

A generic quantitative risk assessment framework for the introduction of bat-borne viruses into the European Union

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**Purpose:**

Bats have been linked to a number of zoonotic diseases such as Nipah Virus (NiV), Ebola Virus (EBOV) and MERS-CoV. In 2014 there have been human cases of NiV in Bangladesh, EBOV in Africa and MERS-CoV in the Arabian Peninsula, with sporadic cases of EBOV and MERS-CoV further afield. Given current anthropogenic activities and an intricately connected global world through trade and travel, it is likely there will be further spill-over of viruses from mammalian reservoirs, with global spread among humans a serious concern.

In order to assess the risk of entry of bat-borne zoonotic viruses to European Union (EU) Member States, a generic risk assessment framework has been developed.

**Methods:**

The model framework combines multiple routes by which bat-borne viruses are most likely to be introduced: human travel, legal importation of both foodstuffs and live animals, and illegal importation of bushmeat. The model does not consider further potential exposure of the virus to humans, livestock or wildlife and the subsequent consequences.

The model was parameterised for NiV and uncertainty in parameter estimates assessed through a series of scenarios.

**Results:**

While the baseline model expected number of years to an introduction event into the EU was 10 years, this decreased considerably if the bat infection prevalence (a highly uncertain parameter) was reduced. Legal trade was consistently the most likely route of entry for all scenarios considered. At a MS level, the Netherlands was the most likely point of entry via legal trade, while the UK was the most likely entry point for human travel, bushmeat and live animals.

**Conclusions/Relevance:**

The model framework described here is a useful tool for initial quantitative prediction of potential risk of introduction to the EU of bat-borne viruses. While the absolute risks should be treated with caution due to the inevitable high uncertainty of parameter estimates, the strength of this model lies in the provision of relative comparisons of routes and overall risk among MSs, as well as analysis of the uncertainty through scenarios. The modular design of the framework allows for future inclusion of additional routes as well as adaptation to other pathogens.