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Application of a quantitative entry assessment model to compare the relative risk of incursion of zoonotic bat-borne viruses into European Union Member States

Verity Horigan\textsuperscript{a,*}, Paul Gale\textsuperscript{a}, Rowena D. Kosmider\textsuperscript{a}, Christopher Minnis\textsuperscript{b}, Emma L. Snary\textsuperscript{a}, Andrew C. Breed\textsuperscript{a}, Robin R.L. Simons\textsuperscript{a}

\textsuperscript{a} Animal and Plant Health Agency (APHA), Department of Epidemiological Sciences, New Haw, Addlestone, Surrey KT15 3NB, United Kingdom
\textsuperscript{b} The Royal Veterinary College, Royal College Street, London, England NW1 0TU, United Kingdom

ABSTRACT

This paper presents a quantitative assessment model for the risk of entry of zoonotic bat-borne viruses into the European Union (EU). The model considers four routes of introduction: human travel, legal trade of products, live animal imports and illegal import of bushmeat and was applied to five virus outbreak scenarios. Two scenarios were considered for \textit{Zaire ebolavirus} (wEBOV, cEBOV) and other scenarios for Hendra virus, Marburg virus (MARV) and Middle East Respiratory Syndrome Coronavirus (MERS-CoV). The use of the same framework and generic data sources for all EU Member States (MS) allows for a relative comparison of the probability of virus introduction and of the importance of the routes of introduction among MSs.

According to the model wEBOV posed the highest risk of an introduction event within the EU, followed by MARV and MERS-CoV. However, the main route of introduction differed, with wEBOV and MERS-CoV most likely through human travel and MARV through legal trade of foodstuffs. The relative risks to EU MSs as entry points also varied between outbreak scenarios, highlighting the heterogeneity in global trade and travel to the EU MSs. The model has the capability to allow for a continual updating of the risk estimate using new data as, and when, it becomes available.

The model provides an horizon scanning tool for use when available data are limited and, therefore, the absolute risk estimates often have high uncertainty. Sensitivity analysis suggested virus prevalence in bats has a large influence on the results; a 90% reduction in prevalence reduced the risk of introduction considerably and resulted in the relative ranking of MARV falling below that for MERS-CoV, due to this parameter disproportionately affecting the risk of introduction from the trade route over human travel.

1. Introduction

Bats are natural reservoir hosts for many viruses which are recognised as serious potential threats to human and/or animal health (Calisher et al., 2006). The bat-borne viruses emerging in the African, Asian and Australian continents have come to the fore more recently with regards to their threat to human health and pandemic potential. Since 2003 there have been a number of large-scale human outbreaks of bat-borne diseases e.g. \textit{Zaire ebolavirus} (EBOV) and Severe Acute Respiratory Syndrome (SARS) in Western Africa and Asia respectively, whilst a significant number of human cases of Nipah virus (NiV) are reported in Bangladesh every year (IEDCR, 2014). Pteropid bats are known to be the natural host of Hendra virus (HeV) (Halpin et al., 2000), a member of the same genus (Henipavirus) as Nipah virus. Since 1994 HeV has been responsible for seven human cases in Australia, four of which were fatal (Smith et al., 2016). Bats have also been linked with Marburg virus (MARV) (Towner et al., 2007), and, more tenuously, with the emerging Middle East Respiratory Syndrome Coronavirus (MERS-CoV) (Memish et al., 2013). Within the European Union (EU), zoonotic incidents of bat-borne viruses have been restricted to European bat lyssavirus types 1 and 2 which have been responsible for less than 10 human cases since 1977 (Fooks et al., 2003). To date, there have only been a few isolated reports of introduction of bat-borne viruses (e.g. MARV, SARS, MERS-CoV) from outside the EU mainly through entry of infected humans (Puzelli et al., 2013; Desenclos et al., 2004; WHO, 2008; Reuss et al., 2014). However, these incidents illustrate that introduction can occur and support the need for some level of surveillance activity to assess the probability of when and where further incidents may occur.

* Corresponding author.
E-mail address: verity.horigan@apha.gsi.gov.uk (V. Horigan).

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incursions may take place.

For most bat-borne zoonotic diseases, primary transmission routes for human infection include direct or indirect contact with bat bodily fluids (Leroy et al., 2009; Luby et al., 2006), or via intermediate animal hosts (Parashar et al., 2000; Hanna et al., 2006). Onward transmission of disease is then possible via human-to-human contact or contact with contaminated fomites or the environment, with nosocomial infections being particularly important in some instances (Baron et al., 1983; Chowell et al., 2014). Disease introduction into the EU could therefore potentially occur from a number of routes, including human travel, illegal and legal importation of food products and transport of live animals. These routes have previously been associated with incursion of other viruses into the EU. For example, human travel and immigration are thought to be the primary reasons why individual Member States (MSs) have a high prevalence of the same Human Immunodeficiency Virus (HIV) subtypes as their historical African colonies (Faria et al., 2012). Classical rabies has been detected in imported domestic pets (Suárez-Rodríguez et al., 2013; McQuiston et al., 2008) and avian influenza (HSNI type A) has been detected in illegal imports of Crested Hawk Eagles from Thailand into Belgium (Van Borm et al., 2005). In the case of trade, illegal importation of food products has been a suggested route of origin for the foot and mouth disease epidemic in the UK in 2001 (Defra, 2001), whilst legal trade in fresh produce, such as fruit and vegetables, has been associated with norovirus (Hjertqvist et al., 2006) and hepatitis A outbreaks (Dentinger et al., 2001). Virus specific transmission characteristics may influence the relative importance of these potential routes of disease introduction.

In terms of government financial resource allocation, it is important to develop methods to assist in efficient targeting of surveillance activities e.g. to inform which pathogen(s) are most likely to enter the EU, where they are most likely to enter and what scenarios would have the most impact with regards to human or animal health and welfare or trade implications. To address these issues, a number of relative risk ranking tools have previously been developed, such as the EU wide DISCONTROLS (2016) and the UK specific D2R2 (Gibbens et al., 2016). However, these tools are qualitative and are generally based on chosen criteria rather than a defined quantitative assessment. There is, therefore, benefit in a quantitative model that can utilise freely available numerical data from datasets on trade and human travel such as Eurostat (2014) and FaoStat (2014).

To address this need, a generic quantitative risk assessment framework for the entry of bat-borne zoonotic viruses to the EU was developed (Simons et al., 2016), considering the pathways: human travel, live animal movement, legal trade of food products and illegal trade of bushmeat. Using current knowledge of virus characteristics such as environmental survival and host incubation periods, the framework was parameterised for NiV, to provide an assessment of the relative risks of transmission through the known pathways of introduction into the EU.

In this paper the model framework is parameterised for a number of other virus outbreak scenarios (MARV, EBOV, HeV and MERS-CoV) and the relative probabilities of introduction to EU MSs are compared and discussed. The impact of uncertainty in the parameter estimates is also investigated through scenario analyses.

2. Materials & methods

2.1. Overview

The entry assessment model parameterised for NiV (Simons et al., 2016), was re-parameterised for five outbreak scenarios (MARV, EBOV, HeV and MERS-CoV), to compare and assess the relative risk of introduction to the 28 EU MSs for these 5 viruses of concern. For EBOV two different outbreak scenarios were considered: 1) Disease geographically distributed in Central Africa, where human outbreaks have previously been relatively limited (cEBOV) (i.e. non-epidemic situation). It is acknowledged that the link between bats and MERS-CoV is more tenuous than initially thought when it first emerged (Memish et al., 2013), but the virus was included here to provide an example of a respiratory coronavirus circulating within the Middle East area. Recent evidence of replication and shedding of MERS-CoV in experimentally infected Jamaican fruit bats (Artibeus jamaicensis) (Munster et al., 2016) and discovery of closely related MERS-like CoV (Anthony et al., 2017) further support the hypothesis that bats are ancestral reservoirs for MERS-CoV. As neither live EBOV nor MERS-CoV virus has been isolated from bats a very low prevalence of infection in bats was assumed. Different prevalence values for all the viruses were considered in the scenario analysis.

The assessment was conducted following the World Organisation for Animal Health (OIE) code for import risk analysis (OIE, 2004). Under traditional OIE guidelines, there are three components of risk assessment: entry, exposure and consequence. This model only considered the entry assessment (i.e. it ceases at the point at which virus is released into the EU) and did not consider subsequent potential exposure of the virus to humans, livestock or wildlife on entry to the EU.

2.2. Model framework

The model has been discussed in detail by Simons et al. (2016). Briefly, the main outputs of the model were a relative estimate of the annual probability of at least one introduction event into each EU MS, $Pr(j)$, and an overall estimate of the probability of at least one introduction event for the EU as a whole. This estimate took into account factors such as the probability an individual unit is infected (or contaminated) in the exporting country, the survival of the virus over the duration of the journey, whether or not the animal/human displays clinical signs and the annual volume of products being imported. The model equations for the various routes are described by Simons et al. (2016). The model was coded in the R software package and is deterministic; as such no stochastic variability of specific parameters was considered in the baseline model.

The relative risk estimate was derived by combining the probability of at least one introduction event from each of the routes included in the model (Fig. 1) from all the potential exporting countries to produce an overall probability for each MS:

$$P_r(j) = 1 - \prod_{r=1}^{k} (1 - Pr(j)),$$

where $R$ is the total number of routes considered for the virus (human travel ($r = 1$), live animal movement ($r = 2$), legal trade of ‘at risk’ products ($r = 3$), illegal trade of bushmeat ($r = 4$) and $Pr(j)$ is the probability of at least one introduction event via route $r$ to MS $j$. The average number of years to an introduction event was calculated, $Y_r(j) = 1/Pr(j)$. In addition the 28 EU MSs were ranked according to their probability of disease introduction, $Zr(j) (1:28)$ by comparing the average number of years, $Y_r(j)$, to an introduction event for each route and MS and ranking the MSs from 1 to 28 accordingly. This provided an indication of where in the EU an introduction event is more likely. Note that the average number of years to an introduction event is based on the input data provided and so does not account for subsequent changes in future years of model factors such as trade patterns or disease prevalence; e.g. for wEBOV it would be assumed that the same number of cases will occur in Western Africa every year as in 2014.

The model considered the four primary routes of introduction based on extensive literature reviews (Simons et al., 2014). While other potential routes exist such as direct exposure from bats through natural migration or accidental exposure via aeroplane strikes, they were not considered here for the viruses of concern. However, as the model...
framework is adaptable, and Eq. (1) is multiplicative with respect to the routes, the choice of routes can be amended and these pathways can be considered in the future, as and when appropriate data become available.

2.3. Parameterisation for individual viruses

The model was parameterised for HeV, MARV, MERS-CoV, wEBOV and cEBOV. The genus Ebolavirus includes five species, each with a single member virus (Kuhn et al., 2013). Due to the potential differences in parameters for the different viruses only Ebola virus (from species Zaire ebolavirus) was parameterised here.

The model considered the probability of introduction to EU MSs from ‘exporting countries’, that is, those in which virus was strongly expected to be circulating in humans, livestock or wildlife (Fig. 2). This was determined from peer-reviewed publications of where the viruses had been reported. For livestock and wildlife, including bats, only positive test results for isolation of live virus or detection of viral RNA were considered (active bat infection). Countries that had reported positive seroprevalence or those which had reported a human case known to have arisen from recent travel to another country were not considered as an ‘exporting country’.

The full details of the generic model parameters are presented in Simons et al. (2016). In this section an overview of the data sources used to parameterise each route is presented.

**Human travel:** Passenger travel data from exporting countries to EU MSs were obtained from the Eurostat dataset aviapaexcc (Eurostat, 2014). For EBOV, MARV and HeV for which outbreaks are sporadic, \( n_{\text{inf}}(k) \) was estimated using the average number of cases per outbreak over a 15 year period. This value was assumed by the authors to encompass all relevant historical data. However, as human cases of MERS-CoV have been reported regularly since March 2012, \( n_{\text{inf}}(k) \) was calculated by dividing the number of reported cases by the number of reporting years assuming a constant rate per year. To account for differences in prevalence between passenger types e.g. business, visiting family, and tourist etc., the baseline prevalence of infection in the exporting country was weighted by the average passenger duration of stay (days) in the exporting country. The ratio of passenger types was assumed to be the same for each exporting country. The sub-clinically infected population was estimated by multiplying the prevalence of infection in passenger type \( i \), \( \theta(i,k) \) by the incubation period of the virus. Passenger detail such as healthcare employees potentially exposed to infected patients or eco-tourists with the intention of visiting bat caves was not accounted for here although it is acknowledged that these factors could influence the risk outcome as has been documented (WHO, 2008).

**Legal trade:** To determine whether a product was considered contaminated, the concentration of virus on the product on arrival to an EU MS was estimated where \( C_{\text{min}} \) is a threshold viral load upon arrival at the EU MS, below which the product was considered not to be contaminated. Note, that this value was set to 1 log10 TCID50 for all viruses as a worst case scenario. The model considered the prevalence of contamination in at risk raw products (see Table 1 for definition), the initial concentration of virus on a raw product in the exporting country and any reduction in viral load between initial contamination of the raw product and arrival in the EU MS, including the effect of processing. The default estimate for the prevalence of contamination in raw products, \( p_{\text{Graw}}(k) \), was based on the estimated prevalence of active virus.
shedding in bats, $p_{BInf}(k)$, the contact rate of the bat with the product, $p_{Bcontact}(k)$ and seasonality of virus shedding, i.e. the proportion of the year that bats can shed the virus. Data on volume of trade from exporting countries to EU MSs were obtained from FaoStat (2014).

**Bushmeat**: In this model bushmeat was assumed to enter an EU MS via aircraft passenger luggage. The volume of contaminated bushmeat entering the EU was estimated by combining the probability of a passenger of type $i$ bringing in bushmeat from exporting country $k$, $p_{BM}(i,j,k)$, and the probability that a consignment of bushmeat was contaminated. The actual number of bushmeat consignments entering the EU from country $k$ was estimated based on the number of bushmeat consignments seized in the EU MS, $N_{seized}(i,j,k)$, and an under-reporting factor accounting for the proportion of passengers luggage that were searched. The under-reporting factor was estimated to be 0.5% based on literature (Falk et al., 2013) and assuming targeted testing of passengers occurs (Simons et al., 2016). The model did not account for
| Parameter Description | Values |
|-----------------------|--------|
| Exporting countries with evidence of virus in human, livestock or wildlife ($k$) | Bangladesh, India, Malaysia, Singapore, Cambodia, East Timor, Indonesia, Thailand |
| Estimated number of human infections in exporting country $k$, in one year, $n_{inf}(k)$ for the scenario | Bangladesh = 27, India = 66, all other countries = 0 |
| Average time to clinical symptoms of the virus (days), $T_{IP}(k)$ | 9, 12.8, 7, 5.5, 8.82 |
| Legal Trade – of at risk products | FaoStat section 8-fruits and derived products, pig and pig products, camel meat and milk |
| Prevalence of active bat infection in exporting country $k$, $P_{bat}(k)$ | 0.20%, 0.47%, 0.29%, 0.10%, 0.10% |
| Proportion of the year bats may shed active virus, $P_{season}(k)$ | 0.33 |
| Initial viral load on product, $C_0(x)$, $\sim$ logNormal$(\mu, \sigma)$ | Mean = 2 log$_{10}$ TCID$_{50}$/ml, Variance = 2.25 log$_{10}$ TCID$_{50}$/ml |
| Half-life of virus in environment, pre-harvesting (h), $CHL_{env}(k,l)$ | 6.15 |
| Half-life of virus during transport (4 °C) (h), $CHL_{trans}(j,k,l,m)$ | 308 |
| Minimum Viral load to consider product contaminated in EU/MS, $C_{min}$ | 1 log$_{10}$ TCID$_{50}$ |
| Live animals: animal species with evidence of infection including serology $s$ | Non-human primate, pig, dog, cat, ferret |
| Probability bushmeat is of species $s$, $P_{bush}(s)$ | 1.5% Bats, 98.5% other species |

*FAO fruits and derived products see: [http://www.fao.org/es/faodef/fdef08e.htm](http://www.fao.org/es/faodef/fdef08e.htm) for definition and classification of commodities.
any virus reduction that may occur from processing bushmeat such as smoking or salting and assumed that the possibility of luggage being searched for bushmeat was the same for each exporting country.

**Live animals**: This route considered the number of animals of species \( s \) arriving from an exporting country \( k \) in one year and the prevalence of live animal infection of species \( s \) in the exporting country to give the probability that at least one infected animal entered a MS. **Numbers of live animal exports from exporting countries to EU MSs** were obtained from the trans-European TRade Control and Expert System (TRACES) database which provides data on the number of animals that are brought into the EU and issued with a Common Veterinary Entry Document (TRACES, 2014).

Virus specific parameter estimates used in the model are given in Table 1. Estimates for NiV are also provided for comparison (Simons et al., 2016). Further information (including references) on these estimates is provided in Appendix A.

The model developed here is deterministic for ease of use in an outbreak situation where rapid parameterisation and data availability for all EU MSs are key requirements. Uncertainty and variability in the model were previously considered for NiV by implementing a series of analyses using alternative parameter values (Simons et al., 2016). It was found that while some scenarios had an impact on the absolute values of probability of introduction of NiV, the relative rankings, of both routes and MSs were more robust. However, the estimate for the prevalence of NiV in bats had considerable impact on the average number of years to an EU introduction of NiV relative to the baseline model and much lower estimates for this prevalence were the only scenarios to have an impact on the relative ranking between the routes. Given this, and the complexity involved in assessing multiple uncertainties between multiple scenarios, the scenarios considered here were a 90% and 99% reduction in the virus prevalence in bats as these reductions both had considerable impact in the previous model for NiV; smaller reductions in virus prevalence had little impact.

### 3. Results

At the EU level the probability of viral introduction was ranked highest for \( wEBOV \) with an overall average prediction of at least one introduction event occurring in one year (Table 2), primarily via human travel and associated illegal importation of bushmeat.

In relative terms, and given the uncertainties in the absolute value estimates, MARV and MERS-CoV were of a comparable risk whilst the introduction event occurring in one year (Table 2), primarily via human travel and associated illegal importation of bushmeat.

In relative terms, and given the uncertainties in the absolute value estimates, MARV and MERS-CoV were of a comparable risk whilst the introduction risk was lowest for HeV.

A 90% or 99% reduction in virus prevalence in the exporting country bat population only affected the risk estimates for the legal trade and bushmeat routes. Consequently, for EBOV and MERS-CoV, which had a relatively high probability of introduction from human travel, the decrease in risk from trade and bushmeat was not sufficient to affect the overall probability of disease introduction. For HeV and NiV, however, where the legal trade and bushmeat routes posed the highest risk in the baseline model the decrease in overall risk was substantial. Human travel replaced legal trade and bushmeat as the route with the highest associated probability for HeV, MARV and NiV introduction when the virus prevalence in bats was reduced by 99% (90% for MARV).

The number of imports of live animals was low for all exporting countries resulting in a relatively low probability of introduction via this route for all viruses (Table 2). Only dromedary camels (Camelus dromedaries) have been shown to be a risk factor for MERS-CoV transmission (Azhar et al., 2014), but as there is no legal trade of live camels to the EU from countries reporting cases of MERS-CoV, the risk from live animals was considered to be negligible.

Within the EU, individual MSs demonstrated different relative probabilities for the various pathogens when the probabilities for all the routes of introduction were combined for each MS (Fig. 3). The probability of introduction for MERS-CoV was quite high across most of the EU MSs, but for other viruses it was mainly focussed in a few MSs, usually in Western Europe with the probability of introduction for MSs from Eastern Europe and Scandinavia generally being much lower (Fig. 3). Overall, the probability of introduction was highest for individual viruses in those MSs with strong historical links to relevant exporting countries, e.g. the United Kingdom (UK) for NiV and France for \( cEBOV \). Such links usually correspond to a relatively large volume of human travel or legal trade movements between the countries. It should be noted that this analysis does not consider movement within the EU after the initial entry.

The countries are ranked according to the probability of introduction for each virus in Table 3. Overall there was a relatively wide variation in the relative ranking of many of the MSs between the different viruses. Different distributions of risk scores were observed between routes but considering the relative ranking of the MSs (1–28), the UK, France, Germany and the Netherlands generally have the highest probability of introduction for all viruses considered here.

### 4. Discussion

The entry assessment described here shows the potential for application of a quantitative model framework for any pathogens, using zoonotic bat-borne viruses as an example. Although a scarcity of data for virus specific parameters resulted in a high degree of uncertainty in the absolute risk values presented, the main strengths of this model lie in the estimates of relative risks between routes of entry and those MSs which are at greater risk of virus introduction. The model has the capability to allow for a continual updating of the risk estimate using new research data as, and when, it becomes available. Any increase in the model risk estimate output would allow the stakeholder to consider employing suitable risk reduction strategies or heightened surveillance providing a rapid and cost-effective response.

Of particular value was the model’s ability to illustrate the relative importance of the different routes of entry between viruses; legal trade of foodstuffs was more important for HeV, NiV and MARV while human travel was more important for MERS-CoV and both EBOV scenarios. These differences could be partly attributed to the virus specific parameters. For example rapid decay of MERS-CoV influenced the relative risk of the transmission pathways; the half-life of MERS-CoV is very short compared to the other viruses (48 min at pre-harvest temperatures (van Doremalen et al., 2013)) so it is unlikely to persist in high numbers on any produce imported via legal trade or in contaminated bushmeat.

The probability of introduction to the EU via the pathways under consideration here varies across the EU at MS level; the UK, France, Germany and the Netherlands often had the highest probability of

### Table 2

| Scenario | Human travel | Legal trade | Bushmeat | Live animals | All routes |
|----------|--------------|-------------|----------|--------------|------------|
| NiV      | 540          | 12 (115, 1147) | 70 (682, 5915) | 51,649       | 10 (83, 344) |
| HeV      | 3202         | 45 (441, 4403) | 123      | 39,299       | 33         |
| MARV     | 18           | 3 (25, 242)   | 5 (25, 44) | 295,015      | 2 (8, 12)  |
| MERS-CoV | 4            | 8.00E+11      | 191      | N/A          | 4 (4, 4)   |
| wEBOV    | 1            | 6 (58, 578)   | 3 (3, 3) | 923          | 1 (1, 1)   |
| cEBOV    | 19           | 240          | 37 (60, 64) | 8259        | 12 (14, 15) |

* The model returned a N/A results due to the probability of introduction being too low to compute.
introduction for all viruses considered. In general those countries which ranked the highest, with regard to probability of introduction (Table 3) corresponded to those with the highest population and the highest ‘disposable income’ (calculated as gross domestic product (GDP) derived from purchasing power parity) (see Appendix B). Other contributory factors could include immigration population densities and trade partner characteristics, both of which frequently have a historical basis. The Netherlands was an exception to this in that it ranked highly in the probability of virus introduction yet only 8th for population density and 7th for GDP (See Appendix B). One explanation for
Table 3
Relative ranking of EU MSs by expected number of years until entry of virus. Minimum, maximum and range in EU MS ranking across all viruses are shown. Columns are highlighted with lower ranking or smaller range in ranking of EU MS having darker grey shades.

| MS (country code) | NiV | HeV | MARV | MERS | wEBOV | cEBOV | min  | max  | range |
|-------------------|-----|-----|------|------|-------|-------|------|------|-------|
| AUT               | 11  | 16  | 16   | 8    | 12    | 22.5  | 8    | 22.5 | 14.5  |
| BEL               | 8   | 7   | 6    | 11   | 1     | 3     | 1    | 11   | 10    |
| BGR               | 17  | 25  | 19   | 20   | 24    | 22.5  | 17   | 25   | 8     |
| CYP               | 19  | 26.5| 13   | 14   | 13    | 11    | 11   | 26.5 | 15.5  |
| CZE               | 14  | 19  | 18   | 12   | 22    | 15    | 12   | 22   | 10    |
| DEU               | 3   | 3   | 7    | 2    | 6     | 2     | 2    | 7    | 5     |
| DNK               | 7   | 14  | 10   | 9    | 23    | 22.5  | 7    | 23   | 16    |
| ESP               | 10  | 9   | 5    | 6    | 4     | 7     | 4    | 10   | 6     |
| EST               | 18  | 28  | 27   | 26   | 27    | 22.5  | 18   | 28   | 10    |
| FIN               | 9   | 12  | 11   | 18   | 25    | 22.5  | 9    | 25   | 16    |
| FRA               | 4   | 5   | 1    | 3    | 3     | 1     | 1    | 5    | 4     |
| GBR               | 2   | 1   | 4    | 1    | 2     | 9     | 1    | 9    | 8     |
| GRC               | 16  | 10  | 9    | 10   | 16    | 12    | 9    | 16   | 7     |
| HRV               | 22  | 20  | 17   | 28   | 14    | 22.5  | 14   | 28   | 14    |
| HUN               | 25  | 18  | 20   | 17   | 20    | 16    | 16   | 25   | 9     |
| IRL               | 15  | 8   | 15   | 7    | 17    | 10    | 7    | 17   | 10    |
| ITA               | 6   | 4   | 8    | 4    | 8     | 6     | 4    | 8    | 4     |
| LIT               | 21  | 23  | 27   | 23   | 9     | 22.5  | 9    | 27   | 18    |
| LUX               | 26  | 26.5| 23   | 27   | 11    | 14    | 11   | 27   | 16    |
| LVA               | 27  | 24  | 27   | 22   | 27    | 22.5  | 22   | 27   | 5     |
| MLT               | 24  | 21  | 21   | 16   | 10    | 13    | 10   | 24   | 14    |
| NLD               | 1   | 2   | 2    | 5    | 5     | 4     | 1    | 5    | 4     |
| POL               | 13  | 13  | 14   | 21   | 15    | 5     | 5    | 21   | 16    |
| PRT               | 23  | 17  | 3    | 15   | 7     | 8     | 3    | 23   | 20    |
| ROU               | 20  | 6   | 24   | 19   | 19    | 22.5  | 6    | 24   | 18    |
| SVK               | 12  | 15  | 25   | 24   | 21    | 22.5  | 12   | 25   | 13    |
| SVN               | 28  | 22  | 22   | 25   | 27    | 22.5  | 22   | 28   | 6     |
| SWE               | 5   | 11  | 12   | 13   | 18    | 22.5  | 5    | 22.5 | 17.5  |

this could be that the Netherlands is serving as a hub for travellers and trade entering the EU and that a reasonable proportion entering the Netherlands are going onto other European countries. It is also possible that more Dutch people, compared to other EU MSs, travel to countries with these viruses. Data from Uganda suggest that in 2012 the Netherlands was the 15th most popular country of origin for tourist arrivals, the only European countries with more arrivals were the United Kingdom and Germany, but Dutch tourists represented a higher proportion of their population (Republic of Uganda, 2013).

Freely available statistical data on trade and human travel for Western Europe were, in general, more complete than for Eastern European MSs. Data for countries such as Estonia, Latvia and Lithuania were lacking for some routes resulting in a low ranking for these countries which may not be a true reflection of the actual risk. It is difficult to determine whether this is a true data gap or if the route genuinely has a low probability of introduction for these countries. This was a particular problem for cEBOV where twelve countries were lacking data for specific routes and, therefore, equally ranked as 22.5.

The generic parameters for which EU wide datasets exist have a relatively high degree of completeness although there is a concern that potentially high risk low volume trade products e.g. camel milk may be under-recorded therefore underestimating the risk via these trade products. Virus specific parameters depend more upon focused research studies and peer reviewed literature and rely upon detection of pathogens in reporting countries. Uncertainty in these virus parameters, in particular, the prevalence of infection in bats in the exporting country, and viral persistence during processing and storage may limit the application of the model by introducing considerable uncertainty. The sensitivity analysis of virus prevalence in bats demonstrated that the results for the relative importance of the routes for EBOV and MERS were quite robust with human travel remaining the route with the highest probability of introduction. With regards to HeV, NiV and MARV, however the sensitivity to the variation in prevalence indicates that further data for this particular parameter would strengthen the model results; this is particularly true of MARV where a 90% reduction in virus prevalence changed the risk ranking order of the routes of introduction. Note that this analysis is to consider the uncertainty about the true prevalence in bats, as such it has no impact on the parameterisation of the human prevalence, which is based on human outbreak data.

It should be noted that the parameterisation of this model uses the best available data at the current time. Some parameters are subject to high uncertainty and the probability of introduction of different viruses will be dynamic, changing over time if a virus spreads amongst different animal species populations or if new human outbreaks occur. Simons et al, previously demonstrated that changes in the exporting country (e.g. if China were to get NiV in the future) or ‘at risk’ product types can have a large effect on the model outputs (Simons et al., 2016). We have demonstrated here that changes in the virus prevalence in bats in the exporting country can have an impact on the average number of years to EU entry for the different viruses and on the relative ranking of the individual routes of entry. We have also highlighted the differences...
in probabilities for two Ebola scenarios; a relatively small non-epidemic human outbreak and a large epidemic scale outbreak. It is acknowledged that the viruses considered here could have differing sensitivity to stochastic variability of specific parameters given the complex dynamics between the routes and viruses. Alternative scenarios could, therefore, be considered in the future.

All risk pathways were given equal weight within the model as the model predicts probability of introduction not risk of human/animal exposure and consequence as stated in the OIE risk assessment (OIE, 2004). For example, the model results suggest that the legal trade (fruit) route has a high probability of introduction for HeV, although human infection from consumption of contaminated fruit is not a proven transmission route for this virus. This route was considered in the model based on the knowledge that fruit bats are known to consume raw fruit in orchards (Eby and Lunney, 2002) and date palm sap is a known route of transmission for NiV (another henipavirus) (Luby et al., 2006; Khan et al., 2012; Nahar et al., 2014). Similarly, there is currently no evidence of human-to-human transmission of HeV but as this has occurred for the Bangladeshi strain of NiV (Gurley et al., 2007) it is plausible that this could occur with or without mutation and adaptation of currently identified strains. Real-time application of the model would allow for removal or addition of pathways if future scientific work provides suitable input data or if trade patterns between third countries and the EU alter. Thus, all pathways were assessed for completeness according to the dogma ‘absence of evidence is not evidence of absence’.

Whilst EU wide trade controls are implicitly accounted for within the model parameters, risk mitigation procedures put in place by individual MSs such as targeted sampling are not taken into account. It is possible that there have already been introduction events of the diseases under consideration here within the EU, but these have remained undetected due to lack of subsequent human/animal infection and/or onward transmission within the individual MS. For example, although the importation of MERS-CoV cases to the EU remains possible, an ECDC risk assessment determined that the risk of sustained human-to-human transmission is low (ECDC, 2015a). However, the outbreak of MERS-CoV in South Korea demonstrated that the potential exists for a serious risk of onward human spread, with >185 cases arising from the importation of 1 human index case (Su et al., 2015).

Validation of such a model presented here is difficult as there are few independent resources for which to compare the results. However, it is of relevance that the five MSs suggested to have the highest probability of introduction of MERS-CoV by the model (Germany, UK, Italy, France and the Netherlands) have already had imported human cases of this pathogen (ECDC, 2014). The model results are also consistent with other reports which predict more imported cases of MERS-CoV to arrive into the EU (ECDC, 2014; WHO, 2014a; Bialek et al., 2014; Poletto et al., 2014). All cases reported outside of the Middle East have had a recent travel history to the Middle East or contact with a case that had travelled from this region (Su et al., 2015). This is in line with the highest probability of introduction for MERS-CoV predicted by this model to be via human travel (Table 2).

Overall, the approach developed here provides a high-level horizon scanning tool for the probability of introduction of bat-borne zoonotic viruses into the EU. The virus scenario with the highest probability was the wEBOV scenario with an overall average prediction of just under one introduction event per year, primarily via human travel. Due to the wide scope of the model, which necessitated using global datasets sometimes with incomplete data, there was a high degree of uncertainty in the absolute risk values presented. A general lack of data on virus specific parameters also contributed to this uncertainty. Thus, the main strengths of this model lie in the comparison of the relative risks between viruses and routes of entry. Whilst there have been several risk assessments carried out for the introduction of individual pathogens into the EU (Rolin et al., 2013; Durand et al., 2013; Mur et al., 2014; Snary et al., 2012) this model was able to assess a range of viruses and could be adapted for other pathogens, as it has the advantage of easy access to a number of relevant databases. The model also allows for a continual updating of the risk estimate enabling the stakeholder to respond in a rapid and risk appropriate manner, for example, by implementing risk-based surveillance and control strategies.

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Appendix A. Virus specific parameterisation

A.1. Ebola

A.1.1. Human travel

Number of human infections in exporting country, nhinf(k). Prior to 2014, human outbreaks of Ebola had been confined to the Sub-Saharan Congo rainforest basin with Uganda, Sudan, Gabon, Democratic Republic of Congo (DRC) and Republic of Congo (ROC) having the most frequent occurrence of infection; in total there had been ~22 confirmed outbreaks resulting in fatal cases (Table A1). The beginning of 2014 saw the largest recorded outbreak of Ebola emerge in Western Africa with Sierra Leone, Liberia and Guinea being the countries most affected. Due to the potential differences in parameters for the different viruses only Ebola virus (from species Zaire ebolavirus), EBOV, is parameterised here. The number of cases per outbreak estimated over a 15 year period was used for nhinf(k). This is estimated at 16,125 for West Africa, 75 for the DRC, 65 for Gabon and 79 for ROC.

Time to clinical signs, Tc(k). The recognised incubation period for EBOV disease is 2–21 days (Del Rio et al., 2014). A review of epidemiological parameters from Ebola outbreaks including incubation period has recently been published (Van Kerkhove et al., 2015). Using a sum of all the estimated means divided by the number of studies the time to clinical signs used is 8.82 for EBOV only (Table A2).

A.1.2. Legal trade import

Bat infection prevalence in exporting country, ping(k). Evidence of EBOV infection in bats (Epomops franqueti, Hypsignathus monstrosus, and Myonycteris torquata) is currently based on seroprevalence and presence of viral RNA.

Table A3 shows the relevant papers that have attempted isolation of EBOV. Combined, 1033 bats were tested with 0 testing positive for viral shedding of Ebola. As such the prevalence of EBOV in bats for this model was assumed to be 0.1%.

Product types (l): The potential for EBOV to act as a foodborne pathogen has been addressed (Bausch, 2011). Parallels have been drawn between the recognised incubation period for EBOV disease is 21 days (Del Rio et al., 2014). A review of epidemiological parameters from Ebola outbreaks including incubation period has recently been published (Van Kerkhove et al., 2015). Using a sum of all the estimated means divided by the number of studies the time to clinical signs used is 8.82 for EBOV only (Table A2).
| Date       | Country          | Number of cases | Number dead | Strain | Likely source | Exposure to: Human-to-human transmission? |
|------------|------------------|-----------------|-------------|--------|---------------|------------------------------------------|
| 1972       | DRC (Zaire)      | 2               | 1           | Zaire | Retrospective identification from 1977 case         | Not with ease                        |
| 1976       | Sudan            | 284             | 280         | Zaire | Index case had bought antelope and monkey bushmeat | Not with ease                        |
| 1977       | DRC (Zaire)      | 1               | 1           | Zaire | No overt link to 1976 outbreak                      | Not with ease                        |
| 1979       | Sudan            | 34              | 22          | Sudan | Index case in same factory                            | Not with ease                        |
| 1980       | Kenya            | 1               | 0           | Zaire | Near Mount Elgon                                    | No secondary transmission            |
| 1980       | Côte d’Ivoire    | 0               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | Yes - non-transmission                |
| 1984       | Gabon            | 52              | 31          | Zaire | Exposure to dead Chimpanzees | Non-natural spread                  |
| 1985       | Gabon            | 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 1992       | Côte d’Ivoire    | 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 2000       | Gabon            | 425             | 224         | Sudan |指数 case had attended burial                | Non-natural spread                  |
| 2001/2002  | Republic of Congo| 59              | 44          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2004       | Gabon            | 65              | 33          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2005       | Gabon            | 60              | 45          | Zaire | Dead chimp found to also be infected                | Non-natural spread                  |
| 2006       | Gabon            | 1               | 1           | Sudan | Healthcare worker flew from Gabon to S. Africa      | Non-natural spread                  |
| 2007       | Gabon            | 0               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 2007       | Republic of Congo| 42              | 24          | Zaire | Exposure to bushmeat                                | Non-natural spread                  |
| 2007       | Republic of Congo| 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 2008       | Gabon            | 65              | 33          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2009       | Gabon            | 60              | 45          | Zaire | Dead chimp found to also be infected                | Non-natural spread                  |
| 2010       | Gabon            | 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 2011       | Gabon            | 425             | 224         | Sudan |指数 case had attended burial                | Non-natural spread                  |
| 2012       | Republic of Congo| 59              | 44          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2013       | Gabon            | 65              | 33          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2014       | Gabon            | 60              | 45          | Zaire | Dead chimp found to also be infected                | Non-natural spread                  |
| 2015       | Gabon            | 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |
| 2016       | Gabon            | 425             | 224         | Sudan |指数 case had attended burial                | Non-natural spread                  |
| 2017       | Republic of Congo| 59              | 44          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2018       | Gabon            | 65              | 33          | Zaire | unusually high number of animals infected            | Non-natural spread                  |
| 2019       | Gabon            | 60              | 45          | Zaire | Dead chimp found to also be infected                | Non-natural spread                  |
| 2020       | Gabon            | 1               | 0           | Côte d’Ivoire | Chimpanzee deaths in wild | No secondary transmission            |

Note: Some outbreaks were considered to be related to different introductions of Ebola virus each related to a hunting episode. At least 2 duikers, 2 chimp, and 2 gorilla carcasses were suspected of involvement in infection of 6 human index patients.
Adapted table from Van Kerkhove et al. (2015) showing estimated time to clinical signs during EBOV outbreaks.

| Year      | Virus       | Estimate | Range         | Study number | Ref                        |
|-----------|-------------|----------|---------------|--------------|----------------------------|
| 1976      | Zaire       | 6.3      | 5.8-6.18      | 318          | (Commission, 1978)         |
| 1976      | Zaire       | 5.99     |               | 262          | (Camacho et al., 2014)     |
| 1995      | Zaire       | 7        | 1-15          | 27           | (Dowell et al., 1999)      |
| 1995      | Zaire       | 6.2      | 5-8           | 5            | (Brooks et al., 1999)      |
| 1995      | Zaire       | 5.3      |               | 315          | (Chowell et al., 2004)     |
| 1995      | Zaire       | 10       |               | 291          | (Lekone and Finkenstadt, 2006) |
| 1995      | Zaire       | 12.7     |               | 23           | (Eichner et al., 2011)     |
| 1995      | Zaire       | 7.8      | 2-19          | 23           | (Ndambi et al., 1999)      |
| 2000      | Sudan       | 12       | 2-21          | 425          | (Okware et al., 2002)      |
| 2000      | Sudan       | 3.35     |               | 425          | (Chowell et al., 2004)     |
| 2000-01   | Sudan       | 12       | 1-12          | 425          | (Francescioni et al., 2003) |
| 2007      | Bundibugyo  | 6.3      |               | 56           | (MacNeil et al., 2010)     |
| 2007      | Bundibugyo  | 7        | 2-20          | 192          | (Wamanal et al., 2010)     |
| 2014-15   | Zaire       | 9.31     | 2-21          | 20           | (Althaus et al., 2015)     |
| 2014-15   | Zaire       | 9.4      |               | 500          | (Team, 2014)               |
| 2014-15   | Zaire       | 11.4     |               | 155          | (Team, 2014)               |
| 2014-15   | Zaire       | 9        |               | 1798         | (Team, 2015)               |
| 2014-15   | Zaire       | 9.9      | 9-11          | 193          | (Faye et al., 2015)        |
| 2014-15   | Zaire       | 12       |               | –            | (Rivers et al., 2014)      |
| 2014-15   | Zaire       | 10       |               | –            | (Rivers et al., 2014)      |
| Total     | All         | 8.6      |               |              |                            |
| Total     | Zaire       | 8.82     |               |              |                            |

Proportion of the year bats may shed active EBOV virus, $p_{season}(k)$. Seasonal climate has been found to be associated with human EBOV outbreaks (Ng et al., 2014). Increased great ape mortality has been frequently reported during the dry seasons of July and December (Pourrut et al., 2007) and the biannual birthing periods of the bat species identified as potential natural reservoirs also occur during the dry seasons when fruit is scarce (Langevin and Barclay, 1990). In the absence of more definitive data the proportion of the year in which bats are presumed to be infectious is estimated as 0.5.

Initial viral load on raw product, $c_0(x)$. The initial concentration of EBOV on the raw product is assumed to be equivalent to that shed by bats. As there have been no successful virus isolation attempts from bats, values are extrapolated from experimental evidence. Nasal washes and oral and rectal swabs from pigs challenged via mucosal exposure with $1 \times 10^6$ PFU of the Zaire strain of EBOV had infectious titres ranging from $1 \times 10^2$ to $1 \times 10^3$ TCID$_{50}$/ml (Kobinger et al., 2011). Infectivity of mucosal wash fluids obtained from monkeys experimentally infected with the Reston strain of EBOV ranged from $<0.7$ log$_{10}$ PFU/ml at initial infection to a maximum of $2.9$ log$_{10}$ PFU/ml in terminal animals (Jahrling et al., 1996). Based on these data the initial viral load used here follows a log normal distribution with mean $3$ log$_{10}$ TCID$_{50}$/ml and standard deviation $1$ log$_{10}$ TCID$_{50}$/ml.

Virus decay in the environment and during transport, CHL$_{env}(j,k)$, CHL$_{trans}(j,k)$. The initial concentration of EBOV on the raw product is assumed to be equivalent to that shed by bats. As there have been no successful virus isolation attempts from bats, values are extrapolated from experimental evidence. Nasal washes and oral and rectal swabs from pigs challenged via mucosal exposure with $1 \times 10^6$ PFU of the Zaire strain of EBOV had infectious titres ranging from $1 \times 10^2$ to $1 \times 10^3$ TCID$_{50}$/ml (Kobinger et al., 2011). Infectivity of mucosal wash fluids obtained from monkeys experimentally infected with the Reston strain of EBOV ranged from $<0.7$ log$_{10}$ PFU/ml at initial infection to a maximum of $2.9$ log$_{10}$ PFU/ml in terminal animals (Jahrling et al., 1996). Based on these data the initial viral load used here follows a log normal distribution with mean $3$ log$_{10}$ TCID$_{50}$/ml and standard deviation $1$ log$_{10}$ TCID$_{50}$/ml.

Minimum Viral load to consider product contaminated in EU MS, $C_{\min}$. Experimental infection of bats with the Zaire strain of EBOV was achieved with an inoculation dose of $10^4.6$ PFU (fluorescent focus forming units) (Swanepoel et al., 1996). Non-human primates (NHP) have been shown to be uniformly susceptible to intramuscular inoculation of $1000$ PFU of the Zaire strain of EBOV (Geisbert et al., 2003; Smith and Wang, 2013). However, doses as low as $50$ PFU were sufficient to cause infection in Rhesus Macaques (Kortepeter et al., 2011) and $100$ PFU of a guinea pig adapted strain of the virus was used to experimentally infect baboons (Ignatiev et al., 2000). Johnson and colleagues (Johnson et al., 1995) reported using a dose of $5.2$ log$_{10}$ of EBOV (Jiax et al., 1995). Rhesus Macaques were aerosol challenged with calculated doses between $743$ and $274,000$ PFU of EBOV delivered as a small-particle aerosol (Twenhafel et al., 2013) whilst a lethal dose of $100$ LD$_{50}$ in African green monkeys and $20–50$ LD$_{50}$ in baboons has been demonstrated (Ryabchikova et al., 1999). As a worst case scenario it is assumed that $C_{\min} = 1$ log$_{10}$ TCID$_{50}$.

A.1.3. Live animals

Species of animal, s. Detection of EBOV by serology and PCR in animals has been recently summarised by Pigott et al. (2014). Dogs and pigs are, so far, the only domestic animals identified as species that can be infected with EBOV (Weingartl et al., 2013; Allela et al., 2005). Although dogs can be asymptomatically infected, they may excrete infectious viral particles in urine, faeces, and saliva for a short period before virus clearance. Pigs have been shown to be susceptible to both the Reston and Zaire strains of Ebola. Conversely, the Zaire strain is also capable of transmission from pigs to Cynomolgus macaques without direct contact (Weingartl et al., 2012). Pigs, challenged with EBOV via mucosal exposure, replicated the virus to high titres mainly in the respiratory tract with shedding observed from oronasal mucosa up to 14 days post-exposure. Transmission to cohabiting naïve pigs was also observed (Kobinger et al., 2011). Animal species in which evidence of natural/experimental EBOV infection has been demonstrated and considered as potentially capable of introducing EBOV into the EU include: pig, domestic dog, Lord Derby's Scaly-tailed Squirrel, Duiker, Non-human primates, small rodents and the shrew (Morvan et al., 1999). Bat species include: Epomops franqueti, Hypsignathus monstrosus, Micropteropus pusillus, Mops (Mops) condylurus, & Hipposideros gigas, Myonycteris (Myonycteris) torquata, Rousettus (Rousettus) aegyptiacus, Rousettus (Rousettus) amplexicaudatus.
### Table A3

| Prevalence |
|------------|
| Ref.       |

**Detection of EBOV in bats.**

| Positive bat species | Country | Sample taken | Test | Number positive | Number tested | Prevalence | Ref.          |
|----------------------|---------|--------------|------|-----------------|---------------|------------|---------------|
| **Ebolavirus (EBOV)** |         |              |      |                 |               |            |               |
| Unknown              | DRC (Zaire) | Spleen, liver, kidney, | Virus isolation | 8 | 0 | 0 | 0 (Germain, 1976) |
| Epomops franqueti, Myonycteris torquata, Epomophorus gambianus, Micropteropus pusillus | Various China | Serum/pharyngeal & ELISA/RT-PCR | 843/143 | 10/0 | (Zaire) | Not attempted | (Yuan et al., 2012) |
| Rousettus aegyptiacus | Bangladesh | Serum/throat, urine/ELISA/WB/ RT-PCR | 273 | 5 (R. leschenaultii) by PCR | Not attempted | (Olival et al., 2013) |
| Macroglossus sobrinus | Malaysia | Faecal swab ELISA | none by PCR | 19 | - | - | (Chandrapala et al., 2015) |
| **Other species** | | | | | | | |
| Epomops franqueti, Hypsignathus monstrosus | Gabon/Congo | Serum/western blotting | 10/0 | (Zaire) | Not attempted | (Pourrut et al., 2009) |
| Epomops franqueti, Myonycteris torquata, Micropteropus pusillus, Mops, | | Serum/liver & spleen ELISA/ RT-PCR | 1468 | 95/0 | | Not attempted | (Pourrut et al., 2009) |
| Epomops franqueti, Hypsignathus monstrosus | Ghana | Serum | 88 | | | | (Hayman et al., 2010) |
| **Invasive species** | | | | | | | |
| unknown | | | | | | | |

### A.2. Hendra

#### A.2.1. Human travel

**Number of human infection in exporting country, nHinf(k).**

Human cases of HeV have been restricted to the state of Queensland in Australia (Table A4). Hendra virus was first described in 1994 since which time 7 human infections have occurred in 45 separate outbreaks with a 57% case fatality rate. No human cases have been reported for the last 6 years (since 2009) which is attributed to horse keepers/vets greater awareness of the disease and an equine vaccination programme. The number of human infections in exporting country k in one year is assumed to be 1.

**Time to clinical signs, TIP(k).** Estimates of average time to clinical signs in humans can be seen in Table A5. Taking an average of all the estimates available, a value of 12.8 days was used for the average time to clinical symptoms of HeV.

#### A.2.2. Legal trade import

**Bat infection prevalence in exporting country, pBats(k).**

In 2011 HeV RNA was detected in up to two-thirds of pooled-urine samples from bats near HeV cases in horses (Plowright et al., 2015). Variable virus excretion has been reported in urine, with prevalence in pooled urine samples collected under roosting flying-foxes ranging from 3–33% in the one-in-four sampling events that yielded positive results. Subsequent studies have detected excretion spikes as high as 60% on rare occasions (Field et al., 2011). Based on documented evidence of virus isolation (Table A6) the prevalence of HeV in bats was assumed to be 0.47%.

**Product types, l.** Whilst there is currently no evidence of human HeV infection as a result of contaminated fruit consumption it is plausible that this could occur with or without mutation and adaptation of currently identified strains. This framework models only the possibility that fruit products contaminated with HeV could enter the EU. All products in the FAOStat database recorded under section 8 fruits and derived products, are therefore included.

**Proportion of the year bats may shed active HeV virus, pseason(s).** Flying foxes appear to excrete HeV at any time of year and spillover in horses can occur in any month but the majority of equine cases (94 confirmed or possible cases as of December 2015 (Smith et al., 2016)) have occurred from June to September suggesting that there is a greater risk of infection at this time (Field et al., 2011). There was an initial coincidence of HeV outbreaks with birthing seasons of Australian fruit bat species and the isolation of HeV from the uterine fluid and aborted foetus of a P. poliocephalus bat indicated that this may be a significant route of infection for horses (Fogarty et al., 2008). However, there now appears to be a temporal clustering of spillovers during the winter...
period with 35/51 spillovers to June 2014 occurring in June, July and August (Goldspink et al., 2015). The proportion of the year that bats are assumed to shed active virus is therefore estimated to be ~4 months or 0.33 of 1 year.

Initial viral load on raw product, c0(x): the initial concentration of HeV on the raw product is assumed to be equivalent to that shed by bats. Virus has been detected in the urine, faeces, saliva and birthing fluids of experimentally infected flying-foxes (Williamson et al., 2000, 1998; Halpin et al., 2011), and in the urine, uterine fluid and foetal tissue of naturally infected free-living flying-foxes (Halpin et al., 2000; Field et al., 2011). Whilst these studies report on prevalence of virus there are no data on quantification of virus in bats available. However, in experimental inoculations of pigs virus titres of 4.6 log10 TCID50/ml were found in nasal swab samples (Li et al., 2010a). Based on these data the initial viral load on the raw product follows a log normal distribution with mean 4.6 log10 TCID50/ml (variance = 1 log10 TCID50/ml in the absence of any other data).

Virus decay in the environment and during transport, Cens(j,k), Crawn(j,k): Using an exponential decay model the half-life of Hendra virus under laboratory conditions was calculated to be 1.85 min, 50.2 and 308 h for 56, 22 and 4 °C respectively (Scanlan et al., 2014). More recent modelling predictions using the same data calculated half-lives of 3.5 s, 2.9 h and 268 h using a Weibull distribution (Martin et al., 2015). When incubated in P. alecto urine (pH ~7) HeV had a half-life of 19 h. at 22 °C and 3 h at 37 °C (Fogarty et al., 2008). The half-life in mango flesh ranged from 0.3 h. at pH3 to 22 h. at pH5 at 22 °C (Fogarty et al., 2008). The calculation of 2.9 h at 22 °C was assumed to be the most accurate for this scenario and this value was therefore used for virus decay in the environment; a value of 268 h was used for decay during transport consistent with the modelling prediction using Weibull distribution.

Minimum viral load to consider product contaminated in EU MS, Cmin: Uniform disease occurred with an inoculation value of 3.4 × 10^6 PFU of HeV for guinea pigs and 6.6 × 10^7 PFU for Landrace pigs whereas an inoculate dose of 2 × 10^7 PFU in Minipigs did not cause uniform fatality (Li et al., 2010b). Horses in a vaccine efficacy study were challenged oronasally with 2 × 10^6 TCID50 in experimental infection with Hendra (Marsh et al., 2011, Middleton et al., 2014) while cats orally challenged with 5 × 10^6 TCID50 succumbed to disease after a 9 day incubation period (Hooper et al., 1997). As a worst case scenario it is assumed that Cmin = 1 log10 TCID50.

A.2.3. Live animals

Species of animal, s. Horses are moved internationally for competition, breeding, slaughter and as companion animals. All horses being permanently exported to Europe from Australia must complete a 30 day pre-export isolation at an approved quarantine stable in Australia. In horses, the incubation period is estimated to be 5–16 days although the incubation period in one horse may have been 31 days (DoH, 2012). Evidence suggests that horses have the potential to excrete virus in nasal secretions up to 2 days before showing signs of infection (Kung et al., 2013) and should be considered as potentially infectious from 72 h prior to onset of clinical signs of disease. Virus is recoverable from infected horse’s urine and saliva for at least 21 days. Transmission of HeV or NiV via semen has not been investigated, although the likelihood of a stallion being infected, clinically healthy and having semen collected for export is considered remote (MAF, 2000).

Experimental inoculation of pigs has indicated that they could be a potential host for HeV (Li et al., 2010b). In a serological survey of 100 swine herds in Queensland, Australia (Black et al., 2001) no HeV antibodies were found in the 500 tested serum samples. Two dogs have tested positive for HeV antibodies on properties where horses developed HeV infection in July 2011 and July 2013. Although the source of exposure for the dogs cannot be definitively ascertained, horse-to-dog transmission is the most plausible scenario. Experimental Hendra virus infections have been performed in horses, cats, ferrets, hamsters, African Green monkeys and guinea pigs all of which developed fatal diseases. Cats from Australia are prohibited from entering the UK unless they are accompanied by a certificate from the Australian Veterinary Authorities confirming that they had not been on a holding where HeV has been confirmed during the 60 days prior to export. Pigs, dogs, cats and horses are all considered in the model.

A.2.4. Illegal trade import: bushmeat

Species of bushmeat, pBMSp(s). Bushmeat is part of the traditional diet of indigenous Australian people whilst Australian game meat plays a part in

| Date       | Country  | Number of cases | Number dead | Likely source | Exposure to | Human-to-human transmission? |
|------------|----------|-----------------|-------------|---------------|-------------|------------------------------|
| 1994       | Queensland | 1               | 1           | Infected horse | Farmer assisted in autopsy of horse. Died 13 months post infection | No |
| 1994       | Queensland | 2               | 1           | Infected horse | Death of horse trainer and severe illness in stable-hand both with close contact with sick horses | No |
| 2004       | Queensland | 1               | 0           | Infected horse | Veterinarian tested positive for Hendra virus after performing a post mortem | No |
| 2008       | Queensland | 1               | 1           | Infected horse | Veterinarian and veterinary nurse were infected after close contact with sick horse. The vet died. | No |
| 2009       | Queensland | 1               | 1           | Infected horse | Veterinarian died after exposure to Hendra infected horse | No |

Table A4
Historical review of HeV human cases.

Table A5
Estimates of average times to clinical symptoms for human HeV cases (days).

| Patient 1 | 1994 | No accurate data |
| Patient 2 | 1995 | 7 |
| Patient 3 | 1995 | 8 |
| Patient 4 | 2004 | 10 |
| Patient 5 | 2008 | 9 or 16 |
| Patient 6 | 2008 | 11 |
| Patient 7 | 2009 | 21 (19) |

* Patient received antiviral treatment which may delay symptoms 1–2 days.
### Table A6
Detection of HeV in bats.

| Positive bat species | Country | Sample taken | Test                        | Number tested | Number positive | Number shedding | Prevalence                        | Ref.                  |
|----------------------|---------|--------------|-----------------------------|---------------|----------------|----------------|-----------------------------------|----------------------|
| *P. alecto, P. poliocephalus, P. conspicillatus, P. scapulatus* | Australia | Uterine fluid | Virus isolation             | 4             | 4              | 4              | targeted surveillance no mention of how many sampling of recently captured sick or injured wild bats | (Halpin et al., 1996) |
| *Pteropus poliocephalus and Pteropus alecto* | Australia | Tissue samples | Virus isolation             | 465           | 2              | 2              |                                    | (Halpin et al., 2000) |
| *P. alecto, P. poliocephalus, P. conspicillatus, P. scapulatus* | Australia | Pooled urine | RT-PCR Virus isolation      | 1672          | 4              | 4              |                                    | (Field et al., 2011) |
|                      | Australia | Tissues & serum | RT-qPCR Virus isolation with q-PCR | 310           | 20             | -              |                                    | (Smith et al., 2011) |
| *Chalinobus, Miniopterus australis, Nyctophilus, P. alecto, P. poliocephalus, P. conspicillatus, P. scapulatus, Saccoelemus flaviventris, Scotorepens, Synconycterus* | Australia | Tissues & serum | RT-qPCR Virus isolation | 45 samples +ve by q-PCR; 30 of these picked for isolation | 4              | -              |                                    | (Goldspink et al., 2015) |

* samples are the same reported in different articles.

### Table A7
Historical review of MARV virus outbreaks to the present day (as of November 2014) (the 2 Koltsovo laboratory infections which occurred in the former Soviet Union have not been included here).

| Date       | Country      | Number of cases | Number dead | Likely source                                                                 | Exposure to | Human-to-human transmission? | Ref.                        |
|------------|--------------|-----------------|-------------|--------------------------------------------------------------------------------|-------------|-----------------------------|-----------------------------|
| 1967       | Europe       | 31              | 7           | Imported African green monkeys (*Chlorocebus aethiops*) from Uganda             | Blood, organs, cell cultures | Yes                     | (Kissling et al., 1970)     |
| 1975       | South Africa | 3               | 1           | Unknown - possibly from Zimbabwe                                               | Visited Sinoa caves 8-9 days prior to onset of symptoms | Yes                     | (Gear et al., 1975)         |
| 1980       | Kenya        | 2               | 1           | Kitum Cave (~70 miles from Lake Kyoga where 1967 monkeys originated)           | Possible bat excretions       | Yes                     | (Smith et al., 1982)        |
| 1987       | Kenya        | 1               | 1           | Kitum Cave (~70 miles from Lake Kyoga where 1967 monkeys from)                | Possible bat excretions       | No                       | (Johnson et al., 1996)      |
| 1998–2000  | DRC          | 154             | 128         | Mine workers in Goroumbwa cave                                                 | Possible bat excretions       | Yes                     | (Bausch et al., 2006)       |
| 2004–2005  | Angola       | 374             | 329         | Unknown                                                                         | Mostly index cases were children possibly from administration of vaccine using contaminated equipment | Yes                     | (Fisher-Hoch, 2005)         |
| 2007       | Uganda       | 4               | 2           | Mine workers in Kitaka cave                                                    | Possible bat excretions       | Possibly                | (Towne et al., 2007)        |
| 2008       | USA/Netherlands | 2             | 1           | Visit to Python cave in Maramagambo Forest                                     | Possible bat excretions       | No                      | (WHO, 2008)                 |
| 2012       | Uganda       | 20              | 9           | Same strain as 2007 outbreak                                                   | 99.3% similar to sequence from bat | Yes                     | (Amman et al., 2014)        |
| 2014       | Uganda       | 1               | 1           | No consumption of bushmeat or contact with bats                                | Healthcare worker             | No                      | (WHO, 2014b)                |
Table A8: Detection of MARV in bats.

| Country                  | Positive bat species                        | Sample taken                  | Number tested | Number shedding | Prevalence | Concentration               | Ref.  |
|--------------------------|---------------------------------------------|-------------------------------|---------------|----------------|------------|-----------------------------|-------|
|                         | Rousettus aegyptiacus                       | liver/spleen tissue           | 1523 (40 RT-PCR) | 7              | 0.40%      | 1 × 10^5 pfu/ml (Towner et al., 2009). |       |
|                         | Rousettus aegyptiacus                       | liver/spleen tissue           | 611 (31 RT-PCR) | 5              | 0.80%      | 1 × 10^5 pfu/ml (Swanepoel et al., 2007). |       |
|                         | Miniopterus fransmani, Hypsignathus monstrosus, Epomops robustus | pooled tissue                 | 381 (12 RT-PCR) | 0              |            |                              |       |
|                         | Gabon & Republic of the Congo               | spleen & lung                 | 1158 (4 RT-PCR) | 0              |            |                              |       |
|                         | Gabon                                       | liver/spleen tissue           | 1380 (9 RT-PCR) | 0              |            |                              |       |
|                         | Kenya                                       | liver/spleen tissue           | 272 (1 RT-PCR)  | pox            |            | No virus isolation attempted due to low viral load |       |
|                         | Uganda                                      | liver/spleen tissue           | 1458 (0 RT-PCR) | pox            |            | No virus isolation attempted due to low viral load |       |
|                         | Uganda                                      | liver/spleen tissue           | 1458 (0 RT-PCR) | pox            |            | No virus isolation attempted due to low viral load |       |
|                         | Uganda                                      | liver/spleen tissue           | 400 (5 RT-PCR)  | pox            |            | 2.25%                        |       |
|                         | Uganda                                      | liver/spleen tissue           | 400 (5 RT-PCR)  | pox            |            | 2.25%                        |       |
|                         | Uganda                                      | liver/spleen tissue           | 1257 (9 RT-PCR) | 0              |            | No virus isolation attempted due to low viral load |       |
|                         | Uganda                                      | liver/spleen tissue           | 22 (7 days with no signi- | 0              |            |                              |       |

A.3. Marburg

A.3.1. Human travel

Number of human infections in exporting country, \( n_{infect}(k) \). Since 1980 MARV outbreaks have originated in Kenya, the DRC, Angola and Uganda (Table A7).

Time to clinical signs, \( T_{infect}(k) \). Data from secondary cases of MARV in Kenya place the median incubation period at 9 days. However the incubation period in index cases following exposure to a reservoir source is calculated as having a mean of 9.8 days (Timen et al., 2009; Amman et al., 2012) with a range of 3–15 days. Based on documented cases of exposure and subsequent infection MARV was calculated to have an incubation period ranging from 3 to 21 days (typically 5–10 days) the range being modulated by factors such as infectious dose and possibly by route of infection (Brauburger et al., 2012). Using data available from historical Marburg cases with precise exposure dates (\( n = 18 \)), the median incubation rate for Marburg was calculated by Pavlin to be 7 days with no significant difference between primary and secondary cases (Pavlin, 2014). The value of 7 days is used in the model.

A.3.2. Legal trade

Bat infection prevalence in exporting country, \( p_{infect}(k) \). The estimate for the prevalence of MARV in bats is based on published information from peer reviewed publications on the isolation of active MARV (Table A8).

The number of bats actively shedding virus is taken as a percentage of the entire pool tested as it is assumed that if no RNA is detectable then virus isolation would be highly unlikely as a direct correlation between RNA levels and the ability to isolate virus has been demonstrated (Towner et al., 2009). Due to the uncertainty surrounding this parameter, the prevalence of active virus shedding in bats was assumed to be \( p_{infect}(k) = 0.29\% \) as a worst case scenario.

Product types, \( l \). MARV has been isolated from Rousettus aegyptiacus, a fruit bat which is known to discard hard particles in their food at foraging sites (Herzig-Straschil and Robinson, 1978). They are known to consume various fruit crops produced for human consumption such as date, fig, apricot and peach. A recent paper succeeded in isolating MARV from both oral and rectal secretions of \( R. \ aegyptiacus \) experimentally infected with virus demonstrating potential avenues for viral shedding (Amman et al., 2015). Thus all products in the FAOStat database recorded under section 8 – Fruits and derived products, are included.

Proportion of the year bats may shed active MARV virus, \( p_{season}(k) \). Retrospective analysis of historical human infections found there was a temporal clustering of infections coinciding with the seasonal pulses in virus circulation in \( R. \ aegyptiacus \) covering 6 months of the year in total (Amman et al., 2012). The observation of these distinct pulses of virus infection in older juvenile bats appears to coincide with the peak biannual birthing seasons. Thus the proportion of the year that bats are presumed to be infectious with MARV is 0.5.

Initial viral load on raw product, \( c_0(x) \): the initial concentration of MARV on the raw product is assumed to be equivalent to that shed by bats. Successful isolation of MARV roughly correlated with tissue samples that had RT-PCR Ct values of 30 or less (> 2000 TCID_{50}/ml) (Amman et al., 2012). The highest RNA level, measured using Ct values, corresponded to an approximate infectious titre of \( 1 \times 10^5 \) pfu/ml (Towner et al., 2009).

Measurements of concentrations of MARV in experimentally
infected guinea pig saliva, urine and faeces showed a virus concentration of 2.3–3.3 log LD50 (median lethal dose) (Chupurnova et al., 2000). The LD50 was calculated to be 5 × 10^{-2} TCID50 of virus for wild type mice (Qiu et al., 2014). However, it should be noted that this will be a rodent adapted strain of the virus. The virus has also been found to be excreted at high levels of up to 10^6 guinea pig infectious doses in urine of experimentally challenged monkeys (Simpson, 1969).

Marburg virus was isolated from oral secretions of *R. aegyptiacus* experimentally infected with virus from a naturally infected bat of the same species (Amman et al., 2015). Viral loads were measured by qRT-PCR analysis of viral RNA and reported as mean TCID50 equivalents. Marburg virus positive oral swabs were obtained on day 4–14 post infection with highest viral loads detected on day 8 (1.32 × 10^3 TCID50/ml equivalents) and cleared from oral secretions by day 14. Based on this data the initial viral load on the raw product follows a log normal distribution with mean 3.12 log10 TCID50/ml (variance = 1 log10 TCID50/ml in the absence of any other data).

Virus decay in the environment and during transport, Cenv(j,k), Ctrans(j,k): In a study on the survival of filoviruses in liquids and on solid substrates the half-life of Marburg virus in liquid media was calculated to be between 5.1 and 6.6 days at +4 °C and ~3 days at room temperature (Piercy et al., 2010). No virus could be recovered from any solid substrate stored at room temperature but at +4 °C the virus had a half-life of ~4.5–5.5 days on glass and ~4.5–10 days on plastic substrates depending on the media in question. From the data available, a mean half-life of 6 days (144 h) is used as an estimate for virus reduction during transport at +4 °C and virus reduction pre-harvesting is estimated at 3 days (72 h) using liquid media data.

Minimum Viral load to consider product contaminated in EU MS, Cmin: Evidence of experimental infection in rodents is not considered here as these models generally use adapted viruses obtained through sequential passage in the rodent species as the wild-type virus does not cause uniform lethality (Bray, 2001). A single intramuscular injection of a common marmoset with as little as 10 PFU of virus has resulted in fatal haemorrhagic disease (Carrión et al., 2011) whilst 1000 PFU has proven to be a uniformly lethal dose of virus (Thi et al., 2014; Geisbert et al., 2007; Hensley et al., 2011; Smith et al., 2013). However doses as low as 2–14 PFU and 99–705 PFU have been reported as causing disease by viral inhalation. The doses were equally fatal but symptoms were delayed by one day in the lower dose group (Alves et al., 2010). When bats were experimentally infected by subcutaneous inoculation with a dose of 10^4 TCID50 MARV there was evidence of infection in all bats although no clinical signs were observed. As a worst case scenario it is assumed that Cmin = 1 log10 TCID50.

A.3.3. Live animals

Species of animals (s): All species of NHPs were considered as susceptible to MARV due to previous research (Simpson, 1969).

A.3.4. Illegal trade import: bushmeat

Species of bushmeat, pBMSp(s). Previous published studies on bushmeat in Europe have not identified bats among seizures of bushmeat sampled (Chaber et al., 2016; Falk et al., 2013). A study reported on the species of bushmeat items confiscated at US ports of entry between 2005 and 2010, suggested that bats accounted for around 1.5% of all bushmeat (Bair-Brake et al., 2013). Thus, in the absence of other information, we assume that 1.5% of bushmeat is bats. The same study suggested that around 6% of bushmeat is derived from NHP which is of relevance here as MARV has been previously transmitted from NHP to humans.

A.4. MERS

A.4.1. Human travel

Number of human infections in exporting country, nHinf(k). Sporadic cases have occurred in Europe and the rest of the world but the index case of these outbreaks has always recently travelled to the Middle East. A large number of cases reported in Saudi Arabia have been nosocomial; the recent outbreak of MERS-CoV in South Korea illustrates the role the hospital environment can play in the spread of pathogens (Park et al., 2015). The number of human infections (Table A9) were taken as the total number (as at November 18th 2016) divided by the period of time over which the infections have been recorded.

Time to clinical signs, Tpr(k). The incubation period of MERS-CoV has been estimated using data from exposure of secondary cases to the index case in a hospital outbreak (Assiri et al., 2013) and using traveller-related clusters (Cauchemez et al., 2014). The median incubation period for confirmed cases in the hospital outbreak was 5.2 days (95% CI 1.9–14.7), and 5.5 days (95% CI 3.6–10.2) for travel related clusters in the UK, France, Italy and Tunisia (Fisher-Hoch, 2005). A figure of 5.3 days is used in this model.

A.4.2. Legal trade import

Bat infection prevalence in exporting country, pBinf(k). Growing serological and molecular evidence suggests that the dromedary camel (*Camelus dromedarius*) is an intermediate species for MERS-CoV (ECDC, 2015b) but the virus is hypothesised to have originated from bats. A MERS-CoV sequence identical to that of the virus isolated from an index-case patient was detected in a faecal pellet from a *Taphozous perforatus* bat sample (Table A10) collected near the home of an index case in an area which is an important date palm production area in Saudi Arabia (Memish et al., 2013). As yet no evidence has been found of actual infection in chiropteran populations.

Product types, l. Some human cases of MERS-CoV infection have had gastrointestinal symptoms including diarrhoea and vomiting. Coronavirus virions have been demonstrated to survive on fresh produce over a period of days (Yepiz-Gomez et al., 2013; Mullis et al., 2012). Thus, it is possible that fruit and vegetables contaminated with coronavirus may be potential vehicles for transmission to humans. Infected bats (or other animals) contaminating raw fruit via saliva or urine whilst foraging for food is considered a risk and thus all products in the FAOstat database recorded under section 8 – Fruits and derived products, are included.

Other legal imports considered as potential risk commodities are camel meat and camel milk. MERS-CoV RNA and antibodies have been detected in milk collected from actively shedding dromedary camels in Qatar providing evidence of the potential for virus transmission (Reusken et al., 2014a). Camel milk imports from UAE to the UK began in 2014 and are transported by plane as a chilled product. The operation is stated to have obtained ISO 20000 certification for both the farm and dairy processing facilities to fulfil the EU import requirements. There have been 6 consignments in 2014 comprising of:
The products are described as having undergone sterilisation and UHT. Camel milk samples, spiked with MERS-CoV, has been shown to be depleted of infectious virus after undergoing heat treatment for 30 min at 63 °C (van Doremalen et al., 2014). There is evidence of only one certificate in TRACES of camelid meat imports into the EU since 2000. This documents 1.183 Kg of wild game camel meat imported from Australia in 2013.

Proportion of the year bats may shed active MERS-CoV virus, p_{season}(k).

Although there is no evidence of viral shedding in bats to observe any seasonal fluctuations, analysis of human infections since the first reporting of MERS-CoV found there was a temporal clustering of infections with a sharp rise in the number of cases in April and May and a smaller peak in August-September. The birthing period for *Taphozous perforatus* is in April and May. In line with the peak in human infections in Saudi Arabia the proportion of the year that the source is presumed to be infectious with MERS-CoV is 4 months or 0.33.

Initial viral load on raw product, c_{0}(x):

Experimental infection of common marmosets with $5.2 \times 10^6$ TCID_{50} MERS-CoV exhibited viral loads of $\sim 6 \log_{10}$ TCID_{50} eq/g in nasal mucosa 6 days after challenge (Falzarano et al., 2014). Respiratory samples gave higher values than blood or other tissues. Camels inoculated with doses of $10^7$ TCID_{50} gave viral titre of maximum of $6 \log_{10}$ TCID_{50} eq/ml of nasal swab samples (Adney et al., 2014). Based on these data the initial viral load on the raw product follows a log normal distribution with mean 5 log_{10} TCID_{50}eq/ml (variance = 1 log_{10} TCID_{50}/ml in the absence of any other data).

Virus decay in the environment and during transport, C_{env}(j,k), C_{trans}(j,k):

The stability of MERS-CoV (isolate HCoV-EMC/2012) was evaluated under three different environmental conditions (van Doremalen et al., 2013). The mean half-life was calculated as: 0.947 (h) at 20 °C 40% humidity and 0.708 h at 30 °C 30% humidity indicating that temperature influences the environmental decay of the virus. In liquid matrices MERS-CoV was found to have a half-life of $\sim 10$ h in milk at +22 °C and 72 h at +4 °C (van Doremalen et al., 2014).

The mean half-life for MERS-CoV in the environment was taken to be 0.773 h, as it was assumed to most accurately mimic a real-life situation whereby fruit contaminated by either infected bat saliva or urine would then be exposed to temperatures of $\sim 30$ °C prior to harvesting (assuming a peak shedding prevalence in April/May and Aug/Sep time). However, after harvest when the fruit is assumed to be kept at $+4$ °C during transport the average half-life time of 72 h, as calculated from milk, is used as virus survival time is assumed to be more similar between solid and liquid matrices.

### Table A9

Global incidence of laboratory confirmed MERS-CoV cases as of 18th November 2016.

| Date of onset/most recent case | Country          | Number of cases | Number dead |
|-------------------------------|------------------|-----------------|-------------|
| 18/11/2016                    | Saudi Arabia     | 1484            | 617         |
| 16/06/2016                    | UAE              | 84              | 12          |
| 13/06/2016                    | Qatar            | 16              | 5           |
| 23/09/2016                    | Jordan           | 35              | 14          |
| 31/05/2015                    | Oman             | 6               | 3           |
| 19/09/2015                    | Kuwait           | 4               | 2           |
| 22/04/2014                    | Egypt            | 1               | 0           |
| 17/03/2014                    | Yemen            | 1               | 1           |
| 22/04/2014                    | Lebanon          | 1               | 0           |
| 18/03/2015                    | Iran             | 6               | 2           |
| 25/09/2014                    | Turkey           | 1               | 1           |
| 12/09/2016                    | Austria          | 2               | 0           |
| 06/02/2013                    | UK               | 4               | 3           |
| 07/03/2015                    | Germany          | 3               | 2           |
| 08/05/2013                    | France           | 2               | 1           |
| 27/05/2013                    | Italy            | 1               | 0           |
| 08/04/2014                    | Greece           | 1               | 1           |
| 05/05/2014                    | The Netherlands  | 2               | 0           |
| 16/05/2013                    | Tunisia          | 3               | 1           |
| 23/05/2014                    | Algeria          | 2               | 1           |
| 09/04/2014                    | Malaysia         | 1               | 1           |
| 01/02/2015                    | Philippines      | 3               | 0           |
| 01/05/2014                    | United States of America | 2 | 0 |
| 02/07/2015                    | South Korea      | 185             | 36          |
| 30/05/2015                    | China            | 1               | 0           |
| 30/07/2016                    | Thailand         | 3               | 0           |

### Table A10

Detection of MERS-CoV in bats.

| Positive bat species                                      | Country | Sample taken | Test | Number tested | Number positive | Number shedding | Ref.                   |
|----------------------------------------------------------|---------|--------------|------|---------------|-----------------|-----------------|-----------------------|
| *Rhinopoma hardwickii*, *Rhinopoma microphyllum*,        | Saudi   | Throat swab, faeces, urine, serum | PCR  | 110 individual bats and 732 roost faeces samples | 1 | 0 | (Memish et al., 2013) |
| *Taphozous perforatus*, *Pipistrellus kuhlii*, *Eptesicus bottae*, *Eidolon helvum*, and *Rosettus aegyptiacus* | Arabia  |              |      |               |                 |                 |                       |
matrices at this temperature than at 30 °C.

Minimum Viral load to consider product contaminated in EU MS, \( C_{\text{min}} \). The only animal models found to be naturally permissive to infection are non-human primates. Rhesus macaques challenged with \( 1 \times 10^7 \text{TCID}_{50} \) (de Wit et al., 2013) and \( 6.5 \times 10^7 \text{TCID}_{50} \) (Yao et al., 2014) showed MERS-CoV related pathology and had detectable levels of viral RNA. Challenge with a total viral dose of \( 5.2 \times 10^6 \text{TCID}_{50} \) caused a severe partially lethal disease in the common marmoset (\( \text{Callithrix jacchus} \)) (Falzarano et al., 2014). Camels inoculated with doses of \( 10^7 \text{TCID}_{50} \) gave viral titre of maximum of \( 6 \log_{10} \text{TCID}_{50} \) eq/ml of nasal swab samples (Adney et al., 2014). As a worst case scenario it is assumed that \( C_{\text{min}} = 1 \log_{10} \text{TCID}_{50} \).

A.4.3. Live animals
Species of animal, (s). There has been documented evidence of MERS-CoV viral RNA (Chu et al., 2014), virus specific antibodies (Alagaili et al., 2014; Briese et al., 2014; Corman et al., 2014; Meyer et al., 2014; Reusken et al., 2014b) and virus isolation (Raj et al., 2014; Hemida et al., 1993) in dromedary camels, both from countries in the Arabian Peninsula and the African continent. According to the EC (Commission Regulation (EC) No 206/2010) no camel imports are allowed from the Arabian Peninsula or countries in Africa where antibodies to the MERS-CoV has been detected in camel sera. However, there is no evidence of camels from approved 3rd countries being tested for the Mers-CoV and, as this virus is suspected of being circulating in camels for some time, it is not impossible that they could be harbouring the coronavirus too. Only dromedary camels were considered as ‘at risk’ for live animal imports to the EU.

A.4.4. Illegal trade import: bushmeat
Species of bushmeat, \( \text{pBMSp(s)} \): Bats, or camel meat, illegally imported as bushmeat from the Arabian Peninsula and Africa could be of potential risk in the transmission of the MERS-CoV. As has previously been stated, in the absence of other information, we assume that 1.5% of bushmeat is bats. It is possible that camel meat could be present in generic ‘red meat’ illegally imported as bushmeat from the Arabian Peninsula.

Appendix B

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