

## SCIENTIFIC OPINION

### Scientific Opinion on Rift Valley fever<sup>1</sup>

EFSA Panel on Animal Health and Welfare (AHAW)<sup>2,3</sup>

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#### ABSTRACT

Based on a comprehensive review of literature and OIE (World Animal Health Organisation) outbreak reports, this scientific opinion reports, first, that there is no evidence that Rift Valley fever (RVF) has spread to previously uninfected countries during the past 10 years. Nevertheless, RVF has moved north within Mauritania, in a desert area. Secondly, maps of Europe and the southern Mediterranean Basin are provided, displaying the geographic distribution of the reported presence of nine potentially competent Rift Valley fever virus (RVFV) vectors of the region, based on a systematic literature review. From environmental and eco-climatic data, predicted presence maps were generated that suggest the suitability of several parts of Europe and the southern Mediterranean Basin for these potentially competent RVFV vectors. Thirdly, to assess the risk of introduction of RVFV into some designated countries in the southern Mediterranean Basin (hereafter defined as the region concerned, RC), especially through the movements of live animals and vectors, a quantitative model was constructed and model parameters were derived based on expert knowledge elicitation (EKE). The EKE model indicates that some hundreds of RVFV-infected animals will be moved into the RC when an epidemic in the source areas occurs. The risk of RVFV entering the RC through the movement of vectors is expected to be small in comparison with the risk of entry through infected animals. Because of a lack of quantitative information on the seasonality of vector abundance and vertical transmission of RVFV within local vector species, the risk of endemicity could not be assessed. However, based on the abundance of the vector *Culex pipiens*, the livestock densities and the temperature in the region, there is a potential for the occurrence of RVF spread in the coastal areas of the RC.

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#### KEY WORDS

Rift Valley fever, Mediterranean Basin, vectors, distribution, risk assessment, introduction, endemicity.

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## SUMMARY

Following a request from the European Commission, the Panel on Animal Health and Welfare (AHAW) was asked to deliver a scientific opinion on the risk of Rift Valley fever (RVF). The first term of reference (ToR) requested an update on the **global occurrence of Rift Valley fever and possible changes in the distribution during the last 10 years**. Although the cyclic occurrence of RVF in endemic areas (once every 5–15 years) makes it hard to observe possible changes in the spatial distribution of RVF over a 10-year period, comprehensive literature review and screening of OIE (World Organisation for Animal Health) outbreak reports indicates that RVF moved north within Mauritania, in a desert area, but no new countries have become infected during the past 10 years. Further, a strong increase in reported outbreaks in South Africa was observed in the last 10 years, which may be partly due to better reporting and registration of RVF outbreaks and does not necessarily indicate an increased risk.

The second ToR requested maps of the Mediterranean Basin displaying the **geographical distribution of potential invertebrate hosts, taking into account their vector competence and seasonal variation in abundance**. First, nine potentially competent RVFV vectors were identified: (i) *Aedes vexans*, (ii) *Ochlerotatus caspius*, (iii) *Ochlerotatus detritus*, (iv) *Culex pipiens*, (v) *Culex theileri*, (vi) *Culex perexiguus*, (vii) *Culex antennatus*, (viii) *Culex tritaeniorhynchus* and (ix) *Aedes albopictus*. A systematic literature review was then conducted to compile presence/absence data and relevant environmental and eco-climatic data for these nine species. All information extracted from the literature was used to generate reported and predicted presence maps. The predicted presence maps show the probability of occurrence of the vectors, which is mainly determined by the amplitude of the daytime and night-time land surface temperature, the set of ecological determinants derived from the systematic literature review, the reported presence and absence data for the vectors as well as two vegetation indices.

The predicted presence maps show that the probability of the presence of *Aedes vexans* and *Aedes albopictus* appears to be medium across large areas of the countries around the Mediterranean Basin. The probability of the presence of *Ochlerotatus caspius*, *Ochlerotatus detritus*, *Culex pipiens* and *Culex theileri* appears to be medium to high in the coastal areas and deltas of the countries around the Mediterranean Basin. The probability of the presence of the *Culex perexiguus* and *Culex antennatus* appears to be high around the Nile Delta.

In the Mediterranean Basin, the largest number of mosquito species and the highest population density are found during summer and autumn (from the beginning of June to the end of September). During winter (from November to March), there is reduced mosquito activity. Geo-referenced data on the abundance of vectors in the southern Mediterranean area are scarce. Only for *Cx. pipiens* were sufficient abundance data found in the literature to generate predicted abundance maps. This species is estimated to be abundant in the coastal areas of the region of concern (RC). To provide improved maps of the seasonal variation in vector abundance in the countries around the Mediterranean Basin, vector collection programmes in these areas would need to be initiated while existing ones should be intensified. Further, detailed laboratory investigations to determine the vector competence of each of the potential vector candidates are needed and field studies are needed to gain further insight on their vector capacity.

The third ToR asked AHAW to assess the **risk of introduction of Rift Valley fever virus (RVFV) into the RC**, especially through the movements of live animals and vectors. The RC, as defined in the mandate, comprises Mauritania, Morocco, Algeria, Tunisia, Libya, Egypt, Jordan, Israel, the Palestinian Territories, Lebanon and Syria. Since RVFV was introduced and is probably still present in Egypt and Mauritania, these two countries were excluded from this assessment. The Veterinary Services of the RC reported that currently (2012–2013) no official import of live animals from RVFV-infected countries into the RC is allowed. Consequently, this assessment concerned only undocumented movements of RVFV-infected animals, using a quantitative model, parameterised by expert knowledge elicitation (EKE). The EKE model indicates that some hundreds of RVFV-infected

animals may be introduced without documentation into RC when an epidemic in the source areas occurs. The number of infected animals moving into the RC from the east source (the Arabian Peninsula and East Africa) would be higher than the number of infected animals moving into the RC from the west source (Central and West Africa). This is mainly due to the higher number of expected movements into the RC, and the shorter duration of the journey from the east source than from the west source. This results in a higher probability of infected animals remaining infectious when entering the RC. Additional to the risk of introduction of RVFV through undocumented movements of infected animals, the possibility that RVFV can be introduced into the RC by vectors moved by wind was assessed. It was concluded that, although introduction of RVFV into the RC by vectors through wind cannot be quantified, it is expected to be small in comparison with the risk of introduction by infected animals.

The fourth ToR requested that the **risk of RVF becoming endemic in the RC** be assessed. The transmission model developed by Fischer et al. (2012) was used to determine the initial epidemic growth rate of RVFV infections, which is an indicator of the potential occurrence of RVFV spread to following virus introduction. The model was assessed using parameters for host, vector and pathogen derived from literature and using the predicted relative abundances of *Cx. pipiens* obtained for ToR 2. Estimates of host densities, which are also needed to assess the risk, were obtained from the FAO (2007) livestock grid. Two scenarios for two different host preferences were applied in the model, and, consequently, two risk maps were generated. The first scenario concerned vectors biting livestock only and the second scenario concerned vectors biting both livestock and other, refractory, hosts. Both scenarios showed that there is a potential for the occurrence of RVFV spread in the coastal areas of the RC as well as on the banks of the River Nile. Because of lack of quantitative information on the seasonality of vector abundance and on the vertical transmission of RVFV within local vector species, survival of the virus during the period with limited vector activity could not be assessed, although this is necessary to assess the risk of endemicity. When these seasonal abundance data and data for other species than *Cx. pipiens* become available in the future, they will need to be included in the model, and then the risk of endemicity can be modelled. Furthermore, when more detailed spatial information is available, the picture may also change, and more detailed risk zones may be distinguished.

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## BACKGROUND AS PROVIDED BY THE EUROPEAN COMMISSION

Rift Valley Fever (RVF) is caused by the RVF virus, a member of the genus *Phlebovirus* (family Bunyaviridae). It is a highly contagious infection of ruminants, with the potential for very serious and rapid spread, irrespective of national borders. It is also a major zoonotic disease, with severe consequences on affected people, potentially leading to death. It is transmitted through the bites of various species of mosquitoes (typically the *Aedes* or *Culex* genera) and possibly midges (*Culicoides*), and through contacts with infective tissues such as blood. It has a strong seasonal pattern, with long silent periods followed by explosive flare-ups when climatic (rain) conditions are favourable to the vectors. RVF has serious socio-economic impact on people's livelihoods, on trade of animals and animal products, on food security in countries where ruminants are the basic source of proteins, and on human health.

The current distribution of the infection is mainly Eastern Africa and Western Africa, but the disease often spreads to the North down the Nile Valley, to the East across the Red sea (where it created a major animal and human health problem in Yemen and Saudi Arabia in 2000–2001), to the South to Madagascar and southern Africa. Due to the multiplicity of possible vectors, wherever cattle and small ruminants are raised and climatic conditions are favourable, RVF may emerge. In areas where competent vectors exist, transmission via these vectors can be important for virus persistence over a long time and overwintering mechanisms may exist. Therefore, most countries free of the infection take strict measures to prevent entry.

Outbreaks of Rift Valley Fever have been reported in the last decade in the Nile valley (up to Egypt), in the east and south of Africa (from Kenya to South Africa) and the Western African region (up to Mauritania). The epidemiology of the disease in Africa, especially sub-Saharan and Sahel region needs to be regularly updated since the evolution of the infection and waves of outbreaks follows a highly complicated pattern. Although officially no new cases have been reported during the last months in Northern Africa, there is still a probability that the disease spread through uncontrolled movements of animals in the region and there is still information indicating that the disease is circulating throughout the region of Eastern Africa with regular incursions in Egypt.

From the information available it can thus be assumed that the disease poses a permanent threat to the EU neighbouring region of the Mediterranean (North Africa and Near East), posing a possible risk to the EU.

RVF is a notifiable disease in the EU in accordance to Council Directive 82/894/EEC and the measures to prevent introduction of and to control RVF are laid down in Council Directive 92/119. No drugs are available to prevent or treat RVF infection in animals; only live vaccines are used in the endemic areas. None of these vaccines have been granted with a marketing authorisation in the EU. All control and eradication measures applicable are based on classical disease control methods, including intensive surveillance, epidemiological investigation, tracing, and stamping out of infected herds, designation of protection and surveillance zones. These measures are combined with strict quarantine and biosecurity measures and animal movement control. Prevention in free countries is reinforced through strengthened import controls.

Concerning the complex epidemiology of RVF, important gaps of information remain about what is the real role of wild animals and vectors regarding the maintenance of RVF virus and their possible transmission to domestic ruminants. Not enough is known about the distribution of potential vectors in the EU neighbouring countries of the Mediterranean as well as in Member States. The presence of RVF in EU neighbouring countries would represent a challenge for animal health risk managers. It is therefore necessary to determine the extent of the problem in order to better manage this risk. In addition, risk managers have to manage areas of uncertainty, such as the role played by vectors or the risk of the disease becoming endemic in the EU vicinity. In order to support the Commission and the Member States in improving the control and eradication measures as regards RVF, scientific evidence from EFSA would be required in this area.

**TERMS OF REFERENCE AS PROVIDED BY THE EUROPEAN COMMISSION**

1. Provide an update on the global occurrence of Rift Valley Fever and possible changes in the distribution during the last 10 years.
2. Provide maps of the region of concern\* and other countries of the Mediterranean Basin (including EU Member States), displaying the geographical distribution of potential invertebrate hosts, taking into account their vector competence and seasonal variation in abundance.
3. Assess the risk of introduction of RVFV into the region of concern\* especially through the movements of live animals and vectors.
4. Assess the risk of RVF becoming endemic, with clinical outbreaks or not, in animal and vector populations in the region of concern\*.

\*Region of Concern (RC): countries of the Mediterranean area neighbouring the EU, namely Mauritania, Morocco, Algeria, Tunisia, Libya, Egypt, Jordan, Israel, the Palestinian Territories, Lebanon and Syria



## ASSESSMENT

### 1. Introduction

Rift Valley fever (RVF) is a mosquito-borne viral disease, mainly affecting ruminants and humans (Davies and Martin, 2006). The disease is caused by RVF virus (RVFV), a virus of the family *Bunyaviridae* and genus *Phlebovirus*, which has been isolated from more than 30 mosquito species (EFSA, 2005). *Aedes* and *Culex* genera, however, are considered to be the main vectors. RVF is widespread in Africa and spread to the Arabian Peninsula in 2000–2001. RVF causes abortion in pregnant susceptible ruminants and high mortality in newborn animals (Chevalier et al., 2010) and during large epidemics, it can have a high impact on public health and the economy in the affected regions (Anyamba et al., 2010). Several detailed reviews on the aetiology, epidemiology, control and prevention of RVF have been published (such as FAO, 2010; EFSA, 2005; OIE, 2007, 2009; AFSSA, 2008; Chevalier, 2010).

In this opinion, an update on the global occurrence of RVF and possible changes in the distribution during the last 10 years is first presented (ToR 1). Secondly, the geographical distribution of potential invertebrate vectors in countries of the Mediterranean Basin is shown and their seasonal variation in abundance is discussed (ToR 2). Next, an assessment of the risk of introduction of RVFV into the region of concern, especially through the movements of live animals and vectors, is described (ToR 3), followed by an assessment of the risk of RVF becoming endemic in animal and vector populations in this region (ToR 4). Finally, conclusions and recommendations are given.

### 2. Global occurrence of RVF

#### 2.1. Methodology

To provide an update on the global occurrence of RVF and possible changes in the distribution during the last 10 years, a literature review was carried out looking into the ecosystems in which RVF has been reported, as well as RVF outbreaks in animals reported in the database (WAHID) of the World Animal Health Information Database (OIE) (from 1996 until June 2012<sup>4</sup>) and human cases<sup>5</sup> reported in the scientific literature (from 1993 up to 2012). The retrieved outbreaks and cases in three consecutive time periods were then mapped and results were discussed with regard to potential changes in spatial distribution over time.

#### 2.2. Results

##### 2.2.1. Ecosystems in which RVF has been reported

Rift Valley fever has been reported in four ecological systems: (i) dambo areas, (ii) semi-arid areas, (iii) irrigated areas and (iv) temperate and mountainous areas.

**Dambos** are shallow depressions, often located near rivers, which fill with water during the rainy season. In Dambo areas, a correlation between heavy rainfall and RVF epidemics has been demonstrated (Linthicum et al., 1999). Transmission from one mosquito generation to another, i.e. “vertical transmission”, has been demonstrated in *Aedes (Neomelanimon) mcintoshi* in these ecosystems (Linthicum et al., 1985). In addition, the virus may survive in *Aedes* eggs (which are resistant to desiccation in the environment over a long period of time) during inter-epidemic and/or dry/cold periods. Owing these two mechanisms, and to extreme rainy events (particularly during El Niño phenomena), the disease may re-emerge every 5–15 years, with only a few infections during the inter-epizootic period (Martin et al., 2007).

**Semi-arid areas**, in which RVF has been reported, are characterised by temporary water points, such as found in northern Senegal or Mauritania. However, in these areas, the virus persistence mechanism

<sup>4</sup> OIE WAHID: data compilation started in 1996.

<sup>5</sup> WHO data were not provided.

remains unclear. It could be related to the survival of the virus in *Aedes* mosquitoes, as demonstrated in East Africa, or to the regular introduction of the virus by nomadic herds coming from neighbouring endemic areas. These possibilities are not mutually exclusive (Chevalier et al., 2005).

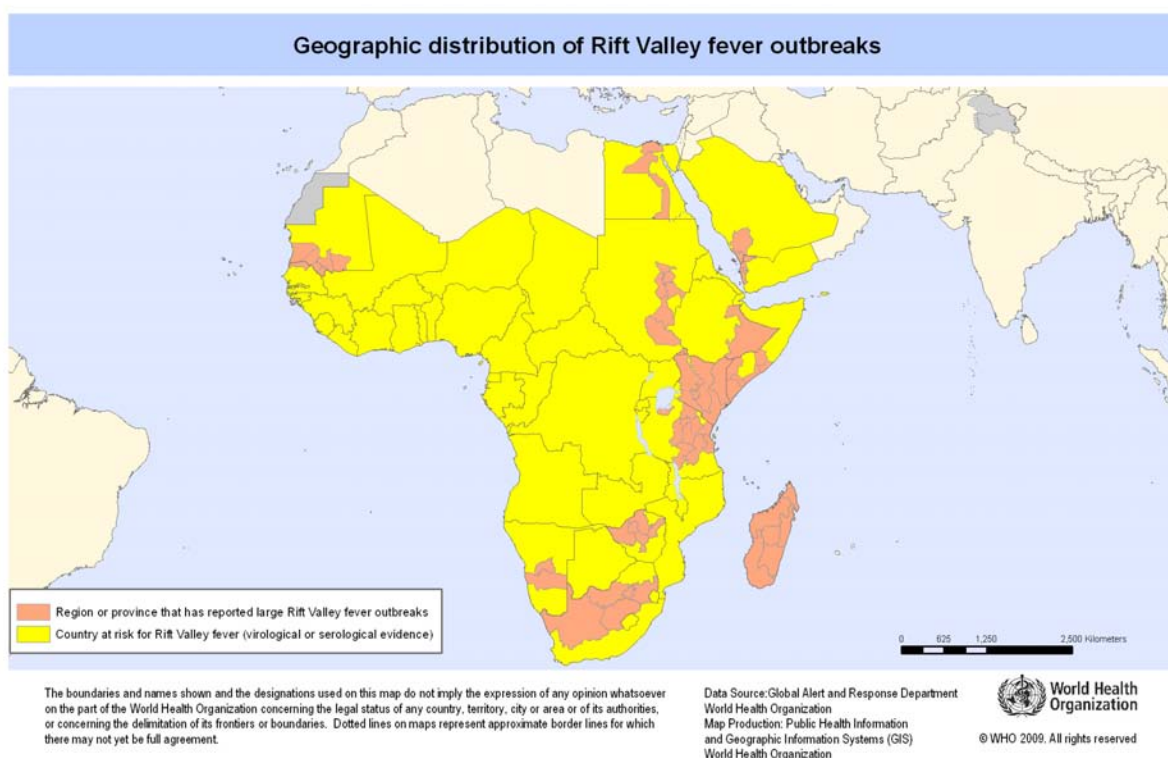
**Irrigated areas** where RVF occurs include the Nile Delta (Egypt) and the Senegal River valley (Senegal, Mauritania), where permanent water bodies favour the development of *Culex* populations, and thus year -long viral transmission (Meegan et al., 1979).

**Temperate and mountainous areas**, such as those found in Madagascar, favour transmission of RVFV by local vectors associated with specific cattle trade practices (Chevalier et al., 2011; Nicolas et al., 2012).

In some of the ecosystems in South Africa and Zimbabwe (Pretorius et al., 1997; Anderson and Rowe, 1998), virus circulation could also be maintained between mosquito vectors and wild ruminants in sylvatic cycles (Chevalier et al., 2011).

### 2.2.2. Geographical distribution of Rift Valley fever

Rift Valley Fever virus was first identified in 1931, in the Great Rift Valley of Kenya. In the past decades, its range has expanded from East Africa across the sub-Saharan region to North Africa and the Arabian Peninsula (Ahmad, 2000). In 2007, RVF was detected in Mayotte (a French overseas territory), part of the Comoros Archipelago in the Indian Ocean, with several clinical cases reported in humans (Sissoko et al., 2009). Figure 1 shows countries considered at risk of RVF based on historical serological and virological evidence and regions that reported epidemics until 2009 (WHO, 2009).



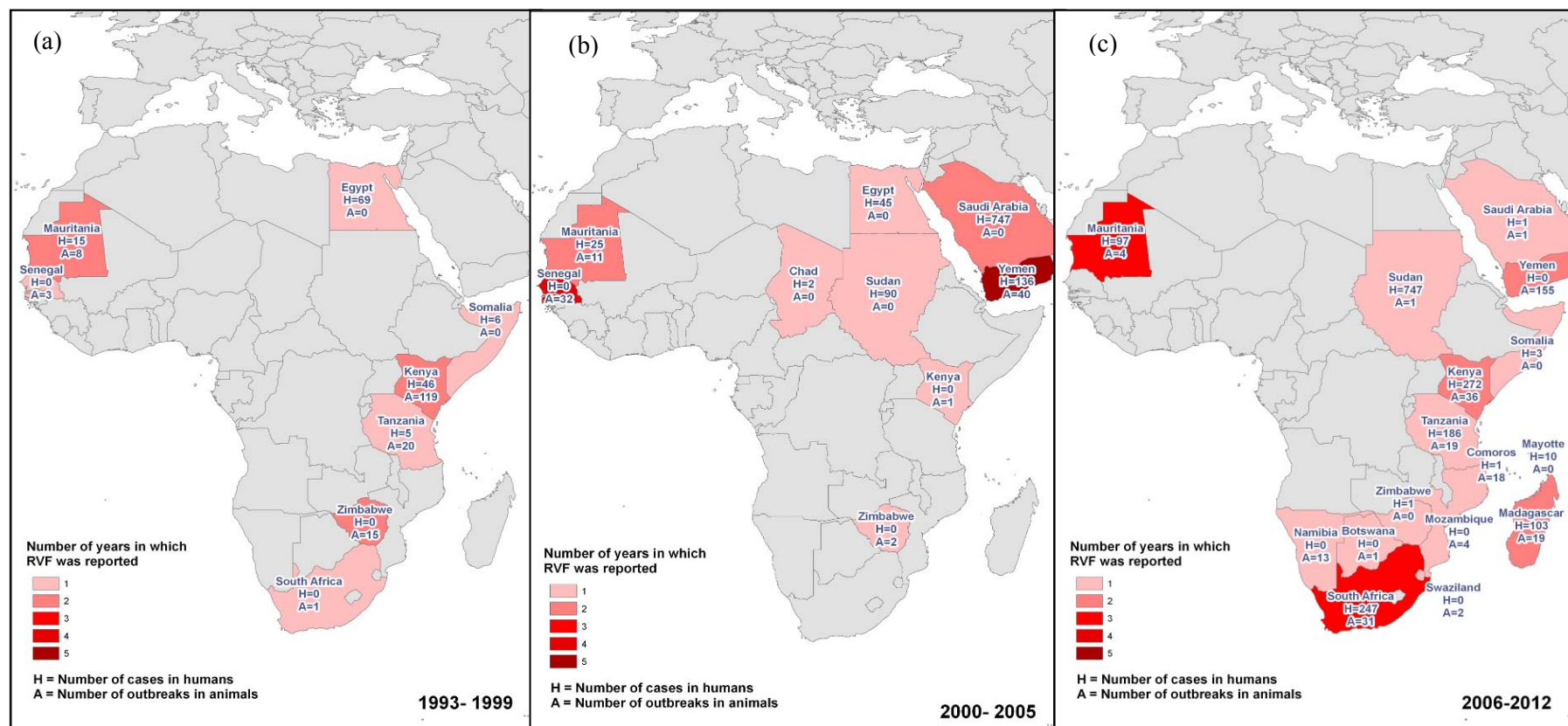
**Figure 1:** Countries at risk of RVF based on virological and serological findings and regions that reported RVF epidemics until 2009 (source: WHO, 2009)

Figure 2a, b and c show the numbers of RVF outbreaks in animals reported by the OIE from 1996 until June 2012, as well as the numbers of human cases reported in the scientific literature during three consecutive periods from 1993 up to 2012. Although these figures may be biased, as RVF outbreaks



and cases may not have been detected or reported, they summarise the best available evidence on the occurrence of RVF. RVF presence has been demonstrated in Egypt in humans and, although Figure 2 shows that Egypt did not report any RVF outbreak in animals to the OIE in the periods indicated on the maps, Kamal (2011) described RVF epidemics in 1977–1978, 1993–1994, 1996–1997 and 2003, involving animal losses and thus suggesting endemic infection in Egypt. This led to the exclusion of Egypt from the RC in the introduction assessment (ToR 3). In addition, Mauritania, where RVF is also endemic (with epidemics in 2010 and 2012), was excluded from the RC in the introduction assessment for ToR 3.

Figure 2 shows the occurrence of RVF in the Arabian Peninsula in the period 2000–2005, which reflects the introduction of RVFV in 2000, most likely caused by importation of livestock from the Horn of Africa. Other notable changes in the distribution of RVF occurred in the southern part of Africa and in the desert region of northern Adrar in Mauritania at the end of 2010 (El Mamy et al., 2011). The latter was caused by ecological changes in the area after heavy rains, making the environment suitable for vectors and virus circulation. The strong increase in reported outbreaks in South Africa may (in part) have been due to the end of an inter-epidemic period and better reporting and registration, following the implementation of the OIE World Animal Health Information Database (WAHID) system in 2005. The cyclic occurrence of epidemics in endemic areas makes it very difficult to draw conclusions on possible changes in occurrence of this disease in sub-Saharan Africa during the last 10 years. Nevertheless, the available information provides no indications of new introductions of RVF into previously uninfected northern countries during the past 10 years. Introduction into the Arabian Peninsula occurred more than 10 years ago and the available information shows a reduced number of reported outbreaks and cases in the period 2006–2012 compared with the period 2000–2005. However, recently (in 2010) in Mauritania, RVF has moved north. This phenomenon is particular not because of its localisation in northern Mauritania (the most northern localisation of RVF epidemics remains in Egypt) but because it occurred in a desert setting following a period of more humid environmental conditions.



**Figure 2:** Reported Rift Valley Fever occurrence in the periods (a) 1993–1999, (b) 2000–2005 and (c) and 2006–2012<sup>6</sup>

<sup>6</sup> The designations and denominations employed and the presentations of the material in this publication do not imply the expression of any opinion whatsoever on the part of EFSA concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers and boundaries.

### 3. Geographic distribution of competent Rift Valley Fever virus vectors in the Mediterranean Basin

#### 3.1. Methodology

To create maps of the RC and other countries of the Mediterranean Basin (including EU Member States) displaying the geographical distribution of potential invertebrate hosts, taking into account their vector competence and seasonal variation in abundance, a stepwise approach was adopted. First, from the literature, potentially competent RVFV vectors (based on field and laboratory observations) were identified. Secondly, based on expert knowledge present in the working group (WG) and AviaGis those competent vectors present in the above-mentioned region were identified. Next, a systematic literature review was conducted to compile all existing presence/absence data of these selected mosquito species. Relevant environmental and eco-climatic data needed to model the distribution and potential areas of spread (for those areas where no presence/absence data were available) were also extracted. All information was used to generate predicted presence maps using Random Classification Forest, which is an empirical modelling technique using field observations to establish the relationship between vector occurrence and prevailing environmental conditions (Breiman, 2001).

The maps show the predicted probability of occurrence of the vector, which is mainly determined by the daytime and night-time land surface temperature, the set of ecological determinants derived from the systematic literature review, the reported presence and absence data for the vectors (the latter if available) as well as two vegetation indices, the normalised difference vegetation index (NDVI) and the enhanced vegetation index (EVI) (Hijmans et al., 2005). Model accuracy was assessed using the area under the receiver operating curve (AUC), which can be roughly interpreted as the probability that a model will correctly distinguish between a true presence and a true absence (Fielding and Bell, 2007).

Predicted presence maps were created for all species with adequate accuracy. Abundance maps could be created only for *Cx. pipiens* as insufficient data were available for the other species. A detailed description of the methodology used is available in the Scientific Report delivered to EFSA by AVIA GIS: <http://www.efsa.europa.eu/en/supporting/doc/412e.pdf>.

#### 3.2. Results

##### 3.2.1. Competent vectors of Rift Valley fever virus in the Mediterranean basin

###### 3.2.1.1. Potential RVF mosquito vectors occurring in the Mediterranean Basin

Of the potentially competent vectors that have been reported in literature (Tables 1 and 2 in Appendix A), the following species were considered relevant for ToR 2: (i) *Aedes vexans*, (ii) *Ochlerotatus caspius*, (iii) *Ochlerotatus detritus*, (iv) *Culex pipiens*, (v) *Culex theileri*, (vi) *Culex perexiguus*, (vii) *Culex antennatus*, (viii) *Culex tritaeniorhynchus* and (ix) *Aedes albopictus*.

***Aedes v. vexans***, a member of the *Aedimorphus* subgenus, has been listed because tropical populations of the related subspecies *Ae. vexans arabiensis* have been found to be infected in the field and incriminated as the main maintenance and epizootic vectors during epidemics in both Senegal (Fontenille et al., 1995; Zeller et al., 1997; Traore-Lamizana et al., 2001; Ba et al., 2012) and the Arabian Peninsula (Jupp et al., 2002). Moreover, it has been shown that some temperate field populations of *Aedes v. vexans* from the United States (Florida, Louisiana) can transmit RVFV under experimental conditions (Turell et al., 2008). Other field populations of the same species from the United States (California, Colorado) and Canada (Turell et al., 2010; Iranpour et al., 2011) were found incompetent despite being tested under identical conditions. This variation in vector competence illustrates the uncertainty surrounding the ability of local populations of a mosquito species to transmit a particular pathogen.

The differences between the Afrotropical and Palearctic/Neartic populations of *Ae. vexans* and the variation in the vector competence of the same species depending on the geographical population tested illustrate the complexity in seeking a prediction of vector competence and capacity based on a literature review. Even though certain traditional African vectors of RVFV are present in Europe, Palearctic populations of these species could exhibit different genetic traits, which may include vector competence for RVFV. Moreover, their relative abundances are different and they have adapted physiologically and behaviourally to the more temperate climate.

In addition, it cannot be excluded that other European vector species not found to be infected by RVFV in the field (obviously because of their absence from endemic regions) and for which competence has not been tested in the laboratory (mostly because of the difficulty of establishing colonies of many of the floodwater *Aedes* species) are competent for RVFV, particularly, among the *Ochlerotatus* subgenus, ubiquitous in the Palearctic region, species such as *Oc. detritus*, which occupies the kind of habitat and exhibit bio-ecological traits that could favour endemic cycles of RVFV transmission, and *Oc. caspius*, which is believed to be the Egyptian maintenance and epizootic vector of RVFV (Turell et al., 1996; Gad et al., 1999). Further, others member of the same subgenus as *Oc. detritus* have similar bio-ecological traits and have shown their competence as RVFV vectors in the laboratory.

*Cx. pipiens* was incriminated as the main epidemic RVFV vector in the Nile Valley (Egypt) based on both field isolates and successful experimental infection in the laboratory (Meegan et al., 1979). Moreover, a recent publication has shown that populations of *Cx. pipiens* from the Maghreb are efficient experimental vectors of RVFV (Amraoui et al., 2012). This species occurs throughout Eurasia, North Africa and North America, displaying a great genetic and phenotypic plasticity. European populations of *Cx. pipiens* may not have the same competence and capacity for RVFV as those present in North Africa.

The same remark applies to three other *Culex* species present in the Mediterranean Basin (*Cx. theileri*, *Cx. perexiguus* and *Cx. antennatus*), whose populations in Africa have been found to be infected in the field and/or competent in the laboratory (McIntosh, 1972; McIntosh et al., 1973, 1980; Linthicum et al., 1985; Gad et al., 1987a, b; Turell et al., 1996). Considering their bio-ecology in terms of abundance, biting activity, feeding habits and longevity, all three of these species could be implicated in RVF transmission in the Mediterranean Basin. Within the *Culex* genus, *Cx. tritaeniorhynchus*, a known RVFV vector that has been identified in the Arabian Peninsula (Jupp et al., 2002), is present in Turkey and Greece (Saminadou and Harbarch, 2013), and presumably in parts of the Balkans.

The list of potential RVFV vectors in the Mediterranean Basin should include the invasive *Ae. albopictus*, which entered Europe in 1979 through international trade (notably in used tyres), with onward spread within southern Europe through ground transport. Although the systematic literature review carried out for this opinion retrieved presence/absence data for this mosquito species in only seven countries around the Mediterranean Basin, according to Medlock et al. (2012), this vector, also known as the Asian tiger mosquito, is now present in at least 22 European states and in Algeria. Laboratory transmission of RVFV by populations of this species from North America (Turell et al., 1988), Cameroon and Reunion Island (Moutailler et al., 2008) has been demonstrated, but *Ae. albopictus* has never been found infected in the field. It has invaded the African continent since 1991, but its presence at present is reported in only five countries of the central region (Nigeria, Cameroon, Gabon, Equatorial Guinea, Central African Republic). Based on its ecological plasticity, overall abundance, long lifespan, multitude of generations per breeding season and non-specific feeding habits, *Ae. albopictus* could be implicated in RVFV transmission.

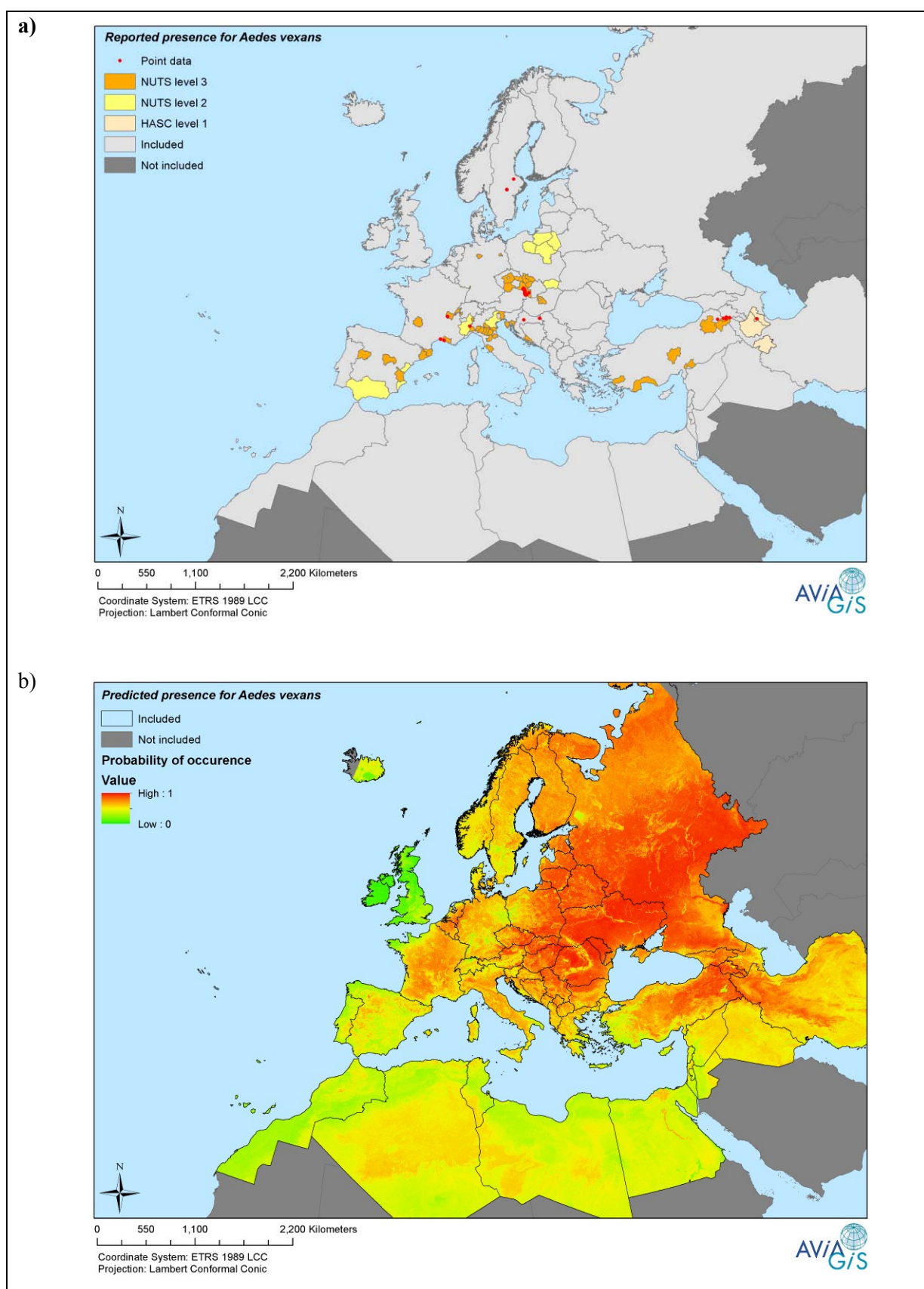
The role of other dipteran species, such as *Culicoides* biting midges, or arthropods, such as argasid and ixodid ticks, has not been taken into account in this report because they are considered only mechanical vectors and their role is therefore thought to be minor compared with that of the other competent vectors.

### **3.2.2. Reported and predicted presence of competent Rift Valley fever virus vectors in the Mediterranean Basin**

For seven of the nine species mentioned above, sufficient data could be obtained for mapping; however, for *Cx. tritaeniorhynchus* and *Cx. antennatus*, fewer publications were available (see Table 3 in Appendix B), making mapping of these species less accurate. Figures 3a–11a show the locations where the vector species have been detected as either point locations, when available, or area (at a NUTS 1, 2 or 3 or HASC1 level), when exact geo-references were not reported. Figures 3b–11b show the predicted presence or absence of the nine RVFV vector species or, in other words the probability that the environment is suitable for their presence.



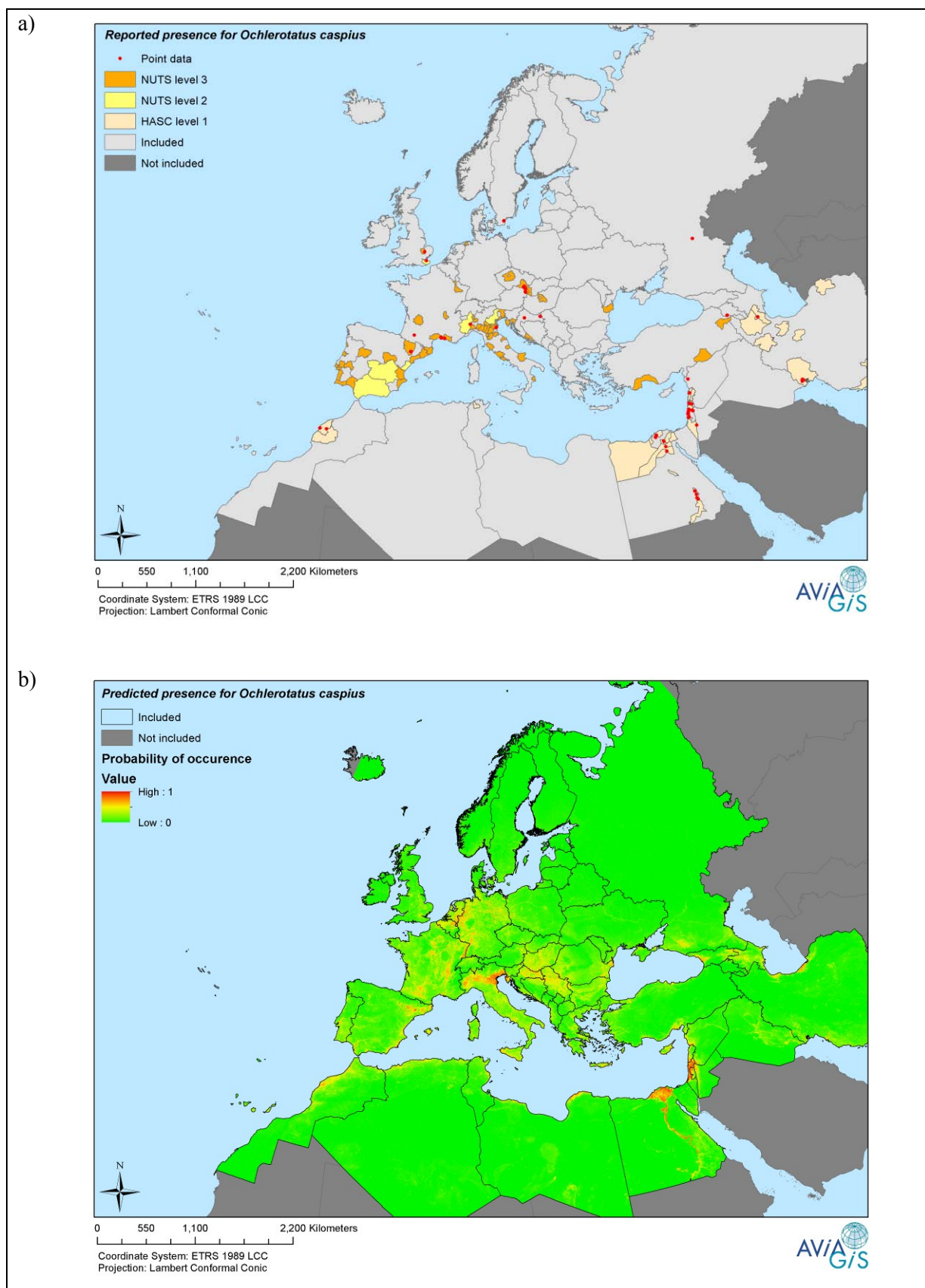
### 3.2.2.1. *Aedes vexans*



**Figure 3:** Reported (a) presence of, and (b) probability of environmental suitability for, *Aedes vexans* in Europe and countries around the Mediterranean Basin

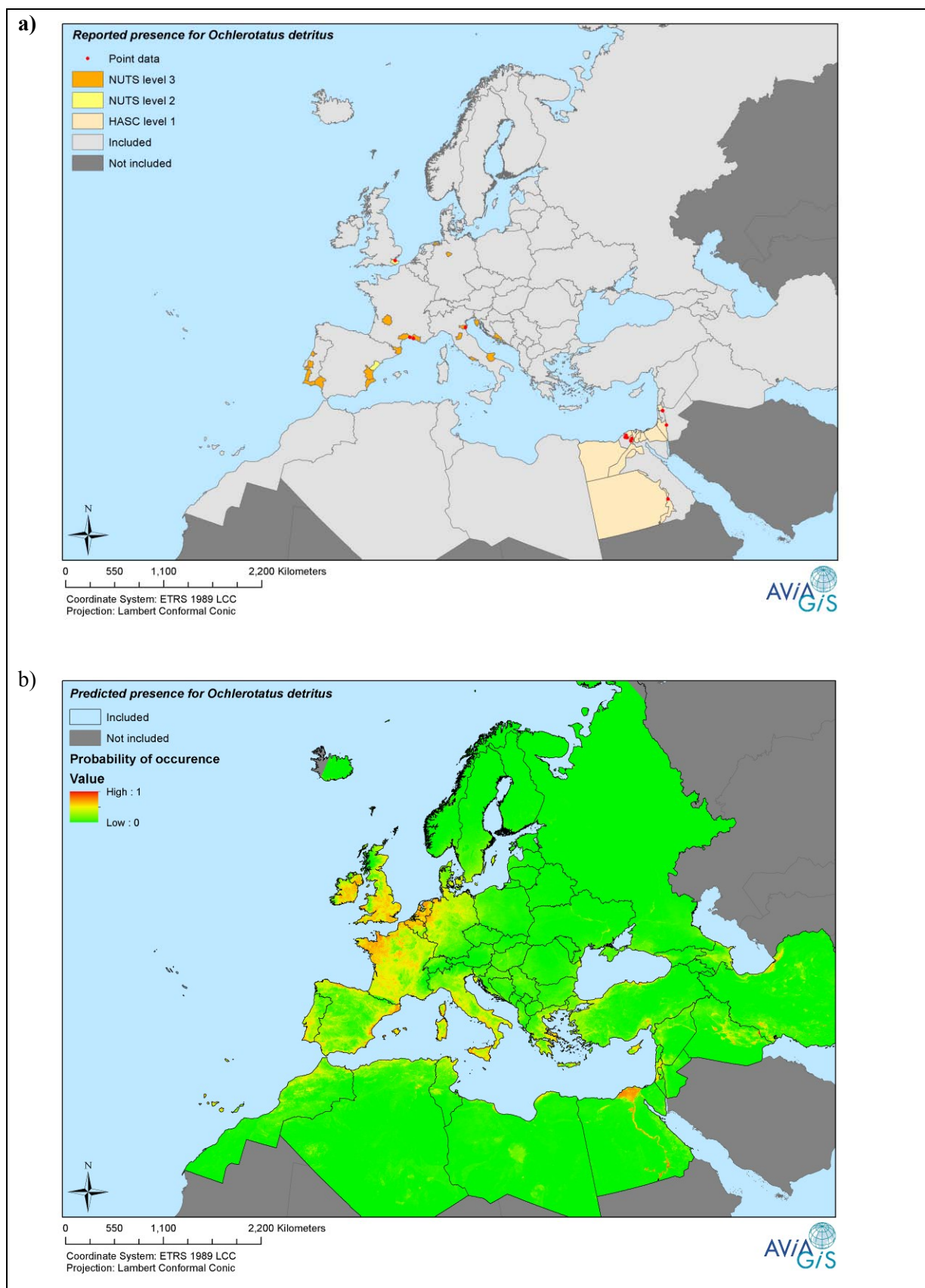


### 3.2.2.2. *Ochlerotatus caspius*



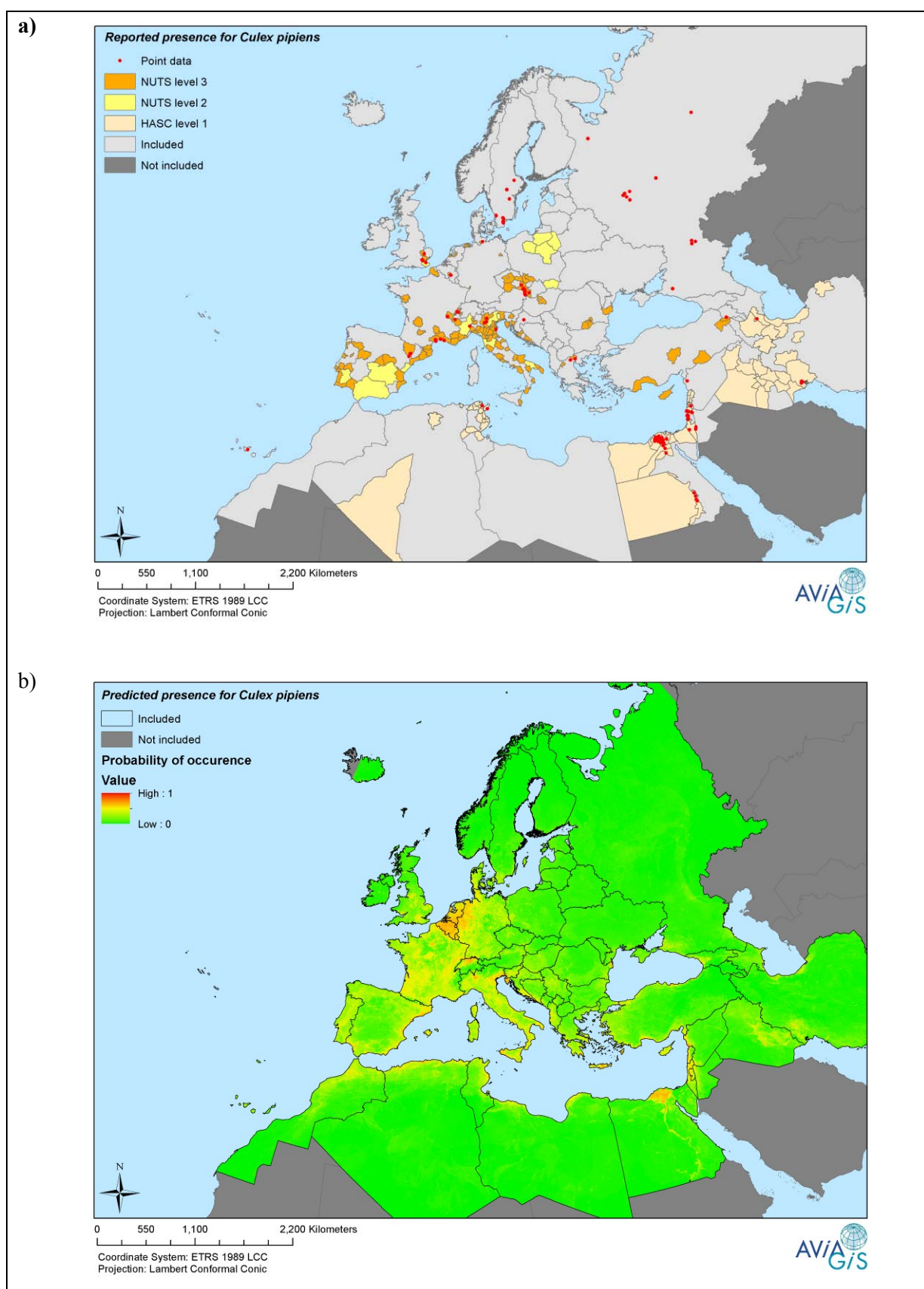
**Figure 4:** Reported (a) presence of, and (b) probability of environmental suitability for, *Ochlerotatus caspius* in Europe and countries around the Mediterranean Basin

### 3.2.2.3. *Ochlerotatus detritus*



**Figure 5:** Reported (a) presence of, and (b) probability for environmental suitability for, *Ochlerotatus detritus* in Europe and countries around the Mediterranean Basin

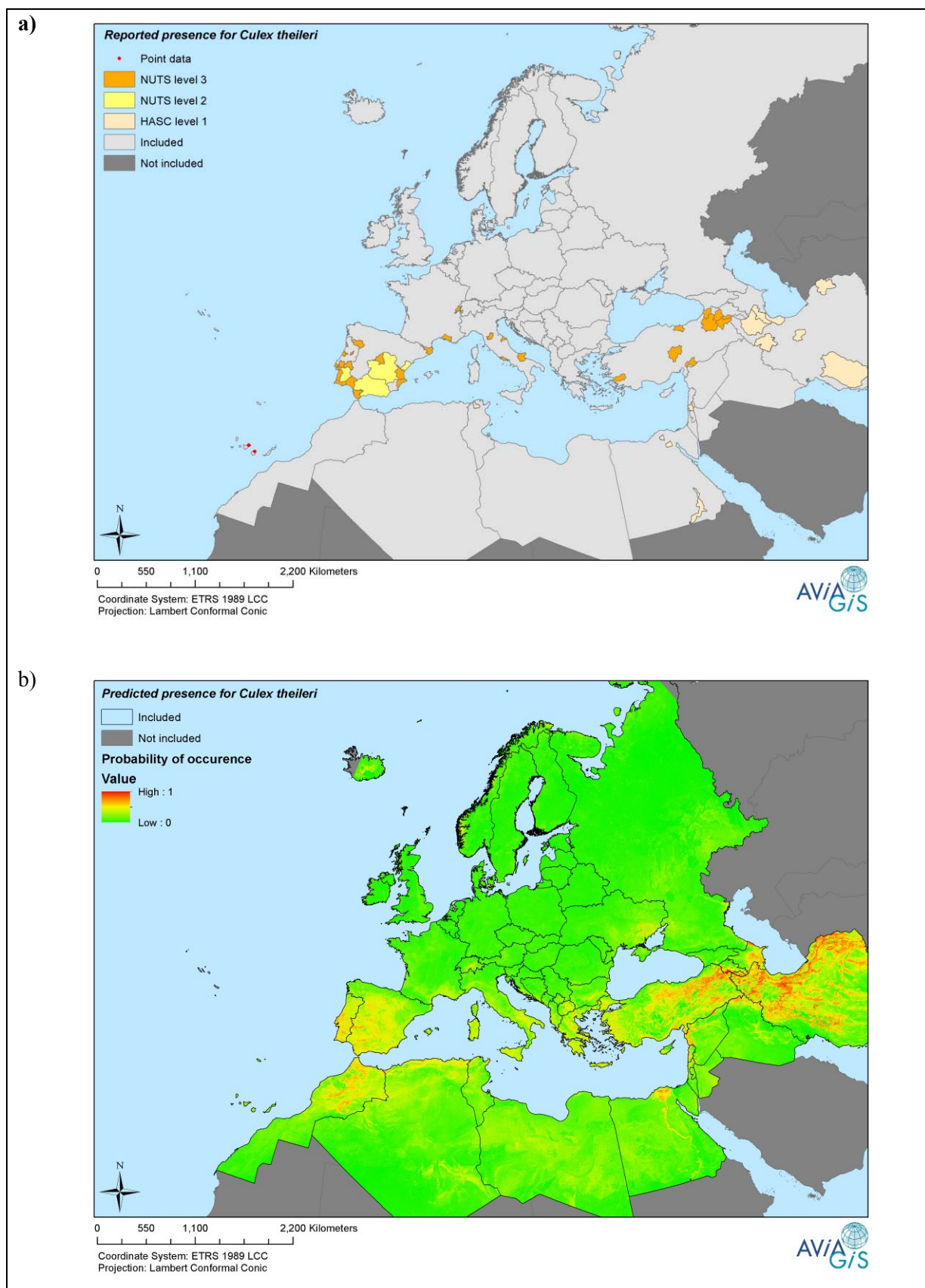
### 3.2.2.4. *Culex pipiens*



**Figure 6:** Reported (a) presence of, and (b) probability for environmental suitability for, *Culex pipiens* in Europe and countries around the Mediterranean Basin

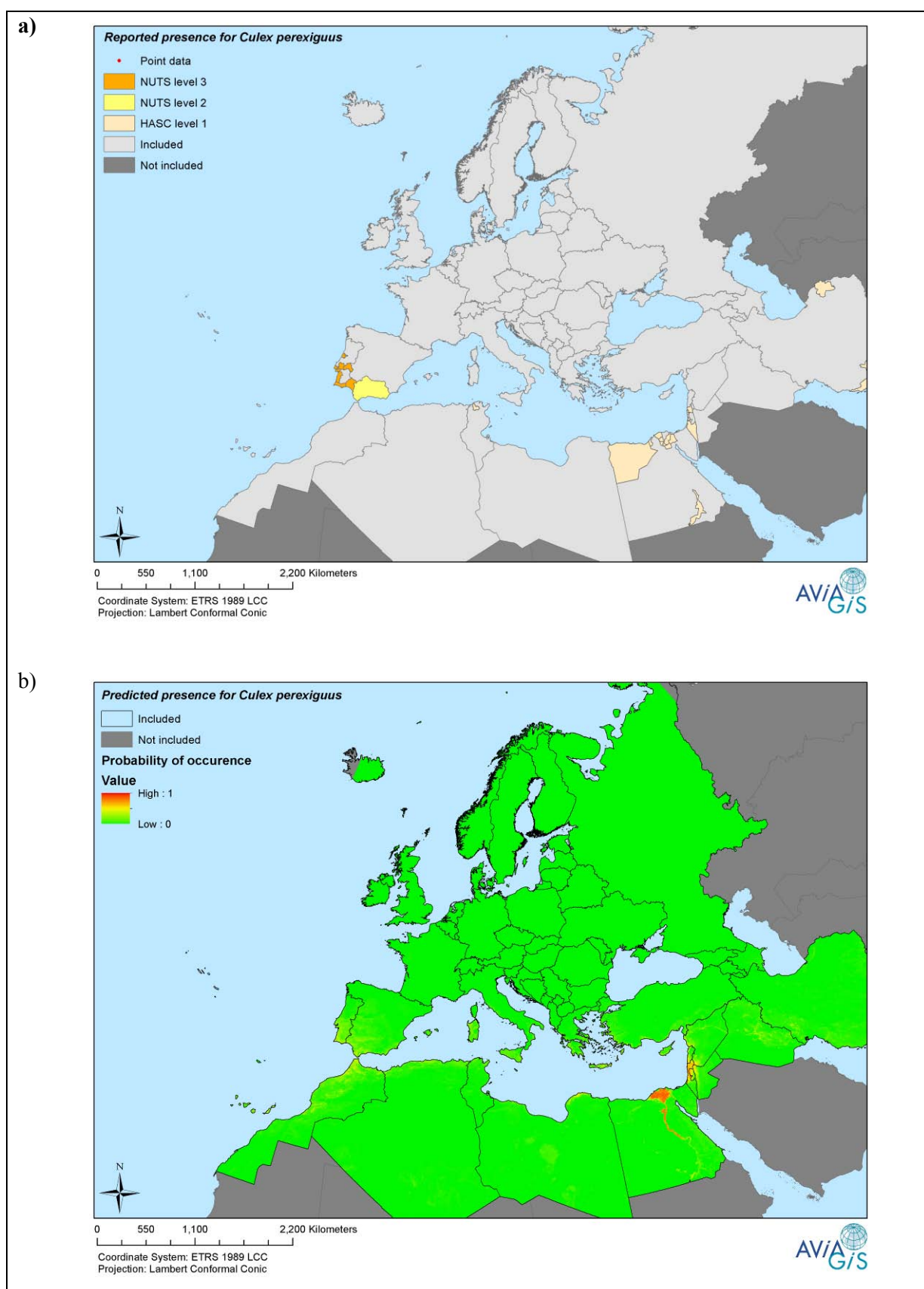


### 3.2.2.5. *Culex theileri*



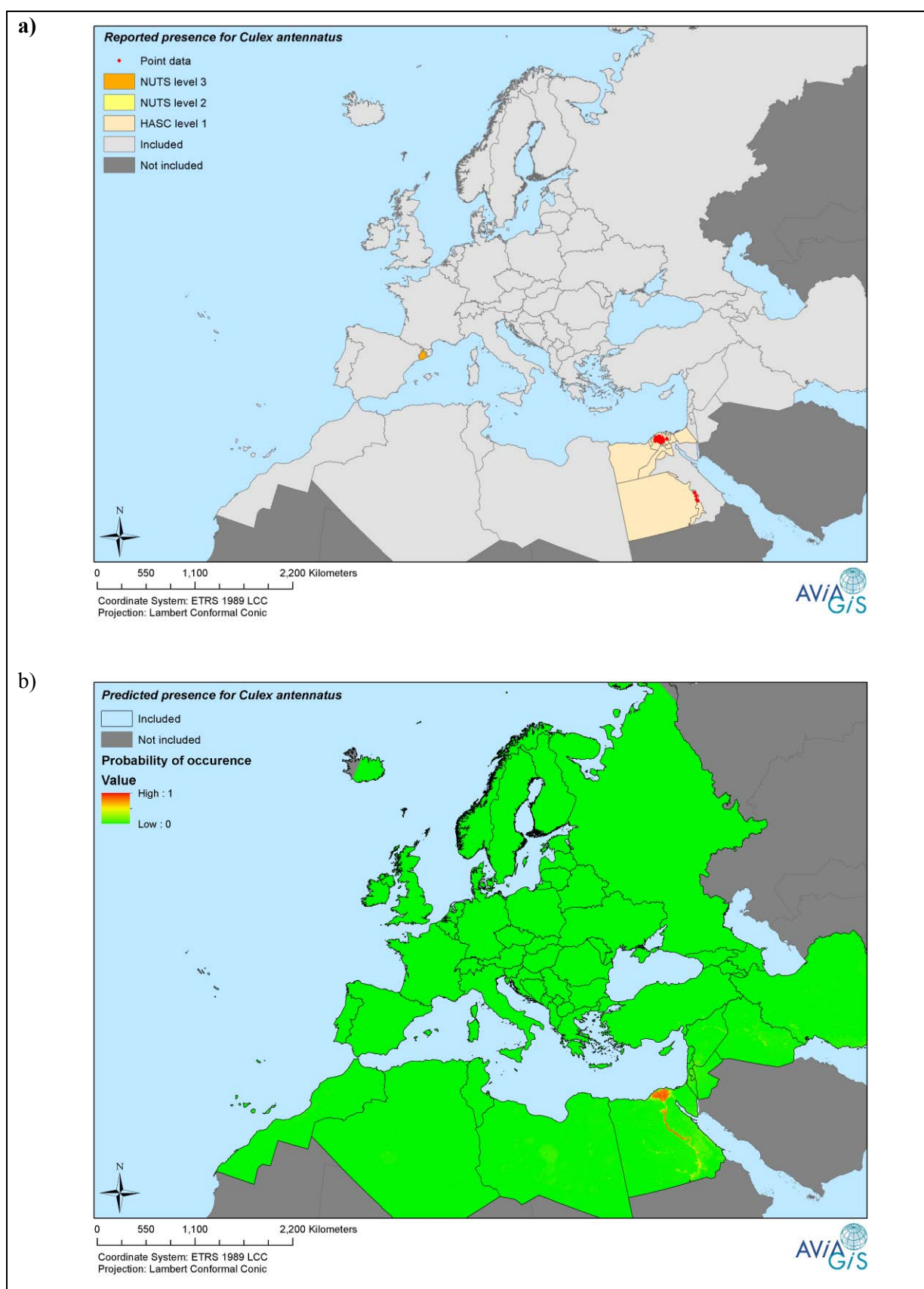
**Figure 7:** Reported (a) presence of, and (b) probability for environmental suitability for, *Culex theileri* in Europe and countries around the Mediterranean Basin

### 3.2.2.6. *Culex perexiguus*



**Figure 8:** Reported (a) presence of, and (b) probability for environmental suitability for, *Culex perexiguus* in Europe and countries around the Mediterranean Basin

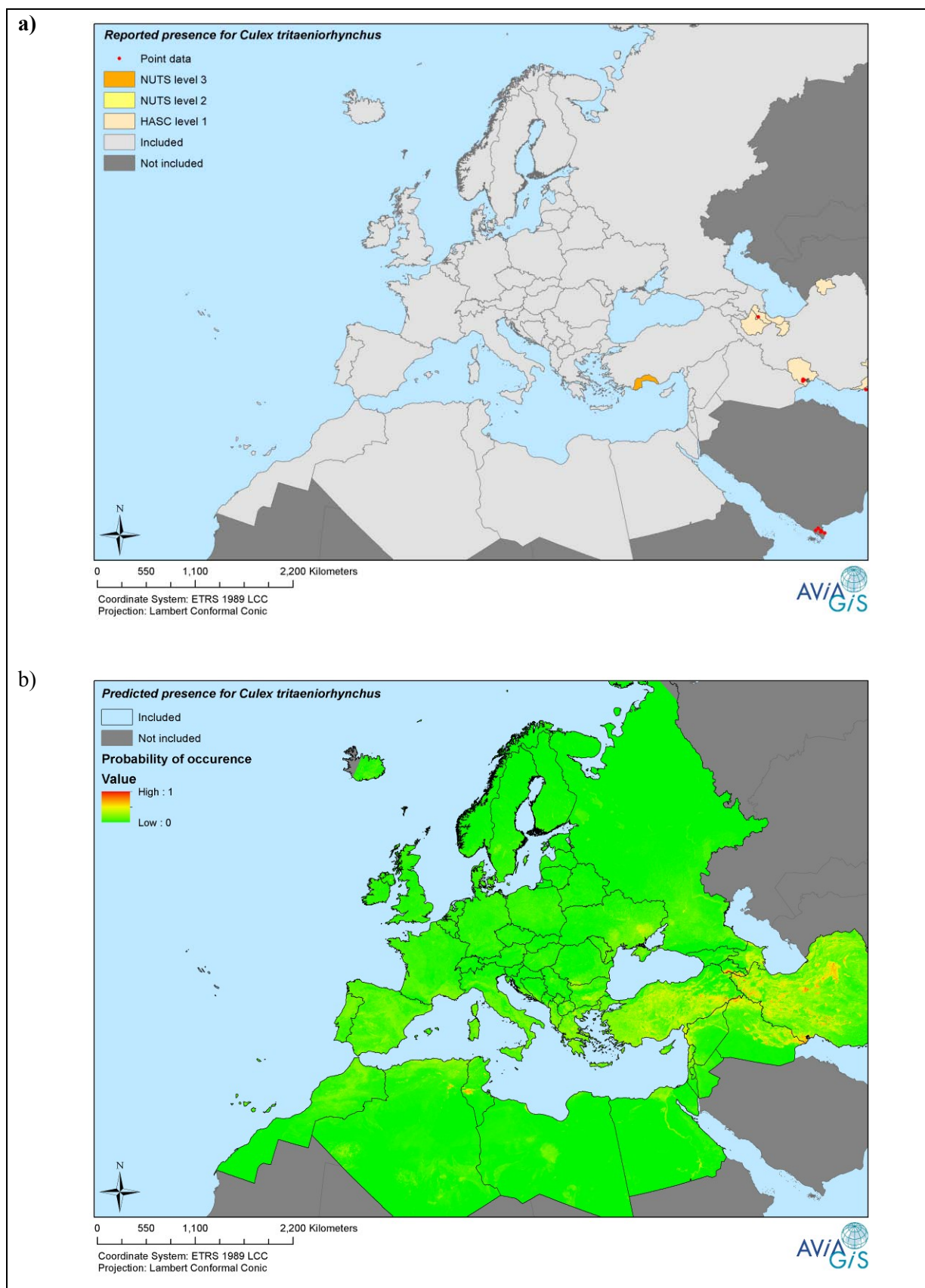
### 3.2.2.7. *Culex antennatus*



**Figure 9:** Reported (a) presence of, and (b) probability for environmental suitability for, *Culex antennatus* in Europe and countries around the Mediterranean Basin

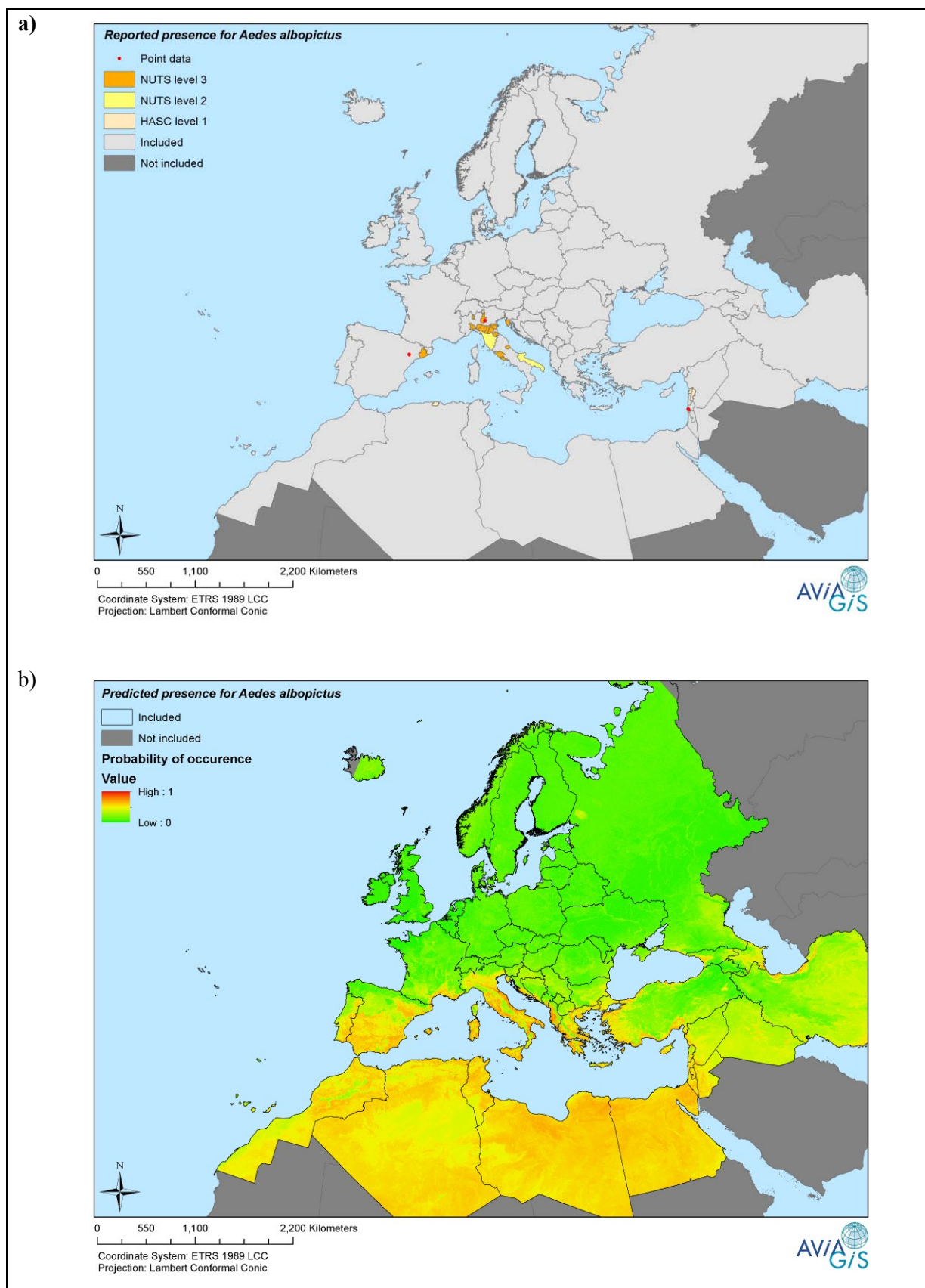


### 3.2.2.8. *Culex tritaeniorhynchus*



**Figure 10:** Reported (a) presence of, and (b) probability for environmental suitability for. *Culex tritaeniorhynchus* in Europe and countries around the Mediterranean basin

### 3.2.2.9. *Aedes albopictus*



**Figure 11:** Reported (a) presence of, and (b) probability for environmental suitability for, *Aedes albopictus* in Europe and countries around the Mediterranean Basin

The predicted presence maps suggest the suitability of several parts of Europe and the southern Mediterranean Basin for the RVFV vectors included in this assessment. Combining the predicted presence maps of all species indicates that some areas are suitable for most of the nine species (e.g. the coastal areas of most countries of the Mediterranean Basin). The predicted presence of *Culex tritaeniorhynchus* and *Culex antennatus*, however, should be interpreted with caution, as they were based on only a few data points (see Table 3 in Appendix B). Moreover, the vector presence maps may reflect some bias due to the sampling design, trapping method, duration and target species. However, the methodology used, which is developed in the Vecmap software, has proved to be a good approach to overcome major biases and enable the use of incomplete datasets (presence only) to make modelling predictions about species distribution.

### 3.2.3. Abundance of competent Rift Valley fever virus vectors in the Mediterranean Basin and its seasonal variation

In general, the vector populations in temperate regions of the northern hemisphere are small during the cooler season (from November to March) and start to increase in early spring. In general, in the Mediterranean Basin, the largest number of mosquito species and the highest population density were found during summer and autumn (from the beginning of June to the end of September). During winter (from November to March), there is reduced mosquito activity.

*Culex pipiens*, which is mainly associated with artificial surfaces and agricultural areas, displays a seasonal thermophilic trend around the Mediterranean Basin, with a rise in spring and peak abundance in the hottest summer months. However, sometimes, owing to low atmospheric humidity, related to continued lack of precipitation, density decreases can be observed during summer. In October, *Cx. pipiens* populations start to decline with the drop in temperature (and also the reduction in the photoperiod, which affects adult activity concomitantly). The other four *Culex* species (*Cx. theileri*, *Cx. perexiguus*, *Cx. antennatus* and *Cx. tritaeniorhynchus*) exhibit the same seasonal trends (Gad et al., 1987a, b, 1989; Harbach, 1988; Margalit et al., 1988; Alten et al., 2000; Orshan et al., 2008).

The floodwater mosquito species (*Ae. vexans vexans*, *Oc. caspius* and *Oc. detritus*) classically show a bimodal seasonality (spring–autumn), with a first peak in early spring (April–May) and a second, more important, peak in autumn (September–October). In some areas, human activities, in particular irrigation and water management, could modify this general pattern. In the Nile Delta, *Oc. caspius* has been found in the spring, summer and autumn with no significant seasonal differences in density (Rifaat et al., 1970).

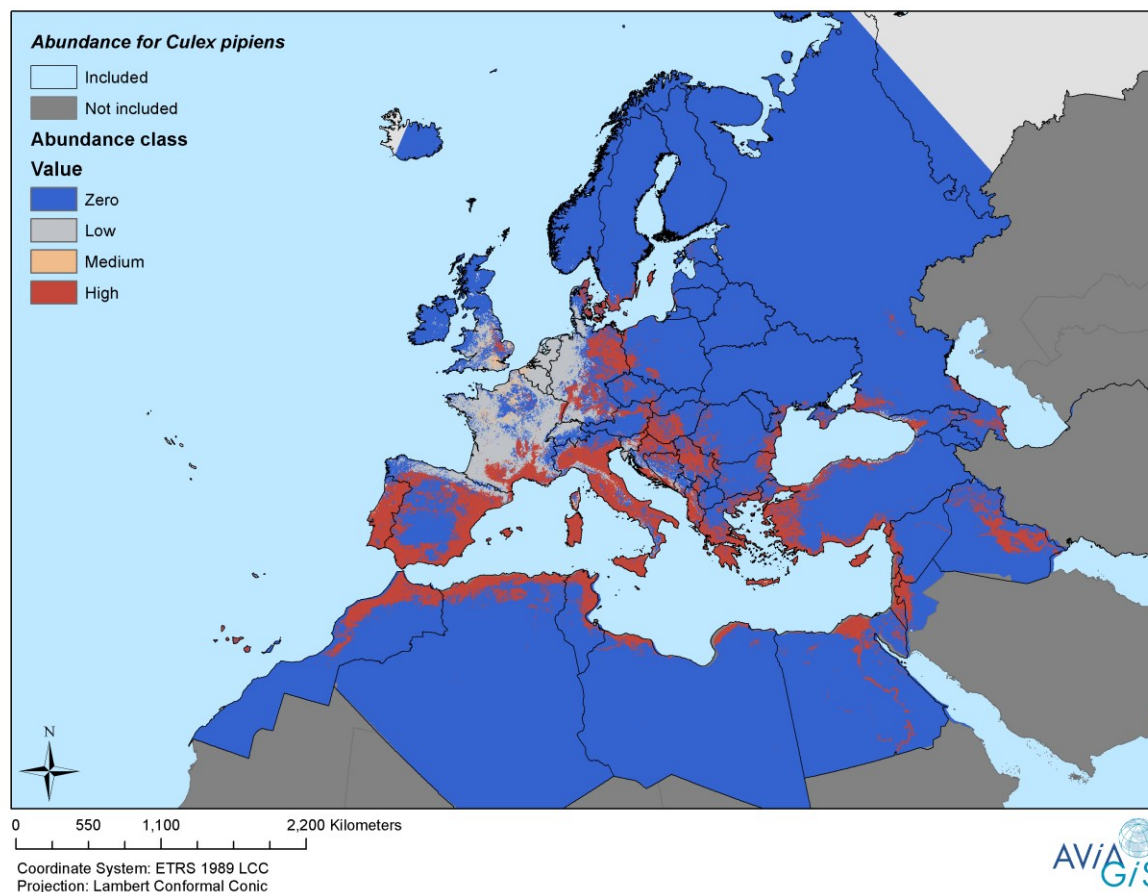
The invasive *Ae. albopictus* is mainly associated with urban areas, as a result of its preference for container habitats (e.g. tyres and vases) in domestic and peridomestic settings. Seasonal monitoring, conducted in Rome (Toma et al., 2003) and in Athens (Giatropoulos et al., 2012), showed that this mosquito is continuously active from mid-spring until the end of November, with a considerably high oviposition and biting activity recorded during summer and autumn (from July to September). Oviposition and biting activity cease from January until March.

The above-mentioned trends are mostly influenced by local climatic conditions, especially by temperature, rainfall and relative humidity, and secondarily by human activities.

Abundance data were extracted from the compiled papers and subdivided into three categories: low, medium and high abundance. The categories were based on a log-transformation in which the low class represent sites with 1–10 specimen per trap, the medium class comprises sites with 10–1 000 specimens per trap and the high class represents all sites with more than 1 000 specimen per trap. Only geocoded records (e.g. point locations) could be used in the modelling approach. Only in the case of *Cx. pipiens* were sufficient records (numerical and spatial) available to create statistically meaningful model outputs. Models were created using random classification forests (Breiman, 2001) for each class separately. The probability maps for each class were then combined with a maximum value compositing procedure, i.e. across the three maps, the maximum probability was selected on a pixel-



by-pixel basis, and the output pixel received the category of the class with the highest probability. In a final step, the abundance map was combined with the probability map. All pixels with a probability of occurrence lower than 0.17 were considered non-suitable for the occurrence of the species. This limit was based on expert opinion. Therefore, the abundance output was multiplied by zero if the value of probability of occurrence was lower than this threshold. All background pixels were assigned a value of -9999 to differentiate between value of zero abundance and background. A more detailed description of the methodology can be found in the scientific report delivered to EFSA by AVIA GIS, <http://www.efsa.europa.eu/en/supporting/doc/420e.pdf>. The predicted abundance map of *Cx. pipiens* is shown in Figure 12.



**Figure 12:** Predicted abundance map of *Culex pipiens* in Europe and countries around the Mediterranean Basin

#### 4. Risk of Rift Valley fever virus introduction into the region of concern, especially through the movements of live animals and vectors

##### 4.1. Methodology

As shown in the response to ToR 1, RVFV infection is already endemic in Mauritania and most likely also in Egypt, and for that reason the RC for the risk assessment of RVFV introduction included only Morocco, Algeria, Tunisia, Libya, Jordan, Israel, the Palestinian Territories, Lebanon and Syria. RVFV can be introduced into a new region by several pathways. Previous assessments have looked into the different potential ways for introduction of RVFV into the EU (i.e. EFSA, 2005). The current assessment considers entry of RVFV only through movement of infected (pre-viraemic and viraemic) animals and movement of infected vectors by wind. Introduction through meat and meat products and introduction through infected humans have not been considered in this assessment, because the ToR specifically focused on movement of animals and vectors. Moreover, RVFV is highly sensitive to low pH and therefore is quickly inactivated in maturing meat and, moreover, meat products are not fed to

ruminants. Additionally, humans are considered dead-end hosts in the epidemiological cycle of RVF and inter-human transmission of the virus has never been described. Introduction of vectors was limited to wind-borne introduction, because this has been reported as a possibility in Egypt. Other routes of vector introduction were considered of minor importance in comparison with the risk of introduction by infected animals (or associated with that risk in the case of vectors travelling with livestock).

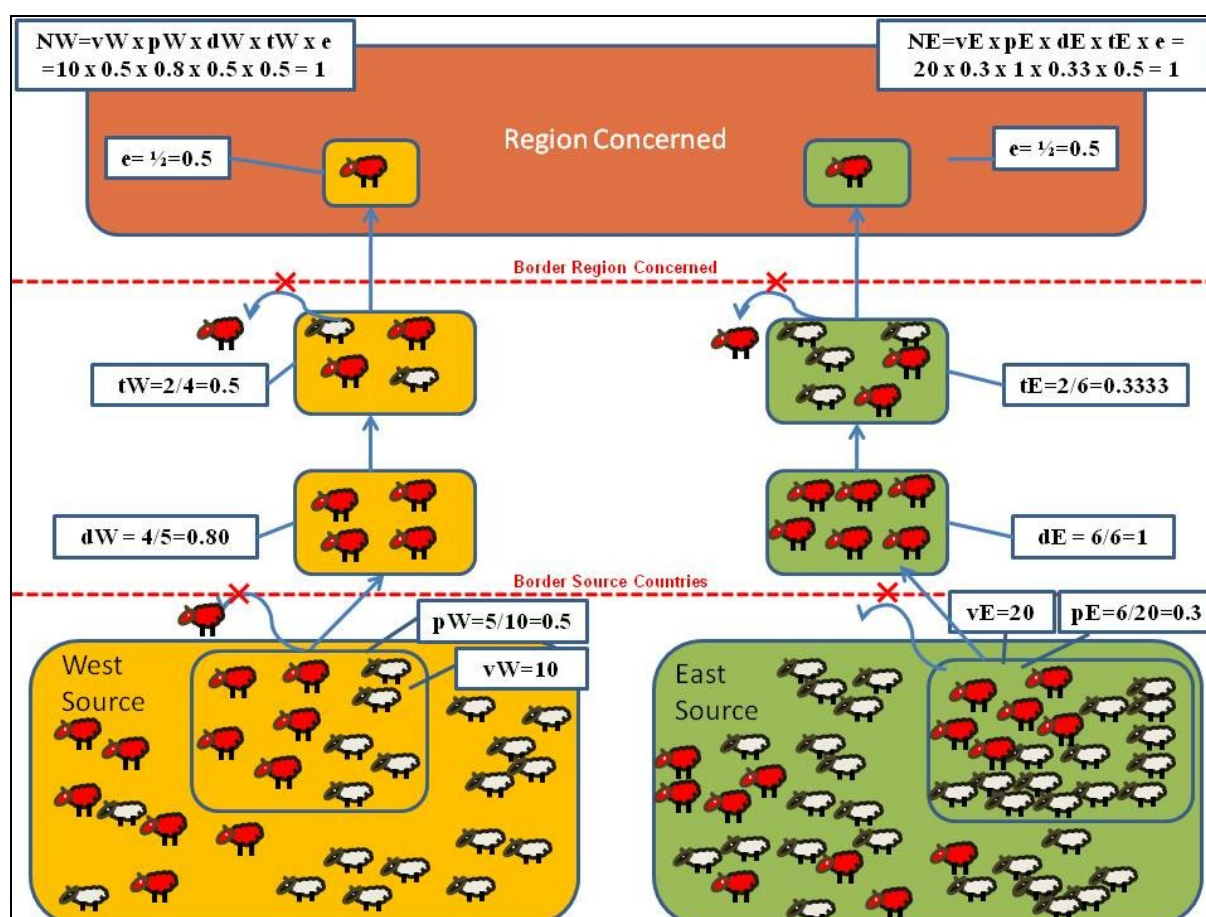
According to reports from the Veterinary Services from the RC (no replies were received from Syria, Libya and Lebanon, however), there is no official trade between RVFV-infected countries and the RC. Consequently, the assessment of the probability of introduction of RVFV by live animals is based on estimated numbers of animals whose movement is undocumented, elicited from expert knowledge. The sources of RVFV introduction into the RC (regions in which RVF has occurred in the past) were divided into three regions.

- the ‘east source’: Ethiopia, Djibouti, South and North Sudan, Egypt, Somalia, Qatar, Saudi Arabia, Yemen, Kenya, Tanzania, Eritrea and Somalia
- the ‘west source’: Senegal, The Gambia, Guinea Conakry, Cameroon, Sierra Leone, Mauritania, Mali, Niger and Chad
- the ‘southern source’: Mozambique, Madagascar, South Africa, Namibia, Zimbabwe, Botswana, Malawi, Swaziland and Zambia.

Experts considered movements of animals of susceptible species towards the RC important only from the east and west source of RVF. The number of infected animals entering the RC without official documentation was modelled as the product of the following parameters:

- the volumes of animals transported from the east and west sources to the RC in 2013 ( $v_E$  and  $v_W$ , respectively),
- the prevalence of RVFV in animals for export in the east and west sources ( $p_E$  and  $p_W$ , respectively),
- the proportions of infected animals that, despite export controls, left the east and west sources ( $d_E$  and  $d_W$ , respectively),
- the proportions of infected animals remaining infected after transport from the east and west sources to the RC ( $t_E$  and  $t_W$ , respectively),
- the proportion of infected animals that entered despite import controls at the RC ( $e$ ).

The model for assessing the risk for introduction of RVFV through the movement of animals is shown in Figure 13 (numbers are fictitious in this example). The year 2013 was chosen for the elicitation since it is generally easier for experts to elicit parameters based on the current situation. However, potential changes in political situation in the RC in the future may have a serious impact on undocumented animal movements. Furthermore, taking into account the cyclic occurrence of RVF every 5–15 years, the epidemiological situation in the source countries may change.



- $vE$  and  $vW$ —the volumes of animals transported from the east and west sources to the RC in 2013
  - $pE$  and  $pW$ —the prevalences of RVFV in animals for export in the east and west sources
  - $dE$  and  $dW$ —the proportions of infected animals allowed to depart from the east and west sources
  - $tE$  and  $tW$ —the proportions of infected animals remaining infected after transport from the east and west sources to the RC
  - $e$ —the proportion of infected animals that are allowed entry on arrival at the RC
- Red ruminants = infected with RVFV; white ruminants = not infected with RVFV.  
M is the number of infected animals entering the RC and, NE and NW are the number of infected animals entering through the Eastern and Western pathway respectively.

**Figure 13:** The model for assessing the risk for introduction of RVFV through the movement of animals (fictitious example)

Distributions of the parameters for the model were constructed through EKE. More details about the EKE process itself have been provided by the Australian Centre of Excellence for Risk Analysis (ACERA, 2006, 2010). This elicitation process followed the Sheffield method and materials and guidance for using this method are contained in the SHELF package, available freely online at <http://tonyohagan.co.uk/shelf>. A detailed report of the EKE workshop is published on the EFSA website: <http://www.efsa.europa.eu/en/supporting/pub/416e.pdf>. Next, probability distributions for the numbers of infected animals entering RC were derived by performing a million simulations of the model using randomly drawn values from the elicited parameter distributions.

Probability distributions of events occurring in the pathway for RVFV to enter the RC through movement of RVFV-infected vectors were more difficult to elicit, as information on this topic is extremely sparse and the WG considered it not possible to elicit such information in the EKE workshop. Therefore, this route of entry of the virus was assessed through a narrative review.



## 4.2. Results

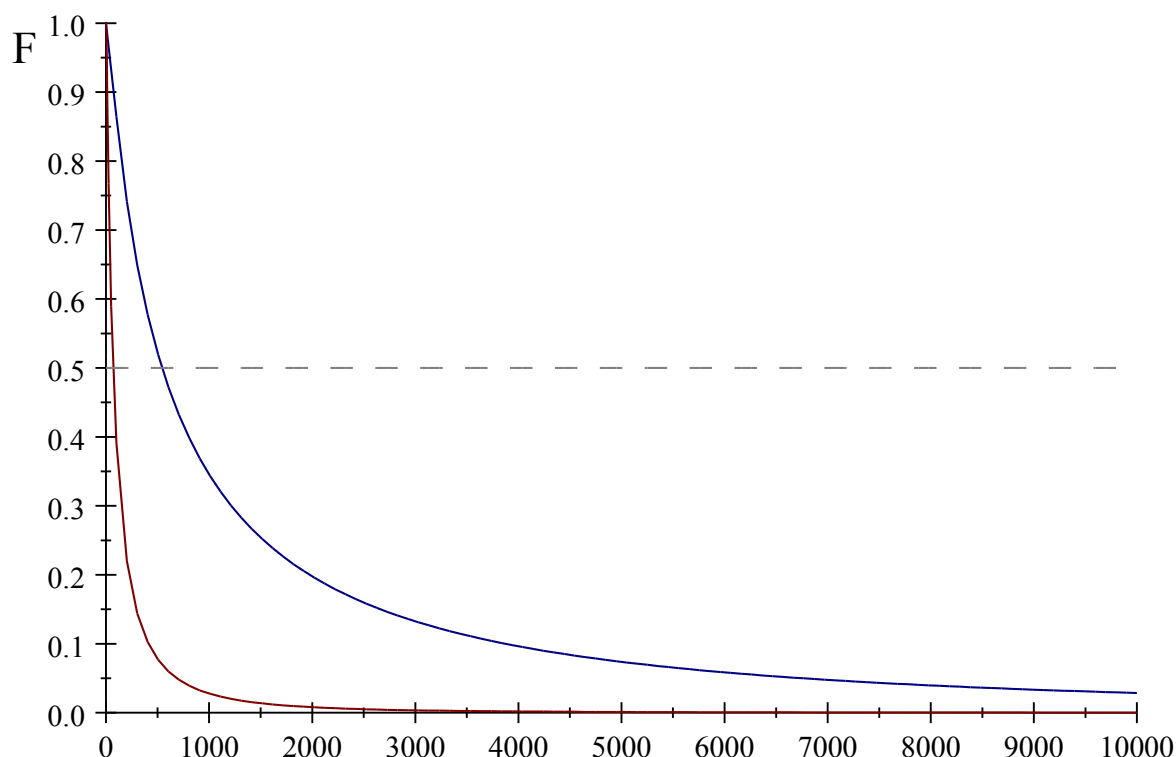
### 4.2.1. Introduction of RVFV via infected animals

Although expert opinion is, by definition, subjective, and the accuracy and uncertainty of the estimates are greatly influenced by a number of factors, such as the group dynamics, expert selection and validation of the results, the EKE workshops provided an overview of the current knowledge of the parameters needed to carry out a quantitative risk assessment for introduction of RVFV into the RC.

The participants, although at first hesitant to provide precise estimates on undocumented movements of infected animals, proved to be very well acquainted with the epidemiology of RVF in their area, and were very familiar with current practices in the trade of animals and traditional farming in their region. Working with probability distributions of estimates, as is embedded within the Sheffield methodology (available freely online at <http://tonyohagan.co.uk/shelf>), should overcome the need to focus on precise numerical values of individual estimated parameters and allows for inclusion of high uncertainty (the range of the distribution) related to the parameters.

The results from the RVFV introduction model based on the outcomes of the EKE workshop indicate that, in a year in which an epidemic occurs in both the east and west sources, the number of RVFV-infected animals introduced into the RC is likely to be in the hundreds, but with substantial uncertainty. The probability distributions for the number of infected animals entering through the eastern (nE) and western (nW) pathway are shown in Figure 14. These curves show log-normal approximations to the million simulations.

The number of infected animals likely to be introduced into the RC from the east source was higher than that from the west source. This is mainly due to the higher number of animals expected to be moved from the east source into the RC, and the shorter duration of the journey, resulting in a higher probability of infected animals remaining infected when entering the RC. Details on all the probability distributions of the individual parameters in the model as well as a list of the most important reasons given by the experts whilst eliciting these parameters can be found in the technical report of the meeting of the AHAW network: <http://www.efsa.europa.eu/en/supporting/pub/416e.htm>



**Figure 14:** The probability values (y-axis) of a least number (x-axis) of undocumented movements of infected animals from the east source (blue line) and the west source (red line) into the RC during a year in which there is an epidemic in the source areas. For example, at a level of probability of 50 % (y-axis), the number of infected animals expected to be introduced by undocumented movements from the east source is 545 or more (x-axis to the right), while this would only be 69 or more from the west source. The data shown are the complementary cumulative distributions of the elicited individual probabilities for each number of movements (<http://www.efsa.europa.eu/en/supporting/pub/416e.htm>)

The conclusion of the experts' analysis of the risk of introduction of RVFV into the RC through movement of infected animals is that it is highly likely that infected animals will be imported unofficially in outbreak years. Trade flows from RVFV-endemic areas towards countries adjacent to the RC (i.e. towards Mauritania, Egypt, Yemen and Saudi Arabia) have already led to introduction of RVFV into these countries in the past, and parallel, undocumented trade flows of ruminants towards the RC can be assumed. Indeed, examples of the spread of other animal diseases in the Middle East and North Africa (MENA) region illustrate that such animal movements do occur. For example, the spread of foot and mouth disease (FMD)-viruses in the region and its impact on the FMD situation in some countries of the RC may be considered as an indicator of animal movements in the region and the risk of introducing infection.

However, regulations implemented in some countries to control FMD might mitigate the risk of introduction of other diseases, RVF included. In Mauritania, FMD-viruses appear to be circulating without being introduced into the direct neighbouring country, Morocco. In addition, animal health legislation in Algeria bans the movements of animals from southern Algeria (where animal density is low and spread occurs only within small communities) to the north of the country (where the highest animal density is found close to the coast). Looking back at the particular FMD SAT2 epidemic that took place in the MENA region in spring 2012, the disease largely spread within Egypt and entered Libya (OIE notification 12/03/2012) and the West Bank/Gaza Strip (OIE notification 19/04/2012), but its presence in Tunisia, where vaccination against FMD was already implemented, was not recorded.

The FMD example could demonstrate an easier existing route for animal movements from the Eastern source compared to the Western source. Therefore, a higher risk of introduction of RVFV from the East could be considered as compared to the West, which supports the assessment by the experts, through the EKE process.

#### 4.2.2. Introduction of RVFV via vectors

When examining pathogen spread by insect movement, it is important to distinguish short-distance dispersal and long-distance dispersal. A review of the literature (Service, 1997) shows that the maximum distance flown actively by mosquitoes is usually between 1 and 5 km, with half of the records being < 1 km. However, while short-distance dispersal seems to be active, translocation of insects over long distances is mainly passive and may be associated with various types of transportation (e.g. ships, trains, aeroplane, etc.) or wind. The probability of introduction of RVFV vectors through human transportation was not assessed separately in this assessment, because it was considered of minor importance in comparison with the probability of movement of RVFV-infected animals. Translocation of insects over long distances by wind is a well-described phenomenon. The current opinion is that such movements can be considered as a part of an active migration during which the insect actively 'climbs' out of its 'flight boundary layer' (a layer in which the wind speed is lower than the insect's flight speed), thus facilitating long-distance wind-borne transport (Reynolds et al., 2006). By this mechanism, insects might carry plants or animal pathogens over long distances.

The probability that an infected mosquito will be carried by wind from one region to another depends on the simultaneous existence of several conditions, i.e. the percentage of infected mosquitoes during an epidemic, the probability that wind is moving in a particularly relevant direction, the probability of the mosquito being carried by the wind, the probability of mosquito survival during its transportation (which depends on humidity and temperature), the probability that it will land in a region inhabited by relevant hosts and the probability of virus transmission to a susceptible host by the mosquito. For a single mosquito, the probability that all these events will take place is extremely low. However, during an epidemic, there will be large numbers of infected mosquitoes and, consequently, the potential of transmission by wind cannot be excluded.

There are several examples of vector-borne infections that support long-distance translocation of pathogens carried by either *Culicoides* or mosquitoes, such as bluetongue virus (Sellers et al., 1978, 1979; Sellers and Pedgley, 1985; Garcia-Lastra et al., 2012) and bovine ephemeral fever (Murray, 1970; Finlaison et al., 2010; Aziz-Boaron et al., 2012). Long-distance transportation of insects can occur over sea and land. Moreover, there are several examples of possible transportation of viruses over deserts (e.g. West Nile virus (Reisen et al., 2004) and lumpy skin disease virus (Yeruham et al., 1995)). More importantly for this opinion, circumstantial evidence suggests that in 1977 RVFV was introduced into Egypt by long-distance wind-borne transportation from Sudan (Sellers et al., 1982; Pedgley, 1983).

Export of cattle and sheep from Sudan to Egypt had been banned in 1975 and 1976, and in 1977 exports went by sea, not through Aswan. Travel of animals to Aswan would have taken too long for animals to remain infectious and the chances of mosquitoes being carried in the vehicles were considered small. It was therefore claimed that the most likely cause of the epidemic was the arrival of infected insects from the south by an unusual long spell of southerly winds at Aswan from July 28 to August 3, when the monsoon spread north from Sudan. However, undocumented movements of camels, which could be infected without showing clinical signs, has been proposed as a possible alternative explanation of RVFV introduction into Egypt in 1977 (Gad et al., 1986).

### 5. Risk of Rift Valley fever virus endemicity in the region of concern

#### 5.1. Methodology

For RVF to become endemic, the virus in a ruminant host population must be capable of spread (the reproductive number,  $R_0$ , must be higher than 1). However, the potential for spread is not sufficient

for RVF to become endemic in a region. Other factors that are important include the size of the susceptible ruminant host population, which needs to be large enough during the vector season to prevent fade-out of the infection. Furthermore, the virus must be able to survive during the season of limited vector activity.

In this opinion, a transmission model developed by Fischer et al. (2012) was used to determine the initial epidemic growth rate of RVFV infections, which is an indicator of the potential occurrence of RVFV spread, following introduction of the virus. The model was assessed using parameters for host, vector and pathogen derived from literature and using predicted relative abundances of *Cx. pipiens* obtained for ToR 2. Estimates of host densities, which were also needed to assess the risk, were obtained from the FAO (2007) livestock grid. Maps of the Mediterranean Basin and the rest of Europe were created, showing the areas at risk of RVFV spread, given introduction of the virus. Because of a lack of information on the seasonality of vector abundance, persistence of the virus during the unfavourable period with limited or no vector activity (winter) could not be assessed. Consequently, the potential for endemicity was not addressed in this assessment. Only the potential for an RVFV to occur, given introduction of the virus, is assessed.

The model assumes homogeneous (i.e. equally likely contact between all vectors and hosts) mixing within each pixel of the risk map. Furthermore, it is assumed that only livestock is susceptible to RVFV infection. Direct transmission was not included in the model, because the importance of this transmission route in the amplification of the disease still needs to be evaluated (Chevalier et al., 2008).

The FAO livestock density maps (FAO, 2007; see Appendix C) for cattle, buffalos, sheep and goats were combined with temperature data for August ([www.worldclim.org](http://www.worldclim.org); see Appendix D) and the abundance estimates of *Cx. pipiens* from ToR 2. The classes of vectors were interpreted as follows: 0, no vectors; 1, 1 000 vectors per km<sup>2</sup>; 2, 10 000 vectors per km<sup>2</sup>; 3, 100 000 vectors per km<sup>2</sup>. The vector was assumed to be active within the temperature range 9.4–32.5 °C (Eldridge, 1968; Madder et al., 1983).

Generally, host preference, although having a genetic basis, is strongly influenced by local host density and availability (Takken and Verhulst, 2013). Spatial and seasonal shifts in host availability can be associated with shifts in the transmission risk of arboviruses such as West Nile virus (Kilpatrick et al., 2006; Simpson et al., 2012). *Cx. pipiens* is present in a large area and consequently presents a large ecological plasticity. Females of *Cx. pipiens* feed on a variety of warm-blooded vertebrates from birds to mammals, including humans. To take these potential changing host–vector ratios into account, two rather extreme scenarios for two different host preferences were applied in the model, and consequently two risk maps were generated for:

- Scenario 1: vectors biting on livestock only and
- Scenario 2: vectors were biting both livestock and other, refractory, hosts.

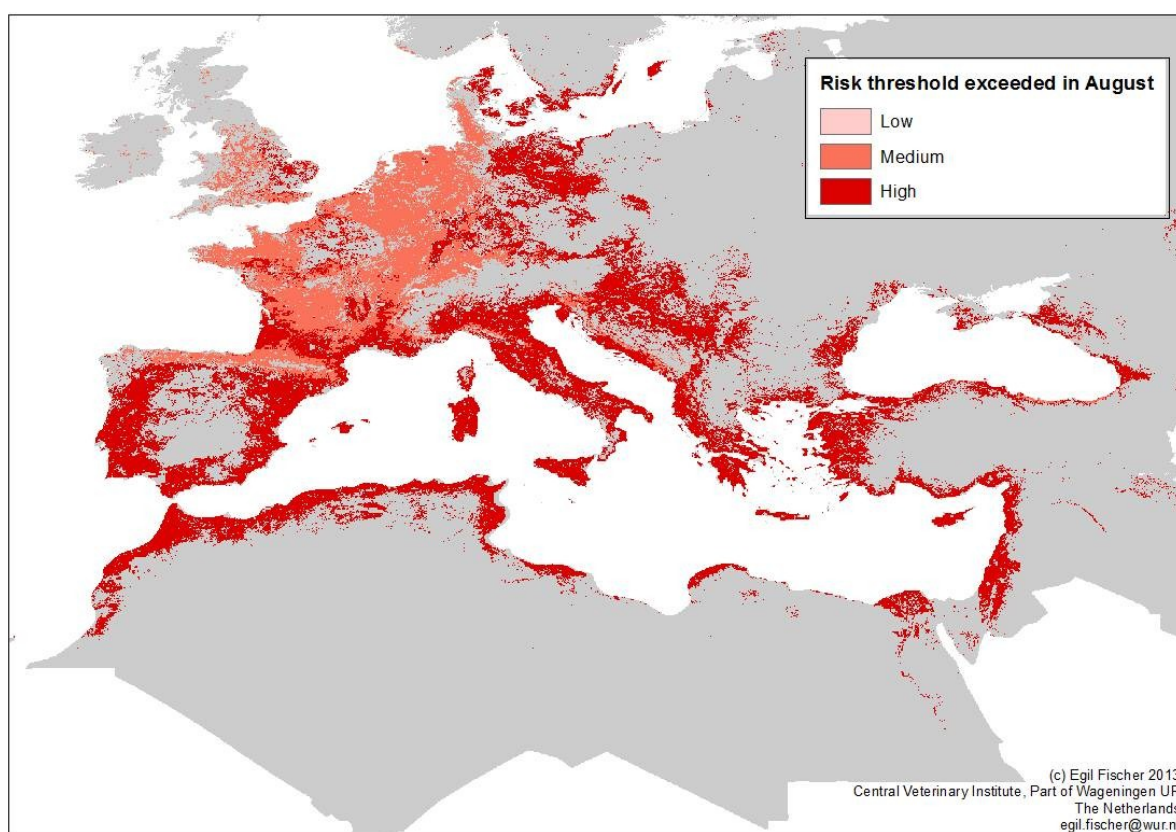
In the second scenario, the numbers of vectors per host (susceptible or refractory) were assumed to be equal. Birds are considered refractory hosts for the RVFV. Given that, of all nine potential RVF vectors, the five *Culex* species are both ornithophilic and mammophilic (Gad et al., 1987a, b, 1999; Balenghien et al., 2006; Muñoz et al., 2012; Osório et al., 2012; Roiz et al., 2012), the host preference in the second scenario could be more realistic for these *Culex* species. The other four mosquito species belonging to the *Aedes* and *Ochlerotatus* genus are mainly mammophilic, however, and bite refractory hosts only occasionally. The host preference used in scenario 1 would have been more appropriate for these species. Unfortunately, abundance data for these mosquito species in the region concerned were too scarce to address this issue specifically. Thus, the two scenarios could be considered as two more extreme options, with reality somewhere in between.

## 5.2. Results

The risk map presented in Figure 15 shows areas subdivided into the risk (likelihood) of exceeding the threshold for transmission of RVFV in August under scenario 1. Risk categories for exceeding the threshold of spread were low (probability < 0.25), medium (0.25–0.75) or high (> 0.75). These results are obtained for scenario 1, i.e. the vectors bite only susceptible livestock.

This resulted in high-risk areas, very similar to the areas where *Cx. pipiens* is highly abundant. This is because the areas with livestock mostly coincide with the areas where *Cx. pipiens* is abundant. Those areas with few animals, vectors or a temperature outside the range 9.4–32.5 °C were excluded (grey areas) from the analysis. According to this scenario, the coastal area of almost the whole of the Mediterranean Basin is at risk of RVFV spread after introduction of the virus, as well as along the River Nile.

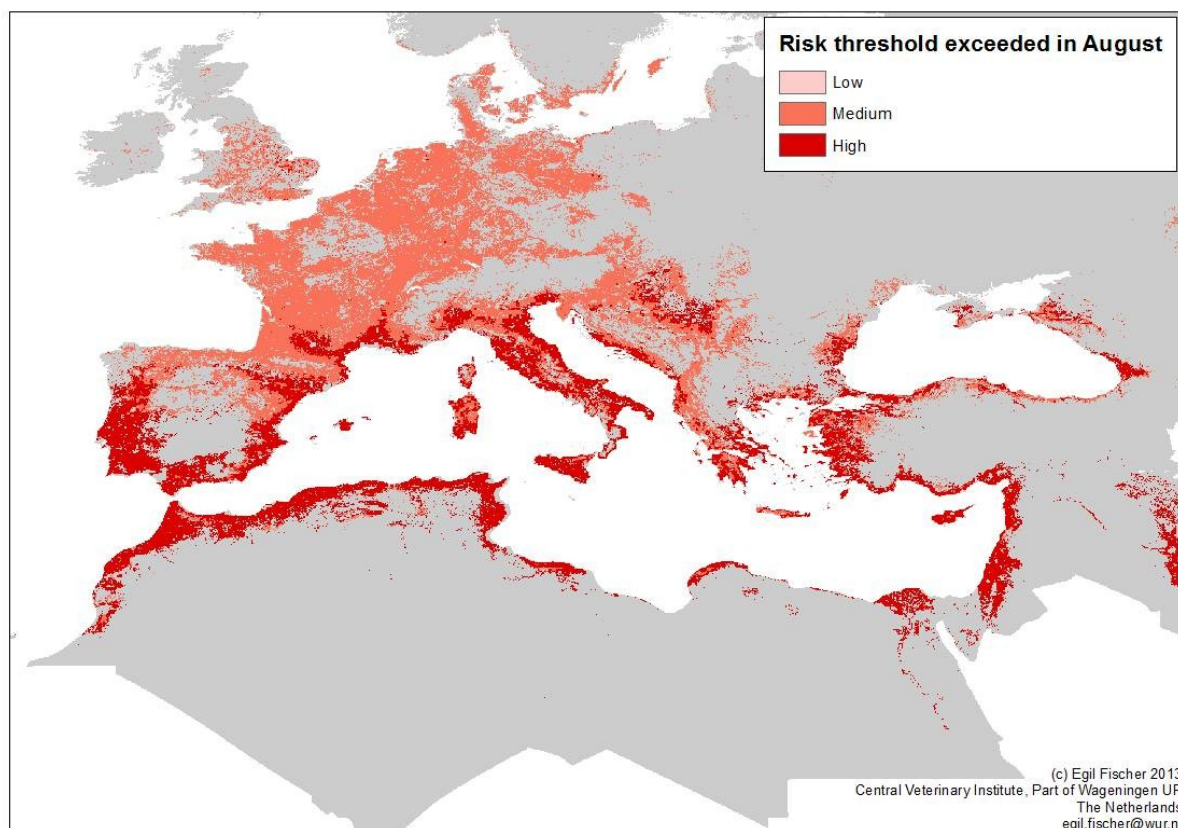
Grey areas: areas excluded for analysis because of absence of livestock or temperatures outside the range in which *Cx. pipiens* is assumed to be active. Sources: livestock abundance data are provided by the FAO livestock grid (FAO, 2007); the abundance of *Cx. pipiens* was generated through the systematic literature review (ToR 2) and high-resolution temperature data were used ([www.worldclim.org](http://www.worldclim.org); see Appendix D).



**Figure 15:** Risk that the threshold for spread of RVFV is exceeded following introduction in August with *Cx. pipiens* as sole vector, biting only susceptible hosts (scenario 1)

Figure 16 presents the risk that the threshold for occurrence of an RVFV spread is exceeded in the Mediterranean Basin and the rest of Europe in August under scenario 2. These results are obtained for scenario 2, i.e. vectors biting both refractory and susceptible hosts with equal preference. In comparison with the first scenario, this led to a lower likelihood that the threshold for occurrence of an RVFV spread will be exceeded in some of the northern areas of Europe, where *Cx. pipiens* is abundant; however, the risk of occurrence of RVFV spread remained equally high in the coastal area of almost the whole of the Mediterranean Basin and along the River Nile.





Grey areas: areas excluded for analysis because of absence of livestock or temperatures outside the range for which *Cx. pipiens* is assumed to be active. Sources: livestock abundance data are provided by the FAO livestock grid (FAO, 2007); the abundance of *Cx. pipiens* was generated through the systematic literature review (ToR 2) and high-resolution temperature data were used (www.worldclim.org; see Appendix D).

**Figure 16:** Risk that the threshold for spread of RVFV is exceeded following introduction in August assuming *Cx. pipiens* as the only available vector, with equal host preference for susceptible and refractory hosts (scenario 2)

Summarising, both scenarios for mosquito host preference led to a high risk of occurrence of RVFV. Spread upon virus introduction into the coastal areas of the RC and along the River Nile. The conclusion of the EKE workshop was that introduction of RVFV in the RC, as used for ToR 3, is highly likely in any year in which there is an outbreak in the source countries. This, combined with the observation that there have been outbreaks in only two countries of the RC, as defined by the mandate, would imply that the probability of spread after introduction is low. This seems to conflict with the results of both scenarios 1 and 2. The EKE model, however, considered only the introduction of RVFV in the region concerned, regardless whether it were to be introduced in a zone at high or low risk of exceeding the threshold for spread.

Factors that might lead to lack of spread upon introduction could be:

- immediate slaughter of animals, e.g. undocumented trade during the Eid al-Adha (the Festival of Sacrifice)
- no or very few susceptible animals in the area of introduction, or introduction of infected animals at times of low vector activity
- existence of vaccination programmes targeting RVF in the RC



- Some outbreaks remaining unnoticed, for example because clinical signs are mild or misinterpreted.

Further, EKE is a subjective assessment. If, for example, the infectious period of host animals is shorter than anticipated in the EKE process, this would result in fewer animals remaining infectious upon arrival after transport, and thus the number of infected animals introduced will have been overestimated. The experts expressed a large uncertainty around some values of the parameters, but judged that they would be extremely surprised if the real values were to lie outside the upper and lower limits of the probability distributions. However, the EKE experts did not address the spatial distributions of the RVFV introductions over the RC.

The transmission model indicates that the coastal area of almost the whole of the Mediterranean Basin, as well as the banks of the River Nile are at risk of occurrence of RVFV spread following introduction. This assessment was based on the abundance data of a single mosquito species (*Cx. pipiens*), which could have led to underestimation of the probability of outbreaks, because the abundance of other vector species was not considered.

Although the possibility of RVFV spread during the vector season is a prerequisite for endemicity, the occurrence of epidemics does not necessarily lead to endemicity. Reduction in the susceptible host density can drive the infection to extinction during the vector season. If this does not occur, the virus needs to survive the adverse season. In northern countries this is the winter, while in subtropical or tropical regions the dry season can cause be unfavourable period with limited vector activity, i.e. an adverse season. The virus can survive this period in the host, e.g. by direct transmission, or in the vector by vertical transmission and survival in resistant eggs of floodwater *Aedes* or in diapausing *Culex* females. To determine the risk of endemicity, the risk of both extinction of the infection during the vector season and survival during the adverse season need to be addressed as well. However, such an assessment requires information on the seasonality of vector abundance and on the possibility of vertical transmission in local vector species and survival of the virus during the period of limited vector activity, information that is currently unavailable for the RC.

## CONCLUSIONS AND RECOMMENDATIONS

### CONCLUSIONS

#### ToR 1

- Although the cyclic occurrence of RVF in endemic areas (once every 5–15 years) makes it difficult to observe possible changes in the spatial distribution of RVFV over a 10-year period, the available information indicates that RVFV moved north within Mauritania, in a desert area, but no countries were newly infected during the past 10 years.
- In the past 10 years, there has been a large increase in reported outbreaks in South Africa, which may be partly due to better reporting and registration of RVF outbreaks and does not necessarily indicate an increased risk.

#### ToR 2

- The probability that the RVFV vectors *Aedes vexans* and *Aedes albopictus* are present across a large part of the countries around the Mediterranean Basin is medium.
- The probability that the RVFV vectors *Ochlerotatus caspius*, *Ochlerotatus detritus*, *Culex pipiens* and *Culex theileri* are present in the coastal areas and deltas of the countries around the Mediterranean Basin is medium to high.
- The probability that the RVFV vectors *Culex perexiguus* and *Culex antennatus* are present around the Nile Delta is high.
- In the Mediterranean Basin, the largest number of mosquito species and the highest mosquito densities are found during summer and autumn (from the beginning of June to the end of September). During winter (from November to March), there is reduced mosquito activity.
- Geo-referenced data on abundance of RVFV vectors in the RC are scarce and data on seasonal variation in this abundance are lacking. *Cx. pipiens* is estimated to be abundant in the coastal areas of RC and the river banks of the Nile River.

#### ToR 3

- RVFV has already been introduced into Egypt and into Mauritania, including, recently, in a more northern area of Mauritania.
- Expert knowledge elicitation indicates that some hundreds of RVFV-infected animals may be introduced into the RC when an epidemic in the source areas occurs.
- The number of infected animals to be introduced into the RC from the east source (the Arabian Peninsula and East Africa) is likely to be higher than the number of infected animals introduced from the west source (Central and West Africa).
- Although the risk of introduction of RVFV into the RC through windborne vectors cannot be quantified, it is expected to be small in comparison with the risk of introduction by infected ruminants.

#### ToR 4

- From the available data it was not possible to assess the risk of endemicity, since seasonal abundance data of the vectors and information on the possibility of virus surviving the vector

adverse season are lacking. It was possible to assess only the potential of RVFV to spread in the RC.

- Depending on the density of livestock and the abundance of *Cx. pipiens*, there is a potential for RVFV spread in the coastal areas of the RC as well as along the River Nile

## RECOMMENDATIONS

### ToR 1

- Implement additional investigations to analyse the movement of RVFV to a desert area in mid-northern Mauritania and to assess any likelihood of disease resurgence in the future in this particular area of the country.
- To better detect changes in the global occurrence of RVF in animals, monitoring, surveillance and reporting of the disease should be enhanced.

### ToR 2

- To provide maps of the seasonal variation in vector abundance in the RC, vector collection programmes in countries of the Mediterranean Basin need to be initiated while existing ones need to be intensified.
- To determine vector competence for each of the potential vector candidates, detailed laboratory investigations are required, including studies of the host preference of the different species.

### ToR 3

- To improve the assessment of the risk of introduction of RVFV into the RC, efforts should be made to quantify the volumes of animals moved into the region.

### ToR 4

- To better assess the risk of RVF endemicity in the RC, seasonal abundance data of the vectors should be collected, their host preference should be established, the possibility of vertical transmission in local vector species should be quantified and the possibilities for the virus to survive the vector adverse season should be investigated quantitatively.

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## APPENDIX

### A. POTENTIAL RVFV VECTORS

**Table 1:** Arthropods species found naturally infected with RVFV

Species	Country (year)	Species	Country (year)
<b><i>Aedes</i> genus</b>		<b><i>Culex</i> genus</b>	
<b><i>Aedimorphus</i> subgenus</b>		<i>annulioris</i> gp.	Madagascar (1979)
<i>cumminsii</i>	South Africa (1982) Kenya (1982) Burkina Faso (1983)	<i>antennatus</i>	Nigeria (1967, 1970) Madagascar (1979, 2008/2009) Kenya (1982) Egypt (2003)
<i>dalzieli</i>	Kenya (1982) Senegal (1974, 1983)	<i>bitaeniorhynchus</i>	Kenya (2006/2007)
<i>dentatus</i>	Zimbabwe (1969) South Africa (1972)	<i>neavei</i>	South Africa (1981)
<i>durbanensis</i> <i>fowleri</i>	Kenya (1937) Senegal (2003)	<i>pipiens</i>	Egypt (1978)
<i>ochraceus</i>	Senegal (1993) Kenya (2006/2007)	<i>poicilipes</i>	Senegal (1998, 2002, 2003) Mauritania (1998–99, 2003) Kenya (2006/2007) Sudan (2007)
<i>tarsalis</i>	Uganda (1944) Uganda (1955)	<i>quinquefasciatus</i>	Kenya (2006/2007) Sudan (2007)
<i>vexans arabiensis</i>	Senegal (1993, 2002) Saudi Arabia (2000)	<i>simpsoni</i>	Madagascar (1979) Kenya (1982)
<b><i>Neomelaniconion</i> subgenus</b>		<i>theileri</i>	South Africa (1953, 1956, 1970, 1974, 1975) Zimbabwe (1969) Kenya (1982)
<i>circumluteolus</i>	Uganda (1955) South Africa (1955, 1981)	<i>tritaeniorhynchus</i>	Saudi Arabia (2000)
<i>lineatopennis</i> = <i>macintoshi</i> (Huang, 1985)	Zimbabwe (1969) South Africa (1975, 1982, 1984) Kenya (1982, 1984, 2006/2007)	<i>univitattus</i>	Kenya (2006/2007)
<i>palpalis</i>	Central African Republic (1969)	<i>vansomereni</i>	Madagascar (1979) Kenya (1982)
<i>unidentatus</i>	South Africa (1975)	<i>zombaensis</i>	South Africa (1981) Kenya (1982, 1989)
<b><i>Ochlerotatus</i> subgenus*</b>		<b><i>Eumelanomyia</i> genus</b>	
<i>caballus</i>	South Africa (1953)	<i>rubinotus</i>	Kenya (1982)
<i>juppi</i>	South Africa (1975)	<b><i>Eretmapodites</i> genus</b>	
<b><i>skusea</i> subgenus</b>		<i>chrysogaster</i>	Uganda (1944)?

Species	Country (year)	Species	Country (year)
<i>pembaensis</i>	Kenya (2006/2007)	<i>quinquevittatus</i>	Uganda (1944)? South Africa (1971)
<b><i>Stegomyia</i> subgenus</b>		<b><i>Coquilletidia</i> genus</b>	
<i>aegypti</i>	Sudan (2007)	<i>fuscopennata</i>	Uganda (1960)
<i>africanus</i>	Uganda (1956)	<i>grandidieri</i>	Madagascar (1979)
<i>dendrophilus</i>	Uganda (1948)	<b><i>Mansonia</i> genus</b>	
<i>furcifer</i>	Burkina Faso (1983)	<i>africana</i>	Uganda (1959, 1968) Central African Republic (1969) Kenya (1989, 2006/2007) Senegal (2003)
<b><i>Anopheles</i> genus</b>		<i>fuscopennata</i>	Uganda (1959)
<b><i>Anopheles</i> subgenus</b>		<i>uniformis</i>	Uganda (1959) Madagascar (1979) Kenya (2006/2007) Senegal (2003)
<i>coustani</i>	Zimbabwe (1969) Madagascar (1979, 2008/2009) Sudan (2007)	<b>Other Diptera</b>	
<i>fusicolor</i>	Madagascar (1979)	<b><i>Simulium</i> spp.</b>	South Africa (1953)
<b><i>Cellia</i> subgenus</b>		<b><i>Culicoides</i> spp.</b>	Nigeria (1967)
<i>arabiensis</i>	Sudan (2007)		
<i>christyi</i>	Kenya (1982) South Africa (1982)		
<i>cinereus</i>	South Africa (1974)		
<i>pauliani</i>	Madagascar (1979)		
<i>pharoensis</i>	Kenya (1982) South Africa (1982)		
<i>squamosus</i>	South Africa (1975) Madagascar (1979, 2008/2009)		

\*Elevation of the subgenus *Ochlerotatus* to generic rank, i.e. *Ochlerotatus* genus (Reinert, 2000).

*Ae. vexans*, *Ae. ochraceus* and *Ae. dalzieli*, which belong to the subgenus *Aedimorphus*, are considered the main enzootic vectors of RVFV in Senegal.

*Ae. cumminsii*, *Ae. circumluteolus* and *Ae. mcintoshi*, which belong to the subgenus *Neomelaniconion*, are considered the main enzootic vectors of RVFV in East Africa.

**Table 2:** Arthropods species that have demonstrated the ability to transmit RVFV in the laboratory (experimental infections)

Species	Mode of transmission	Species	Mode of transmission
<b><i>Aedes</i> genus</b>		<b><i>Anopheles</i> genus</b>	
<b><i>Aedimorphus</i> subgenus</b>		<i>multicolor</i>	Biological
<i>vexans vexans</i>	Biological	<i>pharoensis</i>	Biological
<i>fowleri</i>	Biological	<b><i>Culex</i> genus</b>	
<b><i>Neomelanicion</i> subgenus</b>		<i>annulirostris</i>	Biological
<i>circumluteolus</i>	Biological	<i>antennatus</i>	Biological
<i>lineatopennis</i> = <i>macintoshi</i>	Biological	<i>erraticus</i>	Biological
<i>palpalis</i>	Biological	<i>erythrothorax</i>	Biological
<b><i>Ochlerotatus</i> subgenus*</b>		<i>neavei</i>	Biological
<i>canadensis</i>	Biological	<i>nigripalpus</i>	Biological
<i>cantator</i>	Biological	<i>palpalis</i>	Biological
<i>caballus</i>	Biological	<i>perexiguus</i>	Biological
<i>caspius</i>	Biological	<i>quinquefasciatus</i>	Biological
<i>detritus</i>	Biological	<i>salinarius</i>	Biological
<i>dorsalis</i>	Biological	<i>tarsalis</i>	Biological
<i>excrucians</i>	Biological	<i>territans</i>	Biological
<i>juppi</i>	Biological	<i>theileri</i>	Biological
<i>notoscriptus</i>	Biological	<i>univittatus</i>	Biological
<i>sollicitans</i>	Biological	<i>pipiens</i>	Biological Mechanical
<i>stictitus</i>	Biological	<i>versicolor</i>	Biological
<i>taeniorhynchus</i>	Biological Mechanical	<i>zombaensis</i>	Biological
<i>triseriatus</i>	Biological		
<i>vigilax</i>	Biological	<b><i>Eretmapodites</i> genus</b>	
<b><i>Stegomyia</i> subgenus</b>		<i>chrysogaster</i>	biological
<i>aegypti</i>	biological mechanical	<i>quinquevittatus</i>	biological
<i>aegypti formosus</i>	mechanical	<b><i>Coquillettidia</i> genus</b>	

Species	Mode of transmission	Species	Mode of transmission
<i>albopictus</i>	biological	<i>perturbans</i>	biological
<b><i>Protomacleaya</i> subgenus</b>		<b>Other <i>Diptera</i></b>	
<i>triseriatus</i>	Biological	<i>Stomoxys calcitrans</i>	Mechanical
<b><i>Aedes</i> subgenus</b>		<i>Glossina morsitans</i>	Mechanical
<i>tarsalis</i>	Biological	<i>Lutzomyia longipalpis</i>	Mechanical
		<i>Phlebotomus dubosqi</i>	Mechanical
		<i>Phlebotomus papatasi</i>	Mechanical
		<i>Culicoides variipennis</i>	Mechanical

Note: very few species and individuals within species have been tested owing to the difficulty of establishing colonies of many of the floodwater species (especially those belonging to the subgenera *Neomelanicion* and *Aedimorphus*).



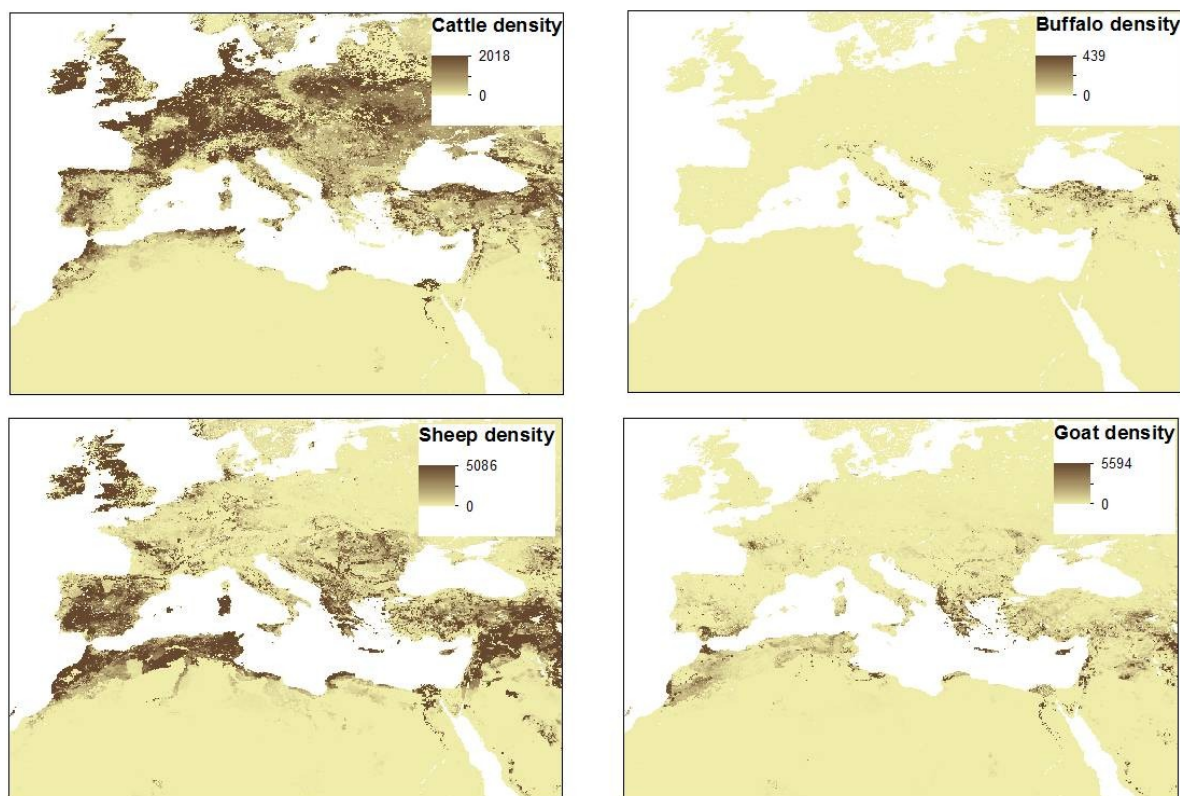
## B. OVERVIEW OF AVAILABLE RECORDS OF RVFV VECTORS IN EUROPE AND THE SOUTHERN MEDITERRANEAN BASIN, EXTRACTED FROM THE SYSTEMATIC REVIEW\*

**Table 3:** Count of presence records per species and per country

Country	<i>Aedes vexans</i>	<i>Aedes albopictus</i>	<i>Ochlerotatus caspius</i>	<i>Ochlerotatus detritus</i>	<i>Culex antennatus</i>	<i>Culex pipiens</i>	<i>Culex theileri</i>	<i>Culex tritaeniorhynchus</i>	<i>Culex perexiguus</i>
Algeria	0	1	0	0	0	5	0	0	0
Belgium	0	0	0	0	0	2	0	0	0
Croatia	20	1	20	5	0	64	0	0	0
Cyprus	0	0	1	1	0	26	1	0	1
Czech Republic	33	0	10	0	0	40	0	0	0
Denmark	0	0	0	0	0	1	0	0	0
Egypt	0	0	34	24	77	107	3	0	56
France	4	0	14	5	0	56	2	0	0
Germany	4	0	1	3	0	8	0	0	0
Greece	0	0	0	0	0	2	0	0	0
Hungary	1	0	1	0	0	1	0	0	0
Israel	0	2	13	2	0	22	1	0	7
Iran	3	0	16	0	0	27	25	10	2
Iraq	0	0	0	0	0	12	0	0	0
Italy	30	28	56	10	0	111	6	0	0
Lebanon	0	5	23	0	0	18	0	0	0
Morocco	0	0	3	0	0	2	0	0	0
Norway	0	0	0	0	0	2	0	0	0
Poland	12	0	2	1	0	20	0	0	0
Portugal	0	0	25	11	0	43	39	0	10
Reunion	0	0	0	0	0	15	0	0	0
Romania	1	0	1	0	0	8	0	0	0
Russia	3	0	2	0	0	36	0	0	0
Serbia	5	0	1	0	0	5	0	0	0
Slovakia	11	0	3	0	0	11	0	0	0
Slovenia	1	0	0	0	0	1	0	0	0
Spain	8	2	24	10	1	33	18	0	7
Sudan	1	0	0	0	0	2	0	0	0
Sweden	10	0	1	0	0	13	0	0	0
Switzerland	2	0	0	0	0	5	1	0	0
Syria	0	1	0	0	0	0	0	0	0
The Netherlands	0	0	0	0	0	2	0	0	0
Tunisia	0	0	1	0	0	57	1	0	1
Turkey	11	0	6	0	0	9	16	4	1
United Kingdom	0	0	2	1	0	4	0	0	0
<b>Total</b>	<b>160</b>	<b>40</b>	<b>260</b>	<b>73</b>	<b>78</b>	<b>770</b>	<b>113</b>	<b>14</b>	<b>85</b>

\*The systematic review was carried out between 1 August 2012 and 31 December 2012. The electronic search of papers was restricted to papers published between 01/01/1990 and 31/12/2012.

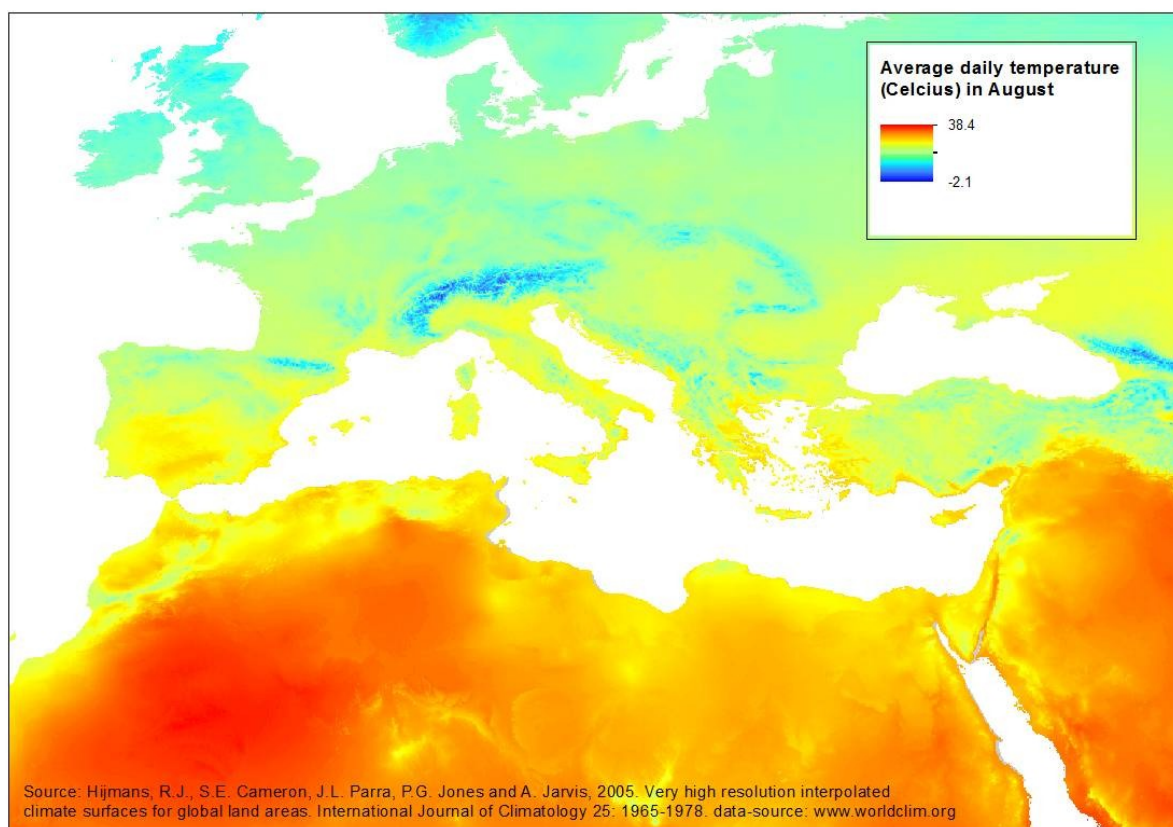
### C. LIVESTOCK DENSITY IN REGION CONCERNED



FAO. 2007. Gridded livestock of the world 2007, by G.R.W. Wint and T.P. Robinson. Rome, pp 131 <http://www.fao.org/AG/againfo/resources/en/glw>

**Figure 17:** Livestock density

#### D. AVERAGE DAILY TEMPERATURE IN THE REGION OF CONCERN



**Figure 18:** Average daily temperature in the region of concern

## GLOSSARY

**Biological transmission:** transmission requiring a persistent systemic infection in the vector that is transmissible through salivation during blood feeding.

**Pixel:** physical point in a raster image, or the smallest addressable element in a display device. It is the smallest controllable element of a picture represented on the screen. The address of a pixel corresponds to its physical coordinates.

**Vector competence:** the ability of a blood-sucking insect to become infected with a pathogen (parasite, virus) after ingestion of an infective blood meal and to transmit this pathogen subsequently when feeding on a vertebrate host.

**Vector capacity:** the combination of vector competence and all exogenous factors of ecological nature that affect it. To be effective, the vector must not only be competent, but have, in a given environment, a favourable bio-ecology for transmission, i.e. to be abundant, to have a longevity sufficient to permit the infected vector to be infectious (duration of the incubation period), to maintain close contact with the vertebrate reservoir (if any) and its vertebrate hosts (trophic preferences), etc. It is only under these conditions that its vector capacity will be high. Variations in vector population density and age are often at the origin of the seasonal pattern of transmission of many vector-borne infectious diseases.

**Mechanical transmission:** transmission that occurs when infectious viral particles are borne on the mouthparts after an interrupted feed on a viraemic hosts and are re-inoculated when the mosquito resumes feeding on a second host. This mode of transmission is especially efficient with the larger haematophagous flies, e.g. horse and deer flies (Diptera: Tabanidae) and tsetse flies (Diptera: Glossinidae), because of the greater surface area of their mouthparts compared with those of a mosquito.

**Random Classification Forests:** an empirical modelling technique using field observations to establish the relationship between vector occurrence and prevailing environmental conditions. This technique generates many classification (categorical response variable) or regression trees (continuous response variable) (Breiman, 2001).

**NUTS:** the Nomenclature of Territorial Units for Statistics, (NUTS) or in French Nomenclature Unités Territoriales Statistiques, is a geocode standard for referencing the administrative divisions of countries for statistical purposes. The standard was developed by the European Union and subdivides the territory of the [European Union](#) into [regions at three different levels](#) (NUTS 1, 2 and 3, moving from larger to smaller territorial units (see also [http://epp.eurostat.ec.europa.eu/statistics\\_explained/index.php/Glossary:NUTS](http://epp.eurostat.ec.europa.eu/statistics_explained/index.php/Glossary:NUTS))).

**HASC:** hierarchical administrative subdivision codes; used to represent the names of country subdivisions, such as states, province or regions.