**S2. Appendix 2**

**Guide to the High Disease Risk Wildlife Market Assessment Framework**

Developed by:

Eric Wikramanayake1, David Olson1, Dirk Pfeiffer2, Ioannis Magouras2, Anne Conan2, Stefan Ziegler3, Timothy C. Bonebrake4

1 WWF Asia-Pacific Counter-Illegal Wildlife Trade Hub (IWT Hub), WWF-Hong Kong, 15/F, Manhattan Centre, 8 Kwai Cheong Road, Kwai Chung, New Territories, Hong Kong SAR, PR China

2 Centre for Applied One Health Research and Policy Advice, City University of Hong Kong, Kowloon, Hong Kong SAR, PR China

3 WWF-Germany, Kaiserstr. 70, 60329 Frankfurt/Main, Germany

4 School of Biological Sciences, University of Hong Kong, Hong Kong SAR, PR China

Direct all questions and correspondence to: Eric Wikramanayake [ericw@wwf.org.hk](mailto:ericw@wwf.org.hk) or David Olson [dolson@wwf.org.hk](mailto:dolson@wwf.org.hk)

**Purpose**

We present a qualitative framework to guide the region’s governments, especially the public health and wildlife sector authorities, to assess markets for their relative risks for potential new incidents of serious emerging infectious diseases associated with the trade in wildlife, and design appropriate policies to curtail and control the wildlife trade, much of which is illegal in most countries.This appendix provides an introduction to the framework and how to use it.

**Introduction to Framework**

The framework is based on available knowledge of different wildlife taxa that are: (1) sourced and traded in the Asia-Pacific Region (e.g., EJF 2003, Lin 2005, Nijman 2010, Greatorex *et al.* 2016, Cantlay *et al.* 2017, McEvoy *et al.* 2019, Scheffers *et al.* 2019, Fukushima *et al.* 2020); (2) known to carry serious zoonotic pathogens; and (3), broad categories of market types and trade chains that exist in the trade.

We acknowledge that what we present can be improved with additional research, literature review, or insights from specialists, as well as field testing. Zoonotic and wildlife trade science is an evolving field and as more information is gathered it will contribute to an improvement of our knowledge about viruses, wildlife primary and intermediate hosts, and the role of wildlife trade chains in zoonoses. This new knowledge can then be used to better inform judgements and adjust and adapt decisions, including those parameters used in this framework. In the meantime, given the urgency to act and assess wildlife markets and prevent another pandemic, this framework can be applied invoking the precautionary principle. We posit that lack of action—once again—is simply too costly and unacceptable.

We have attempted to strike a balance in this framework between keeping it simple enough (Box 1) to make it transparent and adaptable as more knowledge becomes availablle, but to also include enough key variables, based on literature review and consultation with specialists, to make it sufficiently accurate and useful.

**Box 1. Quick 4-step guide to using the framework.**

**Step 1**. Enter Information on numbers of animals of traded taxa in markets into Column E—'Estimated number of animals in market’—in spreadsheet ‘Enter Taxa & Numbers” (Supplementary Material Appendix 1 - Disease Risk Tool). For a specific wildlife trade point of sale, the numbers of animals for sale can be estimated or counted if few. Numbers can be derived from snapshot surveys, averaged from long-term monitoring data, or be based on expert assessments.

**Step 2**. Check disease risk tool matrix of ‘Risk from Traded Taxa’ (Y-Axis) and ‘Trade Chains & Points of Sale’ (X-Axis) that combine the market and taxon risk assessments in the ‘Risk of Wildlife Market’ worksheet from the Supplemental Material Appendix 1: (a) find the risk from traded taxa, (b) define the market, and (c) read the associated risk.

**Step 3.** Estimate and convey the uncertainty of a particular risk evaluation

**Step 4**. Make decision on what action to take based on this Cumulative Risk Factor

**Wildlife Trade Disease Risk Assessment Framework**

This risk assessment framework is meant to gauge zoonotic disease (defined in *Target Zoonotic Pathogens* section below) risk of a given wildlife market or wildlife trade situation. The framework uses two primary types of information:

1. the type of wildlife trade situation along a chain or point of sale in the form of various wildlife markets or points of sale or barter (that is, ‘Market Trade Risk’), and
2. the wildlife taxa and numbers of individual animals for sale in a wildlife trade situation (for example, a wildlife market, or along a trade chain).

**Market Trade Risk**

We begin with the position that all wildlife trade scenarios involving terrestrial vertebrates have some level of zoonotic risk. Some wildlife trade chains or types of sale have features or conditions that exacerbate the risk of zoonotic disease (for example, higher viral loads and virus shedding of individual animals); elevate the transmission risk of pathogens among wildlife, domestic/peridomestic animals, and humans; facilitate mutation and recombination of pathogens into novel forms that may be more infectious, transmissible, or cause more serious harm; and/or increase the risk of rapid and wide spread of infections in human populations after initial infections of a given pathogen. For example, for the latter, features that may increase risk might include crowded markets in urban areas from where people disperse far and wide after shopping, and even roadside stalls that are visited by fewer people can result in high spread as buyers or vendors might disperse far distances over a short period of time, including in public transport.

Based on expert opinion and our own observations, we grouped South East Asian wildlife trade situations into 11 different trade types (Fig. 1). Certain countries or regions may have a subset of these types of trade chains or there may be variations, such as levels of hygiene or number of steps in a trade chain. While the relative influence of these features remains controversial, we assume for the purposes of this analytical tool that this variation will not significantly alter the disease risk rankings for a general type of trade type. If there are enough differences to justify including or changing market types and their characteristics, the framework allows for such change.

Table

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*Figure 1. Asia-Pacific wildlife trade chain or point of sale (‘Market’) qualitative disease risk scoring. Uncertainty for each assigned level is given as high (H), medium (M), or low (L) to denote the level of confidence in the assigned score (screenshot from Supplementary Material Disease Risk Tool).*

General types of wildlife markets and points of sale are assessed for risk based on three variables (Fig. 1). The assessment process is provided in worksheet “Market Type Risk” in the Supplementary Material Risk Analysis Tool. The three variables are:

***Zoonotic Virus Risk (ZVR)***: This is defined as the presence of conditions that increase the amount of a given pathogen or the risk of novel pathogens in wildlife through accumulation of viral loads along a trade chain and through viral shedding and mutation resulting in novel potentially high-risk pathogens. Having high volumes of individual animals crowded together, having live animals kept for a long time, unhygienic conditions stressing animals, other stressors on animals, and a mix of wild species and wild and domestic (or peridomestic or feral) species can amplify the risk (viral load and diversity within an individual animal or a trade chain step as whole) of harmful pathogens (Webster 2004, Johnson *et al.* 2019, Lo *et al.* 2019, Huong *et al.* 2020, IPBES 2020, Sekoai *et al.* 2020). Note, the ZVR does not address exposure/transmission risk, rather it emphasizes high viral loads (for example, due to immunosuppression because of stress due to crowding, presence of many different species and people, and long transport). Thus, there could be a very high risk of accumulation and increase of viral loads in animals because of crowding and mixing of very high and high risk wildlife taxa as they are moved along the trade chains or stored, especially highly stressful conditions (very high score 9-10 based on criteria; high score 6-8; medium score 3-5; low score 0-2).

1. ***Transmission Risk (TR)***: This is defined as the suite of exposure conditions associated with a step in the trade chain that, on average, increases the risk of transmission of a pathogen from animals to humans. Situations where many people interact closely with wildlife on a regular basis are a red flag. Unhygienic butchering practices, butchering and consumption near one another, and lack of running water may also raise transmission risk (Lo *et al*. 2019, Huong *et al.* 2020, IPBES 2020, Sekoai *et al.* 2020). Thus, there could be a very high risk of transmission because of the crowding of the mixing of very high and high risk wildlife taxa in crowded and densely packed (thus elevating transmission risk to people) and unhygienic conditions where wildlife is highly stressed, and there is a high turnover of people through the market, especially in markets that are far downstream along the trade chains (very high score 9-10 based on criteria; high score 6-8; medium score 3-5; low score 0-2)
2. ***Spread Potential (SP)***: This is defined as the conditions or processes associated with a step in the trade chain that increase the risk of rapid and wide spread of infections in human populations (through high human to novel human exposure, that is, many different people are encountered by an infected person) after initial infections by a given pathogen (see Woolhouse 2008, Greatorex *et al*. 2016). Features that could increase risk might include crowded markets in well-connected urban areas, especially where people disperse widely after shopping and come into contact with many others, or even roadside stalls where infected buyers might disperse far distances over a short period of time, including using public transport. Thus, there could be a risk of potential spread of pathogen, based on the numbers and densities of people who used the market, the location and exposure (such as an urban area), and the possible travel distances of people who use the market (potential for travel to far off destinations after purchase, vs local travel) (very high score 9-10 based on criteria; high score 6-8; medium score 3-5; low score 0-2).

We hypothesize that these three variables will adequately classify the risks of potential zoonoses based on the scale or size of the market, the extent of crowding of wildlife that create stressful situations, typical hygiene and sale/butchering conditions, the number and turnover of people through the market, the distance they may travel with wildlife purchases, and where along the trade chain the market would sit that could allow viruses to accumulate and amplify the potential for zoonoses. The contribution of the types and numbers of wildlife being traded are considered in a subsequent step.

Each market type was scored on a scale from 1-10 for each of the three variables (Figure 1). These scores are meant to indicate a qualitative index, rather than reflect a quantitative score. We requested WWF Southeast Asia wildlife trade specialists (N=5; it was a challenge to get more experts) familiar with wildlife market situations in Asia to independently rank each trade situation for each of the three variables. These independent scores were then averaged for each variable. The averaged scores were then summed and divided by 3 (that is, averaged again) to obtain a combined ‘Market Risk’ score from 1-10 for each trade situation (see Column J in “Market Type Risk” sheet in the analytical tool, Supplmentary Material Appendix 1). That score was in turn transformed to a qualitative risk score as: <1 = Lowest Risk; 1-2 = Low Risk; 3-5 = Medium Risk; 6-8 = High Risk; and 9-10 = Very High Risk.

We used a numerical scale, rather than a nominal scale, to assess risks because the former is easier to ‘visualize’ for most people, and the breadth of each category provides for some level of ‘uncertainty’ when assigning a score (see Pfeiffer 2020). For example, for a market that may be considered medium risk, someone may give it a score of 3, while another person may consider it to be 5, although it falls within the same category of ‘Medium risk’. If multiple experts classify the market, the variability can provide an indicator of ‘uncertainty’. However, our risk scale should be considered qualitative.

**Uncertainty**

The level of uncertainty in the assigned scores is given as high (H), medium (M), or low (L). The uncertainty was derived by calculating the standard deviations of each variable for each market or trade situation and using a range of two standard deviations above and below the mean to capture about 95% of the presumed uncertainty. Natural breaks in a distribution of these standard deviations in a bar graph were then used to assign them as high, medium, or low. It is important to convey how much uncertainty assessors have in assigning categories to help inform future refinement of the framework with improved knowledge and for decision-makers considering policies by using this framework (see Institute of Medicine 2013, EFSA 2014, Jakob-Hoff *et al.* 2014, WHO & IUCN 2014, Travis & Smith 2019, Borsky *et al.* 2020, OIE 2020, Pfeiffer 2020).

**Diffuse vs Concentrated Wildlife Trade Activity**

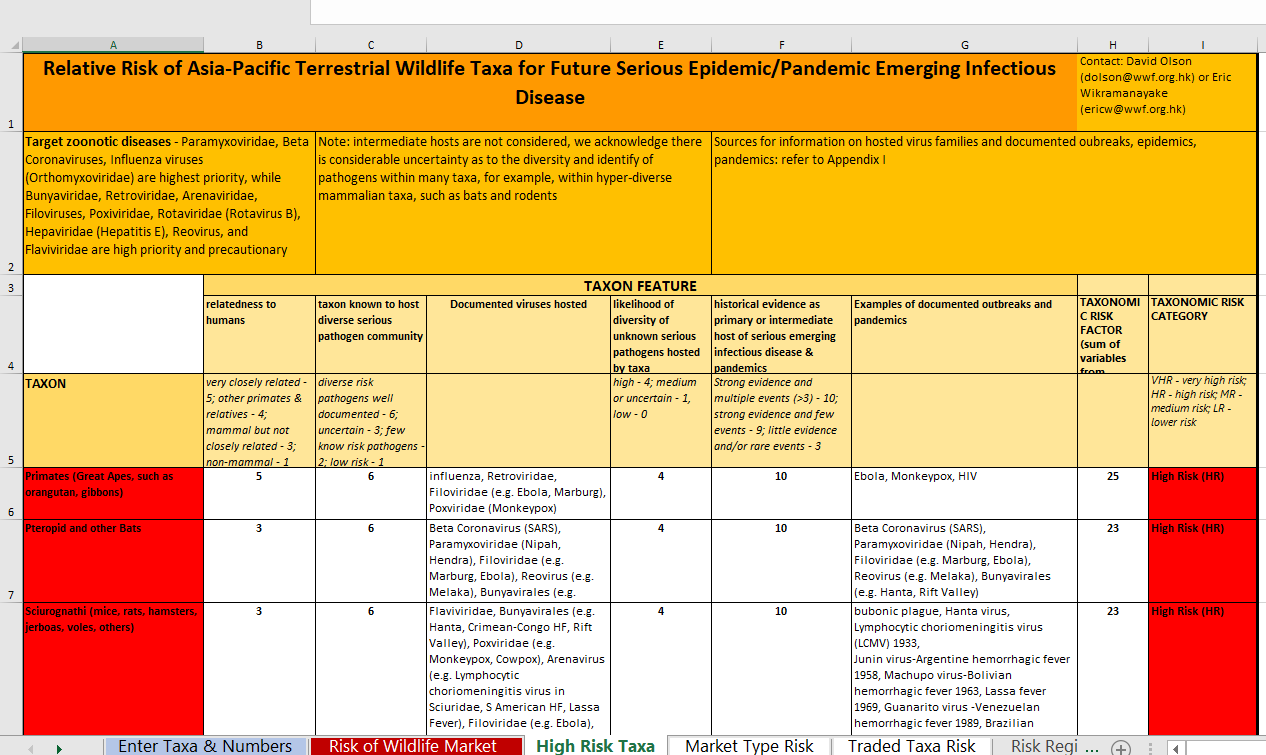
The large concentrations of wildlife (mixed with domestic/peridomesticanimals, at times) in large town and urban wildlife markets represent one end of a continuum of concentrated to dispersed wildlife sales. Though our framework is aimed at assessing risk for individual markets, disease risk could collectively be assessed for multiple sale points across landscapes. For example, in rural villages, there may be ongoing and regular sales of wildlife that collectively amount to high numbers and of diverse species, across a larger area, such as a province, through sales at small, well-dispersed stalls or individual transactions. These tend to occur in the wildland-rural interface areas, involve diverse taxa, and trade occurs largely without refrigeration or high standards of hygiene, increasing the likelihood of zoonotic risk across landscapes. As roads penetrate these frontier areas and increase access, these small stalls become sources for the commercial trade as buyers begin to consolidate stocks for urban markets. Thus, the combined activity of small-scale rural and village wildlife sales a significant contributor to potential zoonotic risk, especially as they often include very high-risk species, such as primates, bats, and some rodents. Laos is one example where larger, concentrated wildlife markets are rare but small-scale wildlife sales in villages and rural areas are common and widespread. The risk assessment tool can address this situation by estimating risk for smaller-scale wildlife sales and their contribution to risk downstream along the trade chains.

**High-Risk Taxa**

The taxonomic groups that are commonly traded in the Asia-Pacific region were assessed for zoonotic risk based on: (1) the likelihood of hosting highly virulent pathogens with a propensity for zoonotic outbreaks (Box 2); (2) the likelihood that they could host a diversity of unknown serious pathogens; (3) historical evidence as primary or intermediate hosts of serious emerging infectious diseases (IPBES 2020; Table 1); and (4) the close relatedness to humans (that is, higher primates) was also considered, on the assumption that they may share similar immune systems and responses that may facilitate zoonotic infection (Figure 2; Arundel *et al*. 1977, Swift *et al*. 2007, Cantlay *et al.* 2017, Greatorex *et al*. 2017, Huong *et al*. 2020, Pruvot *et al*. 2020). The scoring criteria for these variables are provided in the sheet “*High Risk Taxa*” in the analytical tool (Fig. 2, Supplementary Material Appendix 1) and include relatedness to humans, taxon known to host diverse, serious pathogen community, likelihood of diversity of serious pathogens hosted by taxon, and historical evidence of taxon as primary or intermediate host of serious emerging infectious disease and pandemics.

Table 1. *Key sources for disease risk level for different taxa commonly traded in the Asia-Pacific Region.*

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| --- |
| **Primates (great apes, such as orangutan, gibbons) –** Mutombo *et al.* 1983, Warren *et al.* 1999, Nunn *et al.* 2005, Caillaud *et al.* 2006, Childs *et al.* 2007, Davies & Pedersen 2008, Goldberg *et al.* 2008, Keele *et al.* 2008, Burgos-Rodriguez 2011, Essbauer *et al.* 2010, [Calvignac-Spencer](https://www.sciencedirect.com/science/article/pii/S1198743X14641446#!) *et al.* 2012, Ellis *et al.* 2012, Merck Veterinary Manual 2014, Wang & Crameri 2014, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Olival *et al.* 2017, Betsem *et al.* 2011, OIE 2019, Damas *et al.* 2020, IPBES 2020, Jo *et al.* 2020, Johnson *et al.* 2020, Liu 2020, Pruvot *et al.* 2020 |
| **Bats -** Yob *et al.* 2001, Lau *et al.* 2005, Leroy *et al.* 2005, Li *et al.* 2005, Calisher *et al.* 2006, Wang *et al.* 2006, Childs *et al.* 2007, Towner *et al.* 2007, Shi & Hu 2008, Plowright *et* *al.* 2011, Drexler *et al.* 2012, Chan *et al.* 2013, Ithlete *et al.* 2013, Luis *et al.* 2013, Memish *et al.* 2013, Wynne & Wang 2013, Van Doorn 2014, Yang *et al.* 2014, Han *et al.* 2015, Menachery *et al.* 2015, Han *et al*. 2016, Leendertz *et al.* 2016, Baselar *et al.* 2017, Olival *et al.* 2017, Brook & Dobson 2015, Berto *et al.* 2018, Goldstein *et al.* 2018, Wang *et al.* 2018, Fagre & Kading 2019, Li *et al.* 2019, Boni *et al.* 2020, Corrales-Aguilar & Schwemmle 2020, Cupertino *et al*. 2020, Damas *et al.* 2020, IPBES 2020, Jo *et al.* 2020, Johnson *et al.* 2020, Latinne *et al.* 2020, Li *et al.* 2020, Maganga *et al.* 2020, Pereirra *et al.* 2020 |
| **Sciurognathi (mice, rats, hamsters, jerboas, voles, others) –** Childs *et al.* 2007, Shi & Hu 2008, Smith *et al.* 2012, Luis *et al*. 2013, Van Doorn 2014, Han *et al.* 2015, Van Cuong *et al.* 2015, Chaber & Cunningham 2016, Greatorex *et al.* 2016, Han *et al.* 2016, Olival *et al.* 2017, Berto *et al.* 2018, OIE 2019, Strand & Lundkvist 2019, Cantlay *et al.* 2020, Dahmana *et al.* 2020, Damas *et al.* 2020, Huong 2020, IPBES 2020, Jo *et al.* 2020, Johnson *et al.* 2020, McIver *et al.* 2020, Mendoza *et al.* 2020, Pruvot *et al.* 2020 |
| **Primates (monkeys, macaque, loris, tarsier, other non-great apes)** – Maskalyk 2003, Nunn *et al.* 2005, Childs *et al.* 2007, Goldberg *et al.* 2008, Shi & Hu 2008, Essbauer *et al.* 2010, Burgos-Rodriguez 2011, Ellis *et al.* 2012, Merck Veterinary Manual 2014, Chaber & Cunningham 2016, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Olival *et al.* 2017, OIE 2019, Damas *et al.* 2020, IPBES 2020, Jo *et al.* 2020, Johnson *et al.* 2020, Liu 2020, Liu *et al.* 2020, Pruvot *et al.* 2020 |
| **Pangolins** – Childs *et al.* 2007, Shi & Hu 2008, Greatorex *et al.* 2016, Mohapatra *et al.* 2016, Cantlay *et al.* 2017, Gao *et al.* 2019, Liu *et al.* 2019, Gao *et al.* 2020, Han 2020, IPBES 2020, Jo *et al.* 2020, Lam *et al.* 2020, Lehmann *et al.* 2020, Lee *et al.* 2020, Liu *et al.* 2020, Xiao *et al.* 2020, Zhang *et al.* 2020 |
| **Viverids (e.g. civets, mongoose) –** EJF 2003, Enserink 2003, Guan *et al*. 2003, Hung 2003, Zhong *et al.* 2003, Anderson *et al.* 2004, Bell *et al.* 2004, Tu *et al.* 2004, Xu *et al.* 2004, Chen *et al.* 2005, Kan *et al.* 2005, Wang *et al.* 2005, Childs *et al.* 2007, Shi & Hu 2008, Venkatesan *et al.* 2010, Doceul *et al*. 2016, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Damas *et al.* 2020, IPBES 2020, Jo *et al.* 2020, Pruvot *et al.* 2020 |
| **Wild birds –** Mounts *et al.* 1999, Trock *et al.* 2003, Ezenwa *et al.* 2006, Kilpatrick *et al.* 2006, Childs *et al.* 2007, Amonsin *et al.* 2008, Anderson *et al.* 2010, Robinson *et al.* 2010, Edmunds *et al.* 2011, Chan *et al.* 2013, Fournie *et al.* 2013, Kaplan & Webby 2013, Chan *et al.* 2015, Springborn *et al.* 2015, Li *et al.* 2018, Lycett *et al.* 2019, BirdLife International 2020, IPBES 2020, Jo *et al.* 2020, Mollentze & Streicker 2020 |
| **Mustelidae (e.g. weasels, mink, otter, badgers, hog badgers, polecats, marten) –** Childs *et al.* 2007, Shi & Hu 2008, Cui & Holmes 2012, Oreshkova *et al.* 2020, Munnink *et al.* 2020, Shi *et al.* 2020, |
| **Sciuridae (squirrels)** – Childs *et al.* 2007, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Pruvot *et al.* 2020 |
| **Wild pigs & babirussa –** Brown 2000,Chua *et al.* 2000, Wuethrich 2003, Childs *et al.* 2007, Doceul *et al*. 2016, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Jo *et al.* 2020, Pruvot *et al.* 2020 |
| **Eulipotyphla (shrews, moles, moonrats, gymnures, hedgehogs) –** Inoue *et al.* 2009, Corman *et al.* 2014, Földvári *et al.* 2014, Doceul *et al*. 2016, Olival *et al.* 2017 |
| **Wild Cervidae, Moschidae, Bovidae, Tragulidae (selected Artiodactyla) –** Childs *et al.* 2007, Tei *et al.* 2003, Roess *et al.* 2010, Doceul *et al*. 2016, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Jo *et al.* 2020, Pruvot *et al.* 2020 |
| **Wild camels –** Wang *et al.* 2014,Deem *et al.* 2015, Elfadil *et al.* 2018, Sazmand *et al.* 2019, Zhu *et al.* 2019 |
| **Wild Felids –** Childs *et al.* 2007, Shi & Hu 2008, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Jo *et al.* 2020, Pruvot *et al.* 2020, Shi *et al.* 2020 |
| **Wild Canids –** Childs *et al.* 2007, Shi & Hu 2008, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Freuling *et al.* 2020, Jo *et al.* 2020, Pruvot *et al.* 2020, Shi *et al.* 2020 |
| **Ailuridae (red panda) –** Essbauer *et al.* 2010 |
| **Hystricidae (porcupines) –** Childs *et al.* 2007, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Pruvot *et al.* 2020 |
| **Bears –** Childs *et al.* 2007, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Martelli *et al.* 2019, Pruvot *et al.* 2020 |
| **Scandentia (tree shrews) –** Olival *et al.* 2017, Jo *et al.* 2020, |
| **Dermoptera (flying lemurs or colugos) –** Hron *et al.* 2014 |
| **Perissodactyla (e.g., tapir, rhinoceros, asses, horses) & Elephants –** Childs *et al.* 2007, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Olival *et al.* 2017, Pruvot *et al.* 2020 |
| **Hares & rabbits –** Childs *et al.* 2007, Greatorex *et al.* 2016, Cantlay *et al.* 2017, Jo *et al.* 2020, Pruvot *et al.* 2020 |
| **Elephant –** Murphree *et al*. 2011, Olival *et al.* 2017, Pruvot *et al.* 2020 |
| **Marsupials –** Arundel *et al.* 1977, Olival *et al.* 2017 |
| **Reptiles –** Childs *et al.* 2007, Gortazar *et al.* 2004, Chomel *et al.* 2007, Briant *et al.* 2010, Percipalle *et al.* 2011, Andoh *et al.* 2015, Matias *et al.* 2016, IPBES 2020, Mendoza-Roldan *et al.* 2020 |
| **Amphibians –** Gortazar *et al.* 2004, Chomel *et al.* 2007, Schloegel *et al.* 2010, Wombwell et al. 2016, IPBES 2020 |



*Figure 2. The variables and criteria for scoring taxonomic groups for virus risk. Important factors include relatedness to humans, taxon known to host diverse, serious pathogen community, likelihood of diversity of serious pathogens hosted by taxon, and historical evidence of taxon as primary or intermediate host of serious emerging infectious disease and pandemics (screenshot from Supplementary Material Appendix 1).*

The scores for each variable represent qualitative categorical assessments (Row 5, Fig. 2) based on literature and other expert opinions. The scores were then summed (Column H, Fig. 2) to obtain a *Taxonomic Risk Factor* (Column H, Fig. 2). These scores were then translated to a qualitative ‘*Taxonomic Risk Category*’ where scores >20 are considered to be High Risk, >10-20 Medium Risk, and <10 Low Risk (Column I, Fig. 2). Amphibians, Fishes, and Invertebrates are considered to be ‘Lowest Risk’ (Gortazar *et al.* 2004, Chomel *et al.* 2007, Wombwell *et al*. 2016, IPBES 2020). The *Taxonomic Risk Category* assignments are subjective but are based on a review of the technical literature and consultations with specialists. They can be further improved and changed, as necessary, with improved knowledge and additional input from experts.

We note that some taxonomic groups are diverse, such as rodents, and are likely to include species that may be of lower risk than others and that the pathogen communities hosted by some taxa remains poorly known (see Mollentze & Streicker 2020). However, given the severity of economic, health, and social costs and consequences of epidemics and pandemics, as well as current gaps in knowledge about which species host which pathogens, we employ a precautionary principle and presume that until more evidence is available, whole taxa with species that are known to carry high-risk pathogens should be considered risky. This precautionary approach, we hope, will also encourage and catalyze additional epidemiological research to de-list or up-list species, as relevant and appropriate. As the status of these species change, the model can also be adjusted. We use simple, transparent, arithmetic formulas to enable these adjustments.

**Box 2. Target Zoonotic Pathogens**

A key goal is to reduce the frequency and severity of future zoonotic outbreaks, epidemics, and pandemics. This tool emphasizes assessing the risk of serious zoonotic disease outbreaks that have the potential to quickly expand to epidemic or pandemic status. We emphasize the potential of viruses within faunal families to cause a pandemic with unacceptable case lethality (for example, everything above 1% is high) that will disrupt normal life and will be difficult to bring under control. Coronaviruses are clear candidates since they fulfill all criteria (for example, respiratory transmission, asymptomatic Trojan horses) and on the top of that there is no single good vaccine ever developed against (beta) coronaviruses. This is, for example, not true for influenza viruses where there is knowledge about vaccine development and immunogenicity. Thus, the highest priority target zoonotic diseases are Paramyxoviridae, Coronaviridae (Beta Coronaviruses), and Orthomyxoviridae (Influenza viruses). We deem these to have the highest *consequence.* We further consider high priority pathogens to be Bunyaviridae, Retroviridae, Arenaviridae, Filoviridae, Poxiviridae, Rotaviridae (Rotavirus B), Hepaviridae (Hepatitis E), Reovirus, and Flaviviridae. The degree to which actions taken to reduce the risk of the highest priority pathogens causing epidemics and pandemics can reduce the risk of outbreaks caused by the lower priority pathogens or other less serious pathogens remains uncertain. However, to consider the highest and high priority pathogens in risk assessments of taxa and trade situations offers a sensible precautionary approach.

***Definitions***

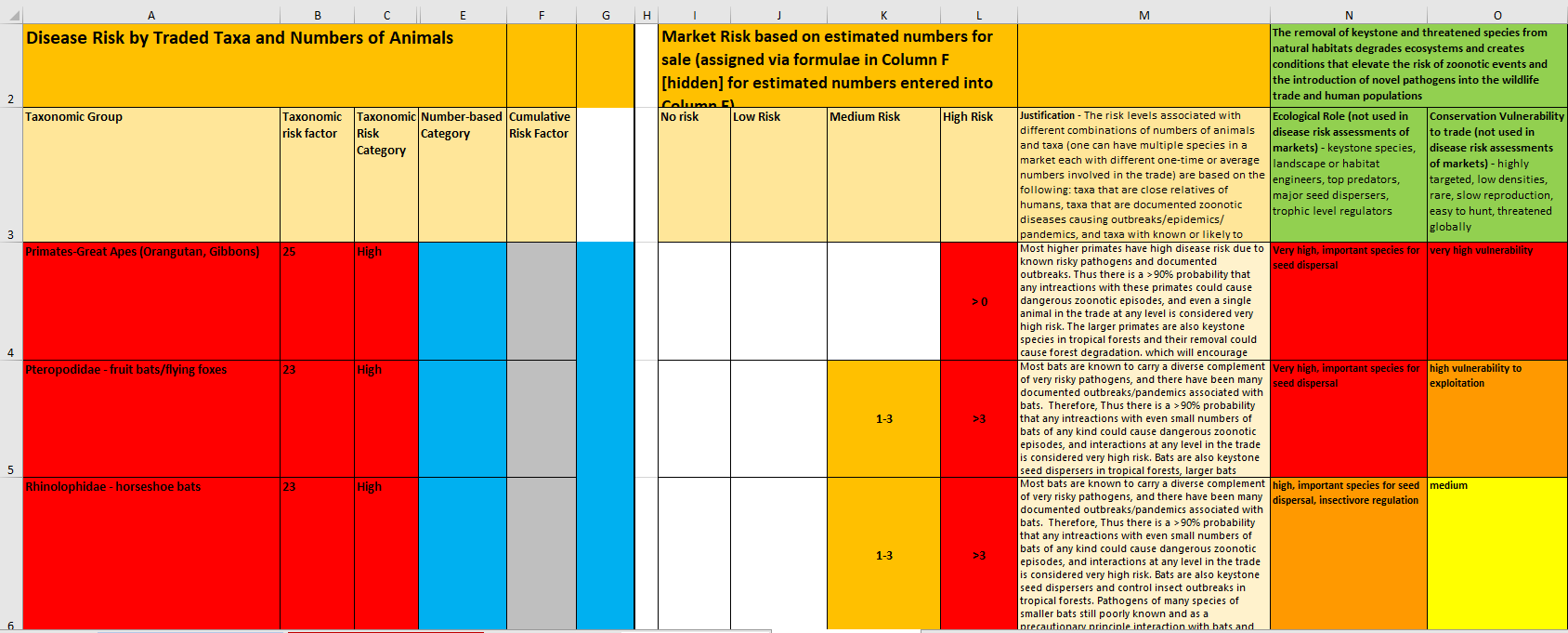
**Presence risk** refers to the propensity of a given wildlife taxon to be host to a high-risk virus or other pathogen. Certain taxa, on average, have a higher chance of hosting high risk pathogens due to their natural history, nature of their immunological tolerances and accumulations of hosted pathogens, known hosted viral diversity, and number of species in the taxon. Taxa documented to harbor high-risk pathogens that have led to serious outbreaks, epidemics, or pandemics in the past are clear high-risk taxa. Great apes and other higher primates are thought to be high-risk, in part, due to the close similarity of their physiologies to humans and the assumption this can facilitate hosted pathogens jumping successfully to humans.

**Consequence risk** refers to the potential of a given zoonotic pathogen to lead to serious outbreaks, epidemics, or pandemics in human populations, all with associated impacts on public health, economies, culture, and socio-political situations in human society. Some features of high risk pathogens that confer high consequence risk are highly infectious transmission rates, transmission pathways via airborne particles in additions to surfaces and direct contact with infected persons, relatively long incubation times, and severe consequences to human health and high mortality in broad age groups.

**Evaluating Risk of Specific Markets or Points of Sale – Traded Taxa Risk**

Taxonomic Risk Categories that represent a pathogen-based risk are then combined with a qualitative index based on the numbers of individuals (particularly live individuals) found in a market, the premise being that a higher number of animals (density may increase with higher numbers in some cases) can amplify the viral load and risk of transmission. The latter index—the ‘*Number-based Category*’ (Column E, Fig. 3, Supplementary Material Appendix 1)—is created by translating the numbers of animals observed for each taxonomic group that are estimated in a market to an index of High, Medium, Low, and Lowest Risk, based on the categories for each taxonomic group as indicated in Columns I, J, K, and L in sheet ‘*Traded Taxa Risk*’ in the analytical tool (Fig. 3, Supplementary Material Appendix 1).

Thus, for example, for the flying foxes or Pteropodidae are known to carry a diverse suite of serious pathogens. If the estimated number of these Pteropid bats in a market is 1-3 individuals, the score would be Medium Risk, whereas if the numbers are >3, it would be classified as High Risk. Thus, any number of these bats in a market would pose at least a medium risk. We recognize that the presence and numbers of individuals of a given taxon may vary from day to day in a particular wildlife market. Thus, market surveys over several days or in different seasons will improve confidence in estimated disease risk, though what constitutes a minimum sample size is not clear presently.



*Figure 3. The variables and criteria for scoring taxonomic groups for risks in the trade and markets (screenshot from Supplementary Material Appendix 1). From worksheet ‘Traded Taxa Risk’ in the excel file. Key sources for assigning disease-risk levels for each taxon are provided in Supplementary Material Appendix 2.*

The numbers of animals found in the market(s) are entered into Column E—'Estimated number of animals in market’—in the analytical tool sheet ‘Enter Taxa & Numbers” (Fig. 4, Supplementary Material Appendix 1). For a specific wildlife trade point of sale, the numbers of animals for sale should be estimated (or counted if few) and the data entered in the relevant column. Note that this is the only place where any data will be entered. These numbers are converted into the qualitative threat categories, based on the categorical classifications in Columns I, J, K, and L in sheet ‘*Traded Taxa Risk*’ (Fig. 3, Supplmentary Material Appendix 1), and entered in Column E via formulas (formulas in Supplementary Material Appendix 1). Information on traded taxa and numbers of animals of each taxon can be derived from snapshot surveys (estimates from site visits over a day or longer period), averaged from long-term monitoring data, or be based on expert assessments. Finally, in the taxa risk assessment, the Taxonomic Risk category and Number-based Category are combined for a Cumulative Risk Factor using the matrix shown in Fig. 5.

**Ecosystem Impact & Conservation Vulnerability**

The justifications for the categories of taxon risks are primarily based on their propensities for harboring serious pathogen communities, but the number-based categories also consider the ecological role of the species and their conservation vulnerability to trade. These justifications are detailed in the Supplementary Material Appendix 1 (Fig. 3 is a screenshot of the relevant sheet), ‘Traded Taxa Risk’ sheet of the analytical tool, in columns M, N, and O.

Deforestation, fragmentation, degradation, and settlement of tropical forests have been identified as significant drivers of emerging infectious diseases (for example, Rulli *et al.* 2017, Wilkinson *et al.* 2018, Guo *et al.* 2019, Gibb *et al.* 2020, Johnson *et al.* 2020, IPBES 2020, Rulli *et al.* 2020). New roads built into once remote tropical forests and other natural landscapes bring in loggers, hunters, and settlers with domestic livestock who may be exposed to novel zoonotic pathogens. Wildlife taken from such areas for the commercial trade can also introduce novel pathogens into human populations. Moreover, the decline or loss of ecologically important species (for example, keystone species, top predators, seed dispersers, ecosystem engineers) through deforestation and hunting degrades ecosystems and subsequently creates conditions that elevate the risk of zoonotic events that typically accompanies deforestation. For example, the decline or loss of wild forest felids and canids can lead to an increase in rodents that carry a variety of zoonotic pathogens, creating an environment that elevates zoonoses risk. Many species and higher taxa are threatened by hunting, snaring, and collecting driven by the wildlife trade (Duckworth *et al.* 2012, IPBES 2019). Examples include primates, wild cats, wild canids, and elephants. Farming wildlife maintains demand for threatened species that, in turn, drives exploitation of wild populations. Thus, trade in such species should end. The risk categorizations based on animals in markets reflect this.



*Figure 4. Data entry worksheet in the proposed risk analysis tool (screenshot from Supplementary Material Appendix 1 tool). All data from market surveys should be entered into Column E in this worksheet, ‘Enter Taxa & Numbers’, against the respective wildlife taxon. Numbers can be based on counts or estimates. The numbers entered are an example.*

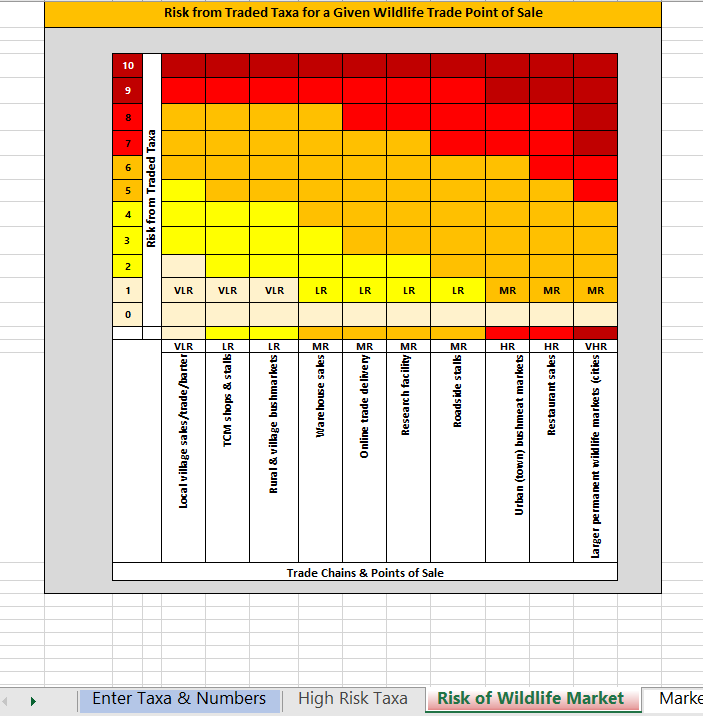
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | **Taxa Risk** | | | |
| **Market Risk** | **High Risk** | **Medium Risk** | **Low Risk** | **Lowest risk** |
| **High Risk** | Very High Risk | High Risk | Medium Risk |  |
| **Medium Risk** | High Risk | Medium Risk | Low Risk | Low Risk |
| **Low risk** |  | Medium Risk | Low risk | Lowest Risk |

*Figure 5. Matrix of taxon risk categories used to derive the Cumulative Risk Factor.*

**Combining market & taxon risks**

As a final step, we combine the market and taxon risk assessments in a graphic presentation, as indicated in the analytical tool sheet ‘*Risk of Wildlife Market*’ (Fig. 6, Supplementary Material Appendix 1). The risk categories are plotted on a matrix of risks from the traded taxa (Y axis) and the respective markets or points of sale (X-axis). One identifies the type of wildlife trade situation that best describes the wildlife market or point of sale being evaluated (on the X-Axis) and trace upwards in the Y-Axis direction until the letters appear in the relevant box (determined by the wildlife taxa risk weighting) that connote lowest, low, medium, high, or very high risk.

This matrix provides a first assessment of the disease risk associated with a specific wildlife market or point of sale. The risk levels could vary over time as different combinations and numbers of taxa are traded over time in a given location, but we assume, on average, that a similar set of taxa and numbers of animals traded will occur over time in any given venue. Improvements in hygiene, regulation, and sale and butchering practices could diminish risk to some extent, but we assume that such mitigations will not be sufficient or occur in time within the region to override the substantial risk from legal and illegal trade chains involving high risk taxa or the risks posed by bringing together many wild animals of different species together in close quarters interacting with many people.



*Figure 6. Graphic presentation of risks from traded taxa and trade chains (Supplementary Material Appendix 1). The VLR (beige cells), LR (yellow cells) and MR (orange cells) letters in this example estimate the trade situation as either low risk or medium risk for a combination of traded taxa and trade chain type. High Risk (HR, red) or Very High Risk (VHR, dark red) might be relevant for other combinations.*

**Addressing Uncertainty**

Uncertainty in risk assessments can arise from a lack of information, data, or knowledge or from high variation inherent to a process or interaction in question. It is important to clearly convey the level of uncertainty when assigning relative risk attributes to different features or processes in a wildlife trade chain (Dufour *et al*. 2011, Institute of Medicine 2013, EFSA 2014, Gale *et al*. 2014, Jakob-Hoff *et al.* 2014, Travis & Smith 2019, Borsky *et al.* 2020, OIE 2020, Pfeiffer 2020). The uncertainty associated with a risk level estimated for a specific wildlife trade market or point of sale should be derived from a reasonable combining of uncertainties in individual steps or features of the given trade chain. This allows decision makers to be informed of the uncertainty in the decision deliberations and individual probability and uncertainty estimates to be scrutinized by experts and stakeholders with respect to their validity. Uncertainty estimates can be easily revised in this way.

Uncertainty estimates should reflect the strength of scientific evidence that informed a qualitative risk estimate. In a risk pathway modelling process one combinies the probabilities across the sequence of conditionally dependent steps. Probabilities expressed as numbers between 0 and 1 can be multiplied with each other if it is proven that the underlying events are independent of each other. However, in a qualitative risk assessment, the combination involves an element of opinion, but it needs to be justified by logic. The product of two qualitative probability estimates should not be higher than the lower of the two as an underlying principle (Pfeiffer 2020).

We apply high, medium, or low uncertainty levels to our estimates of TR, SP, and VZR for assessing the risk associated with different wildlife trade chains or points of sale. We considered and attemped to identify uncertainties associated for each of these three features at each step of a trade chain (for example, hunter to middleman to transporter to urban warehouse to transporter to urban market to buyer), but this introduced inordinate complexity. We also identify higher taxa for which we have higher or lower uncertainty in our risk estimates (*High-Risk Taxa* sheet of the analytical tool, Supplementary Material). We define our uncertainty levels as follows (adapted from Pfeiffer 2020):

**Low** –There are solid and complete data available; strong evidence is provided in multiple references; authors report similar conclusions.

**Medium** – There are some but no complete data available; evidence is provided in small number of references; authors report conclusions that vary from one another.

**High** – There are scarce or no data available; evidence is lacking or not provided in references but rather in unpublished reports or based on observations, or personal communication; authors report conclusions that vary considerably between them.

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