 2010a; Nowak, 2010b; Rataj et al., 2011).

![Figure 2. Ixodes ricinus nymph attached to a patient (courtesy of the authors)](image)

At least, 27 tick-borne viruses have been described in Europe (Hubálek & Rudolf, 2012). Some of them cause serious diseases (i.e. Tick-Borne Encephalitis Virus, TBEV), while others (i.e. Eyach virus) are less pathogenic or seem to be associated (serological data) with infrequently reported human infec-
TBEV is a single-stranded RNA virus that belongs to the *Flavivirus* genus, family *Flaviviridae*. Virions are of small size (40-60 nm), with lipid envelope and spherical structure (Figure 3). TBEV has three main subtypes: European, Siberian, and Far Eastern (Mansfield *et al*., 2009). Some authors also include Louping ill virus in the TBE complex (Grard *et al*., 2007).

**Figure 3:** Structure of the mature phase of Tick-Borne Encephalitis virus (courtesy of the authors).

TBEV has been identified in several species of ticks and *I. ricinus* (European subtype), *Ixodes persulcatus* (Siberian and Far-Eastern subtypes) and *Ixodes ovatus* (Far-Eastern subtype in some areas of Japan) are recognized vectors (Figure 4). The virus has transovarial and transestadial transmission in ticks. Thus, the arthropod acts as vector and reservoir. Nevertheless, some authors defend the necessity of the co-feeding (transmission of pathogens between two ticks that feed very near on a host at the same time) for the viral infection to persist (Randolph, 2011). In addition to ticks, small mammals such as rodents of the genera *Apodemus* and *Myodes* (bank vole) (Süss, 2011) may act as amplifiers of the infection and, probably, as reservoirs (if the microorganism may persist in the rodent for a long time). Transmission of the infection occurs mainly by tick-bites, but cases of infection by the ingestion of contaminated, not pasteurized milk have been also reported (Süss, 2011).

TBE is the main viral disease transmitted by ticks in Eurasia, where cases of the disease have been reported in at least 32 countries (Süss, 2011). The disease is distributed in endemic foci in middle latitudes from Japan to France, and it has been also reported in South of the Scandinavian countries, North of Greece, Anatolia and Central and Northern China (Figure 5) (Petri *et al*., 2010; Süss, 2011; Ergunay, 2011). The incidence of infection is increasing, even reaching 400% increase in countries without vaccination programme (Süss, 2008).
Figure 4: *Ixodes ricinus* specimens waiting for hosts over vegetation. Left to right: Larvae and nymphs; two females; a male (courtesy of the authors).

Figure 5: Known distribution of cases of Tick-Borne Encephalitis Virus (modified from Süß, 2011 and Dobler *et al.*, 2012). Countries with autochthonous cases of the disease are shown in green. Countries without reported cases of illness but where the virus has been amplified from ticks and/or from cattle are shown in blue.

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Up to date, the presence of TBEV has not been detected in the Iberian Peninsula, although conditions are ideal for the circulation of the virus: Vectors (*I. ricinus* is the tick species that more frequently bites humans in the North of the Iberian Peninsula) as well as reservoirs are part of the faunal diversity. In addition, the presence of the Louping ill virus (closely related to TBEV) has been confirmed in countries such as Spain (González *et al.*, 1987; Balseiro *et al.*, 2012). Furthermore, the possibility of co-feeding of
larval and nymphal *I. ricinus* in Spain has been reported (Barandika *et al*., 2010), and we have observed co-feeding in birds from La Rioja (northern Spain) (Figure 6).

![Figure 6. *Ixodes ricinus* nymph and larva feeding on a Eurasian Blackcap (*Sylvia atricapilla*) captured in Spain (courtesy of the authors).](image)

The disease has a biphasic febrile clinical course. After an incubation period ranging from 7 to 14 days, appears the initial phase or viremia that lasts from 2 to 4 days. In this phase the symptoms are not very specific (fever, anorexia, headache, nausea, myalgia and arthralgia). After around 8 days of remission, a second phase that affects the central nervous system, causing meningitis and/or encephalitis and/or radiculitis may appear. The mortality rate is 0-3%, and patients may have important neurological sequelae (Mansfield *et al*., 2009). In some cases, TBE may co-exist with Lyme borreliosis since both diseases share ecological niche and vector. Clinical laboratory findings are nonspecific and may include leukopenia, thrombocytopenia, discrete elevation of transaminases at a first stage and later, elevation of leukocytes (Figure 7).

In the first phase, the virus can be detected by reverse transcription polymerase chain reaction (RT-PCR) techniques or by culture from patient specimens (cerebrospinal fluid, serum and/or heparinized plasma). This last procedure requires a Biosafety Level 3-Laboratory. In the following stages diagnosis is based on the detection of IgG and IgM antibodies using enzyme-linked immunosorbent assay (ELISA). This technique has cross reactions with other flaviviruses antibodies, and it is not useful if the patient has been previously vaccinated (Mansfield *et al*., 2009).

Prevention measures of TBE are to avoid tick-bites and the ingestion of unpasteurized milk. There are vaccines for primary prophylaxis of the infection that have showed to be very effective in endemic areas.

### 3 Crimean-Congo Hemorrhagic Fever Virus (CCHFV)

CCHFV, which is the causal agent of the CCHF, belongs to the *Nairovirus* genus, family Bunyaviridae. Virions are spherical, approximately 90-100nm in diameter, with lipid envelope and three genomic segments (S, M and L) of single-stranded RNA and negative polarity (Figure 8). Up to 8 different genotypes are known (Ergonul & Whitehouse, 2007).
Figure 7. Clinical and laboratory course of Tick-Borne Encephalitis Virus (courtesy of the authors).
CCHF is, after dengue, the arboviral disease with the greatest importance in human health due to its wide geographic distribution (Africa, Asia and South-Eastern Europe), the risk of acquisition, and its potential high percentage of mortality (up to 30%, and even >60% in outbreaks) (Khan et al., 1997; Ergonul, 2006; Ergonul, 2012).

The virus circulates in a cycle of enzootic tick-vertebrate-tick in which there is no evidence that cause disease in animals. Humans become infected through tick bites, by crushing infected ticks, after contact with a patient with CCHF during the acute phase of infection, or by contact with blood or tissues from infected livestock.

CCHFV has been isolated from at least 33 tick species belonging to the genera: *Hyalomma*, *Amblyomma*, *Rhipicephalus*, *Boophilus*, *Ixodes*, *Dermacentor*, *Haemaphysalis*, *Argas* and *Ornithodoros*, but most of them are not competent vectors. *Hyalomma marginatum* is considered the most important vector of the disease (Figure 9) (Turell, 2007). This tick species acts as reservoir since CCHFV is transmitted transovarial and transtadially. Small mammals (rodents) are also major reservoirs. Larger mammals and some birds such as ostriches seem to be important for the epidemiology of the virus (Ergonoul & Whitehouse, 2007). Birds harboring infected ticks suggest the dispersion of the virus during migrations, as it has been published by our group (Palomar et al., 2013), among others (Lindeborg et al., 2012). Although recent studies report low environmental suitability for the survival of foreign immature *H. marginatum* ticks introduced in Spain by migratory birds (EFSA, 2010; Bosch et al., 2012), the average temperatures recorded in spring in northern Spain during 2011 would have allowed ticks to molt.

Since the first documented and confirmed cases of CCHF in Crimea (1944) and Democratic Republic of the Congo (1956), outbreaks have been reported in the Balkans (Albania, ex-Yugoslavia), Bulgaria, Turkey, Iran, Iraq, United Arab Emirates, Saudi Arabia, Kuwait, Oman, Pakistan, Afghanistan, Former USSR, China, Uganda, Namibia, South Africa, Tanzania, Senegal, Kenya, Mauritania and Burkina Faso (Ergonul, 2006). More recently, cases of infection have been also described in Sudan, Greece, Georgia and India (Papa et al., 2008; Zakhashvili et al., 2010; Aradaib et al., 2011; Patel et al., 2011; Ergonul, 2012) (Figure 10). In addition, seroepidemiological studies in healthy population have evidenced the circulation of the virus in countries such as Turkmenistan, Nigeria, Egypt, Madagascar, Hungary, France, Portugal, Benin, Zimbabwe, Guinea, Cameroon, Congo and Romania (David-West et al.,

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**Figure 8.** Structure of the mature phase of Crimean-Congo Hemorrhagic Fever Virus (courtesy of the authors).
Figure 9. *Hyalomma marginatum* specimens. A: Larvae (unfed and engorged); B: Nymphs; C: Male; D: Engorged female (courtesy of the authors).

Figure 10. Known distribution of cases of Crimean-Congo Hemorrhagic Fever Virus, year 2012. Countries with autochthonous cases of the disease are shown in green. Countries without autochthonous cases of illness but where the virus has been amplified from ticks and/or from cattle are shown in blue.
1974; Smirnova et al., 1978; Blackburn et al., 1982, Gonzalez et al., 1989; Andriamandimby et al., 2011; Ergonul, 2012; Ceianu et al., 2012). Furthermore, imported cases of CCHF have been diagnosed in other European countries such as England, Germany and France (Jauréguiberry et al., 2005; ECDC 2008; Tall et al., 2009).

Generally, the CCHF infection courses in four phases. The incubation period varies between 3 and 7 days after the acquisition of the virus. Fever (39-41°C), headache, myalgia and dizziness may appear for about 3 days during the prehemorrhagic period. In the hemorrhagic period (2-3 days following the onset of the disease), ecchymosis and petechiae of the skin and mucous membranes, as well as gastrointestinal bleeding are common. This phase may cause the death of the patient. During the period of convalescence (about 10 days), breathing difficulties, tachycardia, loss of hair, hearing or memory may be present in survivors (Ergonul, 2006; Ergonul, 2012). Thrombocytopenia, leukopenia and increased levels of lactate dehydrogenase, some aminotransferases and creatinine phosphokinase (CPK) are the typical clinical laboratory findings. Alterations in coagulation may be observed (Figure 11).

Cell cultures (only sensitive in the first five days of infection and carried out in a Biosafety Level 4-Laboratory) as well as RT-PCR assays from blood samples (sensitive in the first 9 days of infection) and the detection of IgG antibodies by ELISA (from the first week and up to 5 years) are used for diagnosis of CCHF.

There is no commercial vaccine or demonstrably effective treatment. Nevertheless, the use of ribavirin for the treatment is recommended (Ergonul, 2012).

4 Situation in the Iberian Peninsula (Southwestern Europe)

The climatic and geographic heterogeneity of Southwestern Europe, located between two very contrasting areas such as Eurasia and Africa, is responsible for the high diversity of habitats and their biological richness, with abundant and diverse tick populations, and accordingly, their associated diseases. The changes of the environmental conditions (climatic and anthropological changes) could favor the establishment of new populations of ticks and their tick-borne pathogens (Estrada et al., 2012a). In this context, we will focus on the Iberian Peninsula, which is located in Southwestern Europe and has environmental and climatic conditions that favor the presence of several tick species (up to 29 species of hard ticks have been identified) and reservoirs, and where numerous tick-borne diseases have been reported. Some of them, such as Lyme borreliosis, Mediterranean spotted fever and Dermacentor-borne, necrosis, erythema and lymphadenopahy (DEBONEL) are endemic or very prevalent in our environment (Oteo et al., 2000a; Oteo & Portillo, 2012).

The presence of CCHFV and TBEV in European areas with climate conditions, vegetation and fauna similar to those in the Iberian Peninsula (Hubálek & Rudolf, 2012), along with the presence of tick populations recognized as main vectors of these viruses (*I. ricinus* and *H. marginatum*), the increasing number of human tick-bites from these tick species observed in our area (Figure 12), the previous detection of Louping ill virus (closely related to TBEV) in ticks and livestock (González et al., 1987; Balseiro et al., 2012), the import of livestock and pets, and the existence of febrile syndromes and encephalitis cases of unknown etiology after tick-bites have made necessary monitoring the presence of these viruses in our country. Moreover, the Iberian Peninsula is a stopover or breeding site in the migratory routes of several bird species (Hoyo et al., 2004), and migratory birds have been demonstrated to be carriers of infected ticks (Palomar et al., 2013). The existence of the co-feeding has been also suggested (Barandika et al., 2010), and this phenomenon has been observed by our group (Figure 6).
Figure 11. Clinical and laboratory course of Crimean–Congo Hemorrhagic Fever (courtesy of the authors).
The reasons for the absence of these viral diseases in Southwestern Europe are unknown, and even febrile syndromes and encephalitis cases may have been misdiagnosed. Thus, an investigation aimed to detect TBEV and CCHFV in ixodid ticks from La Rioja (North of Spain) and other Spanish provinces is being performed at the Centre of Rickettsiosis and Arthropod-Borne Diseases, Area of Infectious Diseases, Hospital San Pedro-Centre of Biomedical Research from La Rioja (CIBIR), Logroño, Spain. This project was funded by the “Fondo de Investigación Sanitaria”, Ministry of Science and Innovation (PS09/02492), Spain. The following sections detail the methodology and results obtained from January 2010 to June 2012. Other study about the risk of TBEV infection was carried out in the same area (Barandika et al., 2010).

4.1 TBEV in Spain

Ticks belonging to *I. ricinus* species were captured from vegetation (blanket dragging technique) and mammals (cows and deer) during years 2010 and 2011. Collected specimens, except larvae (n=1,055), were processed for the study of the presence of TBEV in La Rioja. A total of 1,000 nymphs and 1,020 adults were grouped in pools of 10 or 5 individuals, respectively. Samples were homogenized and RNA was extracted using RNeasy Mini Kit (Qiagen, Hilden, Germany) according to the manufacturer's recommendations. Reverse transcription to cDNA was performed using Omniscript RT (Qiagen, Hilden, Germany). The presence of TBEV was tested using qPCR for the detection of a fragment of the non-coding 3’ region (Schwaiger & Cassinotti, 2003).

TBEV was not found in any samples. Our results agree with those obtained in a previous study carried out in ticks from the North of Spain (Basque Country and La Rioja) (Barandika et al., 2010). Nevertheless, these data support but do not confirm the absence of the virus in Spain (Stefanoff et al., 2012).

Disease surveillance plans should be followed. As previously stated, in Spain there are established tick populations of the TBEV vector (*I. ricinus*) and reservoirs (small mammals), the phenomenon of co-feeding occurs (our observation; Figure 6), as previously suggested (Barandika et al., 2010), and the circulation of a subtype of the virus (Louping ill) transmitted by the same tick species has been demonstrated in our environment (González et al., 1987; Balseiro et al., 2012). Furthermore, in Europe, TBE and
Lyme borreliosis have similar distribution (epidemiology), and Lyme borreliosis is endemic in the North of Spain (Oteo et al., 2000a).

4.2 CCHFV in Spain

From the end of 2009 to mid-2012, removal of *H. marginatum* specimens from cattle and poultry was carried out in La Rioja. In addition, *Hyalomma lusitanicum* specimens were collected over deer in the province of Cáceres (Southwestern Spain) in November 2010. A total of 473 *H. marginatum* adult specimens were processed. Specimens were grouped in pools of 10 specimens or individually if immature, homogenized and RNA was extracted using RNeasy Mini Kit (Qiagen, Hilden, Germany) according to the recommendations of the manufacturer. Reverse transcription to cDNA was performed using Omniscript RT (Qiagen, Hilden, Germany). Conventional PCR and qPCR assays for the amplification of different fragments of the S segment of CCHFV were performed (Midilli et al., 2007; 2009; Burt & Swanepoel, 2005; Atkinson et al., 2012).

CCHFV was not detected in *H. marginatum*, but it was found in *H. lusitanicum*. Two out of 12 analyzed pools were positive using a fragment of the S segment (211 bp) as PCR target (Midilli et al., 2009). Only one sequence could be obtained. When compared with those deposited in GenBank, it showed 98% identity with CCHFV strains from Sudan and Mauritania (Estrada-Peña et al., 2012b). These results were confirmed by the National Centre for Microbiology (Instituto de Salud Carlos III, Madrid, Spain).

This is the first detection of CCHFV in Southwestern Europe (Figure 10). The genetic identity with African strains, allowed us to hypothesize about the presence of the virus in Spain and the arrival of CCHFV-infected ticks through migratory birds (Estrada-Peña et al., 2012b). Furthermore, in April 2011 bird ringings were carried out in Zoula (Morocco), which is on the route of birds that migrate from central and southern Africa to Europe in spring. Ticks parasitizing these birds were collected for the investigation of CCHFV. A total of 52 *H. marginatum* specimens (all immature stages) were studied. RNA was extracted using AllPrep DNA/RNA Mini Kit (Qiagen, Hilden, Germany). Reverse transcription to cDNA was performed using Omniscript RT (Qiagen, Hilden, Germany). A total of 6 pools were tested by PCR as previously described (Midilli et al., 2009) and four pools yielded positive results, showing a minimum infection rate of 7.7%. Sequences (n=3) obtained from the S fragment (211 bp) were identical each other, and homologous (100% identity) to Sudan AB1-2009 and Mauritania ArD39554 strains, showing almost 99% identity with those previously detected in ticks from Cáceres (Palomar et al., 2013). These PCR-positive pools contained ticks removed from long-distance migratory bird species that nest and/or make stopover in the Iberian Peninsula. This is the first detection of CCHFV in Morocco (Figure 10). The study confirms the role of birds as dispersal of infected ticks, and supports the theory of the entry of the virus in the Iberian Peninsula through migratory birds coming from Africa (Palomar et al., 2013) (Figure 13).

The data presented herein confirm the need to establish a CCHFV surveillance plan for European countries with risk of receiving bird populations from Africa, such as Spain or Portugal. Furthermore, healthcare workers should be informed about the CCHF and the clinical picture in the potential “endemic” areas. Moreover, potential risk groups (healthcare workers, hunters, farmers…), and potential reservoirs (livestock) should be further investigated.
Figure 13. Map showing some of the migratory routes of birds from Central and South of Africa to Zouala (Morocco), and from there to Southwestern Europe.

In summary, these data suggest that the TBEV could establish in the Iberian Peninsula although, to our knowledge, it has not been detected in our area. In addition, the circulation of the CCHFV has been demonstrated and the risk of acquiring CCHF exists in Southwestern Europe. To raise awareness of healthcare workers is crucial in risk areas, and TBEV and CCHFV surveillance systems are required.

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