



# Zoonotic Potential of International Trade in CITES-Listed Species: Addendum



**Addendum to  
JNCC Report  
No. 678**

**Prevalence of CITES-listed taxa associated with WHO R&D  
Blueprint priority diseases in legal and illegal international wildlife trade  
Addendum to: Zoonotic potential of international trade in CITES-listed species**

**UNEP-WCMC & JNCC**

**August 2022**

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**ISSN 0963 8091**

Prevalence of CITES-listed taxa associated with WHO R&D Blueprint priority diseases in legal and illegal international wildlife trade: Addendum to: Zoonotic potential of international trade in CITES-listed species

**Prepared** for JNCC as an Addendum to JNCC Report No.678

**Published** August 2022

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**Citation** UNEP-WCMC and JNCC. 2022. Prevalence of CITES-listed taxa associated with WHO R&D Blueprint priority diseases in legal and illegal international wildlife trade. Addendum to JNCC Report No. 678: Zoonotic potential of international trade in CITES-listed species. Cambridge and Peterborough, UK.

**Contributing Authors** Stafford, C., Szopa-Comley, A.W., Pavitt, A., Vitale, J., Hunter, K., McAlpine, J., Littlewood, A.H.L. & Malsch, K.

**Acknowledgements** We are grateful to Guy Clark (UK Border Force) for providing the UK national seizure data analysed in this report, and to TRAFFIC International for providing data from the TRAFFIC International Wildlife Trade Portal. This study was funded by JNCC and the Department of the Environment, Farming and Rural Affairs (Defra).

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**UN Environment Programme World Conservation Monitoring Centre (UNEP-WCMC)** 219 Huntingdon Road, Cambridge CB3 0DL, UK  
Tel: +44 1223 277314 [www.unep-wcmc.org](http://www.unep-wcmc.org)

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## Executive summary

In May 2021, UNEP-WCMC and JNCC published a study (JNCC Report No. 678) investigating the zoonotic potential of international trade in CITES-listed species. This addendum aims to begin to address two of the key recommendations made in the study, namely:

- (1) to conduct further analyses that explore the **prevalence in trade of CITES-listed taxa that are associated with pathogens considered to pose a relatively higher risk to human health**, for example, those that have the highest likelihood of developing into an epidemic/pandemic or that cause particularly severe disease in humans; and
- (2) to explore the presence of CITES-listed taxa associated with zoonotic risk in **illegal trade**.

To address the first recommendation, we explored the prevalence in reported international trade of CITES taxa that have been associated with 11 diseases considered by the World Health Organization (WHO) to pose the greatest public health risk due to their epidemic potential and the absence of sufficient countermeasures<sup>1</sup>, known as the **WHO R&D Blueprint priority diseases (henceforth ‘priority diseases’)**. We explored this over a ten-year period (2011 to 2020), focusing on trade in live animals as a commodity that is generally considered to carry a greater risk of zoonotic spillover. The key findings of this analysis were as follows:

- (1) Of the 270 animal families that include at least one species in the CITES Appendices, **31 families (11%) include at least one taxon associated with a priority disease**. These families belong to three classes (Mammalia, Aves and Reptilia), with Mammalia as the class containing the highest proportion of CITES families associated with at least one priority disease (29% of mammalian families that contain at least one species in the CITES Appendices were associated with at least one priority disease). Artiodactyla (even-toed ungulates), Carnivora and Primates were the three mammalian orders with the highest number of CITES families associated with priority diseases.
- (2) Restricting the list of diseases considered in the analysis to the 11 priority diseases decreased the proportion of CITES families that include a taxon association with a zoonotic disease across all four classes in which associations were detected in UNEP-WCMC and JNCC (2021); however, **the implications of this more focused approach were most pronounced in the proportion of bird and reptile families in which associations were recorded** (68% of bird families were found to contain at least one taxon associated with a zoonotic disease in UNEP-WCMC and JNCC (2021), compared with 12% of bird families found to contain at least one taxon associated with priority diseases only; 58% compared with 3% of reptile families for each type of association, respectively). This is likely due to the absence from the Blueprint list of a small number of zoonoses that have been found in a wide number of bird and reptile species, such as Chlamydiosis and Salmonellosis.
- (3) **Whilst all 11 priority diseases were associated with at least one CITES family, only ten diseases were associated with CITES families found in legal international trade as live animals** (the exception being Lassa fever).

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<sup>1</sup> COVID-19, Crimean-Congo haemorrhagic fever, Ebola virus disease and Marburg virus disease, Lassa fever, Middle East respiratory syndrome coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS), Nipah and henipaviral diseases, Rift Valley fever and Zika virus.



Approximately 3% of all (re-)exporter-reported transactions in live animals recorded in the CITES Trade Database between 2011 and 2020 involved families associated with at least one priority disease; these transactions involved at least 1.12 million individuals, which represents 1.65% of all live animals reported by number in direct CITES trade over this period (a small proportion of trade in live animals in the CITES Trade Database was reported by weight or volume).

- (4) **Of the 2005 CITES-listed species reported in live, international trade between 2011–2020, 49 were directly associated with a WHO R&D Blueprint priority disease.** Trade in these species represented 1.5% of all live animal transactions reported in the CITES Trade Database over this period and involved over 575 000 individual animals.
- (5) **Transactions recorded in the CITES Trade Database involving live animals belonging to families associated with one or more priority diseases were dominated by mammals** (55% of (re-)exporter transactions between 2011 and 2020) **and reptiles** (42%), with birds accounting for the remaining 3% of transactions in families associated with priority diseases. While Varanidae was the top family associated with priority diseases in terms of the number of transactions as well as the number of individuals in trade, this family contained only one species with a direct association with a priority disease (*Varanus niloticus* and Zika virus), and it should be noted that the role that this species could potentially play in zoonotic spillover of this disease is unclear (Gutiérrez-Bugallo *et al.* 2019). In contrast, the second and third most traded families associated with priority diseases, the Cercopithecidae (Old World monkeys) and Felidae (cats), have been associated with eight and six of the 11 priority diseases, respectively.

In order to begin to address the second recommendation, an initial assessment of the presence of families associated with priority diseases in **illegal trade** was conducted by searching for the presence of families associated with priority diseases in three datasets:

- (1) seizures of live animals upon import to the United States of America (hereafter United States), 2009 to 2018 (as recorded in the United States Fish and Wildlife Service Law Enforcement Management Information System (LEMIS) and submitted for inclusion within the CITES Trade Database (under source I); data were extracted from the CITES Trade Database directly....);
- (2) seizures of live, unlicensed specimens of species included in the CITES Appendices and/or United Kingdom (hereafter UK) Wildlife Trade Regulations made at the UK border, 2013–2021 (as recorded in the UK national seizure database); and
- (3) seizures and instances of smuggling/illegal trade of live specimens recorded in TRAFFIC International's Wildlife Trade Portal, 2013–2021.

This analysis of seizures found that taxa belonging to 30 of the 31 CITES families associated with one or more priority diseases were present in illegal trade of live animals; the only family not identified was Rhinocerotidae. Data from TRAFFIC International's Wildlife Trade Portal identified seizures in far more priority disease-associated families (30) than US seizure data (8) and UK seizure data (3), which is unsurprising given the TRAFFIC dataset's wider geographic scope. The class Mammalia contained the highest number of families in which seizures of live individuals of priority disease-associated taxa have been recorded (22 families associated with priority diseases across all three datasets).

While this analysis goes partway towards fulfilling the recommendation to explore the prevalence of CITES-listed taxa associated with zoonotic risk in illegal trade, the

**incorporation of additional datasets from other sources of illegal trade data**, such as EU-TWIX, Africa-TWIX, and other similar repositories, will create a fuller picture of potential risk. Future analyses could also consider factors such as other ‘higher-risk’ commodity types (e.g. meat), trade routes, and estimated volumes of illegal trade, as well as the impact that factors such as concealment methods may have on spillover risk. Such research however would have to account for reporting biases and other uncertainties such as whether seizure records truly reflect the composition of illegal trade as a whole.

Similar caveats to those outlined in UNEP-WCMC and JNCC (2021) apply to the analyses contained in this addendum, including sampling and reporting biases for both species and pathogens; the fact that zoonotic spillover may not have been confirmed in all species/disease associations included in our dataset; and the fact that this study does not take into account variations in risk caused by differing conditions in rearing, housing, or transport of wildlife products. Given the continual new characterisation of associations between diseases and animal hosts and the inclusion of emerging diseases such as COVID-19 in the list of priority diseases, the recommendation in UNEP-WCMC and JNCC (2021) for the creation and maintenance of a **central repository of disease/species associations covering the full range of zoonotic pathogens and their associated diseases** remains particularly pertinent.

The identification and collation of available data on disease/taxon associations was highlighted by the CITES working group on the *role of CITES in reducing risk of future zoonotic disease emergence associated with international wildlife trade* as a potential future area of work for CITES to jointly undertake with the World Organisation for Animal Health (OIE). It is hoped that studies such as this one can help to provide a foundation for this work as well as other joint CITES and OIE workstreams, should a joint program of work be agreed to between these two partners, and contribute more broadly to work by the Quadripartite partnership (the World Health Organisation (WHO), the Food and Agriculture Organisation (FAO), the World Organisation for Animal Health (OIE) and the United Nations Environment Programme (UNEP)) to develop a Global Plan of Action for One Health.

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## 1| Introduction

In May 2021, UNEP-WCMC and JNCC (2021) published a study investigating the zoonotic potential of international trade in CITES-listed species. The study took a preliminary look at the prevalence in legal international trade of CITES-listed taxa that have been associated with at least one zoonotic disease, outlining the key trade routes and taking an in-depth look at two commodities that were considered to have particularly high potential for zoonotic spillover: live animals and meat. The study looked at prevalence across a broad range of pathogen types, and included all zoonotic diseases identified through a literature search in its analysis regardless of their severity or transmissibility.

Two of the key recommendations made in this report were:

- (1) To conduct further analyses that focus on exploring the prevalence of pathogens that might be considered to pose a relatively higher risk to human health, for example, those that have the highest likelihood of developing into an epidemic/pandemic or that cause particularly severe disease in humans

and

- (2) To explore the prevalence of CITES-listed taxa associated with zoonotic risk in illegal trade.

This addendum aims to begin to fulfil these recommendations, by (1) investigating the prevalence in legal international trade of CITES-listed taxa associated with zoonotic diseases that have been identified by the World Health Organisation (WHO) as posing the greatest public health risk; and (2) taking a preliminary look at the presence or absence of CITES-listed taxa associated with these diseases in three illegal trade datasets. In both cases, our analyses focus on trade in live animals, as the commodity that is generally considered to carry a greater risk of zoonotic spillover.

### 1.1 Legal international trade in CITES-listed taxa associated with zoonotic diseases that pose the greatest public health risk

In order to focus our analysis on CITES-listed taxa associated with pathogens that pose a relatively higher risk to human health, we restricted the investigations in this addendum to the prevalence in international trade of taxa that have been associated with the WHO's Research and Development (R&D) Blueprint priority diseases (hereafter 'priority diseases'). The R&D Blueprint for Action to Prevent Epidemics is a global strategy, developed by a broad coalition of experts convened by WHO, that aims to reduce the time between the identification of a public health emergency of international concern and the availability of appropriate measures (e.g. effective tests, vaccines, and medicines) that can be used to avert a crisis (WHO 2016). The list of priority diseases maintained by WHO is focused on those which pose the greatest public health risk due to their epidemic potential, and/or for which there are no or insufficient countermeasures (WHO 2016). As of January 2022, the priority diseases are:

- COVID-19
- Crimean-Congo haemorrhagic fever
- Ebola virus disease and Marburg virus disease
- Lassa fever

- Middle East respiratory syndrome coronavirus (MERS-CoV) and Severe Acute Respiratory Syndrome (SARS)
- Nipah and henipaviral diseases
- Rift Valley fever
- Zika
- Disease X (represents the awareness that the next international epidemic could be caused by a pathogen currently unknown to cause human disease.)

Our study looks at the prevalence of CITES trade in families that contain taxa associated with all diseases in this list with the exception of Disease X, which cannot be included by definition.

## 1.2 Presence of CITES-listed taxa associated with WHO R&D Blueprint priority diseases in illegal trade

As noted in UNEP-WCMC and JNCC (2021), illegal trade has been postulated to carry a higher risk of zoonotic spillover than legal trade. This is because, while legal international trade is often subject to sanitary controls at numerous points in the supply chain, animals and animal products traded illicitly are not subject to such checks and are more likely to be stored in cramped or poor conditions that can increase the possibility of exposure to pathogens and suppress an animal's immune response (Rosen & Smith 2010; ROUTES 2020). Smugglers may also seek to evade animal health provisions such as quarantine, to which legal trade is subject. Gaining a strong understanding of which species are associated with high-risk zoonotic diseases and which of these are most likely to be present in illegal international trade is therefore a key component of managing the threat posed; however, illegal trade data are not as readily available as legal trade data and can be challenging to interpret, with substantial biases coming into play around enforcement effort, detection, reporting, and the quality of data recorded (see Sas-Rolfes *et al.* 2019; UNODC 2020).

Our preliminary analysis into the prevalence of CITES-listed taxa that have been associated with priority diseases in illegal trade therefore takes a simplified approach of looking for the presence or absence of taxa associated with these diseases across three datasets:

- (1) seizures of live animals upon import to the United States, as recorded in the United States Fish and Wildlife Service Law Enforcement Management Information System (LEMIS) and submitted for inclusion within the CITES Trade Database (under source I), 2009–2018;
- (2) seizures of live, unlicensed specimens of species included in the CITES Appendices and/or UK Wildlife Trade Regulations made at the UK border, 2013–2021; and
- (3) seizures and instances of smuggling/illegal trade of live specimens recorded in TRAFFIC International's Wildlife Trade Portal, 2013–2021.

While the same seizure event may occur in more than one dataset, our focus on presence or absence only negates potential issues caused by double counting.

The analysis is intended to be a first step towards understanding the potential public health risks associated with the illegal wildlife trade, but it is important to note that it does not make inferences of risk based on the *volume* of illegal trade in these species. Each of the three datasets is subject to particular caveats that are outlined in more detail in the methods and results sections, and the findings of this analysis should be interpreted bearing these in mind.

## 2| Methods

### 2.1 Taxon/disease associations

Our study used the taxon/disease association dataset compiled in UNEP-WCMC & JNCC (2021), supplemented by the results of an additional search for taxon/species associations for the 11 WHO R&D Blueprint priority diseases. The supplemental search used the following search string: “wildlife AND host AND [priority disease] AND (zoonoses OR zoonosis OR zoonotic)” in Google Scholar; any taxon/disease associations identified in the first ten papers returned by the search string that met the criteria below were added to the initial dataset. For the purpose of this report, associations for ‘henipaviral diseases’ were restricted to the two viruses in this genus that have been reported to infect humans: Nipah virus and Hendra virus (Cousins & Ustianowski 2021).

The inclusion criteria for studies outlining taxon/disease associations to be included in the dataset were as follows:

1. The study directly sampled taxa for the presence of a particular pathogen, OR,
2. The study was a review paper of known associations detected through serological assays or viral isolation with PCR detection; AND
3. Associations in the study were specific to the level of taxonomic family or below.

The complete set of papers used to compile the dataset of taxon/disease associations used in our analysis can be found in Addendum Annex A. As with UNEP-WCMC and JNCC (2021), we excluded disease/taxon associations that were from domesticated species<sup>2</sup>. CITES-listed taxa were mapped to CITES taxonomy using Species+, all other taxa were mapped to IUCN or Catalogue of Life taxonomy.

As with UNEP-WCMC and JNCC (2021), unless otherwise stated it should be noted that the presence of an association within a ‘CITES family’ means that an association between one or more priority diseases and either the family, a genus within that family, or a species within that family was found within the literature. Our justification for using a principally family-level approach is that species within the same family are likely to carry similar zoonotic diseases (Davies & Pedersen 2008), but not all species are equally well studied in the context of zoonotic risk, with research effort shown to be a major predictor of detecting species-disease associations (Olival *et al.* 2017; Becker *et al.* 2020 and references therein; Johnson *et al.* 2020). The approach taken means that all species of the family in which the association was detected are considered to carry a *potential* spillover risk, regardless of whether a direct association with a priority disease has been recorded at the species level. Associations also ‘carry over’ to the family regardless of whether the taxon in which the association was recorded is CITES-listed. For example, if a direct association is recorded between *Sus scrofa* (which is not itself CITES-listed) and Severe Acute Respiratory Syndrome (SARS), all other members of the Suidae are deemed to be potentially associated with this disease.

It is also important to note that an association with a specific disease in our dataset does not necessarily imply that a known spillover event has occurred between humans and that particular taxon. Non-human primates, for example, have been identified as the most

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<sup>2</sup> *Bos taurus*, *Canis lupus familiaris*, *Camelus bactrianus*, *Camelus dromedarius*, *Capra hircus*/*Capra hircus aegagrus*, *Cavia porcellus*, *Equus asinus*, *Equus caballus*/*Equus ferus caballus*, *Felis catus*, *Lama glama*, *Mustela furo*/*Mustela putorius furo*, *Ovis aries aries*, *Sus domesticus*, *Vicugna pacos*.



important enzootic<sup>3</sup> amplification hosts for Zika virus in the sylvatic cycle of the disease<sup>4</sup>; however, there are records of infection in other classes, including birds and reptiles (Gutiérrez-Bugallo *et al.* 2019). Gutiérrez-Bugallo *et al.* (2019) note that there is scarce information regarding the viremia levels different hosts can develop, and that there is a very limited understanding of the contribution of these latter two groups to Zika transmission. Our analysis is therefore taking a highly precautionary approach, which assumes there may be risk even if a spillover event has not yet been recorded. As with UNEP-WCMC and JNCC (2021) we also acknowledge that the geographic ranges of diseases and host species may not completely overlap, and that, for vector transmitted diseases (e.g. Crimean-Congo haemorrhagic fever), the analysis does not take into account the distribution of known insect vectors. The results of our analysis should be interpreted in the context of these limitations.

## 2.2 Analysis of legal trade in CITES families associated with WHO R&D Blueprint priority diseases

Data on both direct and indirect trade in current CITES-listed animal taxa were downloaded at the shipment-by-shipment level from the CITES Trade Database (<https://trade.cites.org/>) on 15 February 2022. Trade data terms and units were standardised; only shipments reported as live animals (term code LIV) were included in the analysis<sup>5</sup>. Sources as defined in CITES Resolution 12.3 (Rev. CoP18) on *Permits and Certificates* were grouped for analysis as follows: wild-sourced trade ('W', 'U', and no source specified), captive-produced trade ('C', 'D', and 'F'), trade in ranched specimens ('R'), and other ('X', 'I', 'O') (see <https://cites.org/sites/default/files/notif/E-Notif-2019-072-A1.pdf> for details of specific source codes). All purpose of transaction codes (i.e. the reason the specimen(s) were traded) were included<sup>6</sup>.

Throughout the report, figures denoting the number of trade **transactions** are based on both direct and indirect trade, and unless otherwise noted are (re-)exporter-reported only.

**Quantities** traded were converted to gross exports (i.e. quantities reported by the exporter and importer are compared based on data aggregated by taxon, term, unit, importer, exporter, source and year; whichever quantity is largest is used in the analyses) and are based on direct trade only.

## 2.3 Presence of CITES families associated with WHO R&D Blueprint priority diseases in illegal trade

We investigated the presence of taxa associated with priority diseases in illegal trade using three datasets:

- (1) seizures of live animals recorded in the United States Fish and Wildlife Service Law Enforcement Management Information System (LEMIS), and submitted for inclusion within the CITES Trade Database under source I (2009–2018) (hereafter referred to as United States seizure data);

<sup>3</sup> Enzootic diseases are those which are maintained at a regular baseline level, without the need for external inputs.

<sup>4</sup> The cycle involving nonhuman animal hosts and insects

<sup>5</sup> A small number of transactions involving taxa belonging to CITES families associated with priority diseases had an unspecified term code (equivalent to 0.004% of all live transactions involving taxa from priority-disease associated CITES families). While these transactions could have involved live animals, we focus only on trade where there was no uncertainty regarding the involvement of live animals.

<sup>6</sup> Commercial (T), Zoo (Z), Botanical garden (G), Circus or travelling exhibition (Q), Scientific (S), Hunting trophy (h), Personal (P), Medical (M), Educational (E), Reintroduction or introduction into the wild (N), Breeding in captivity of artificial propagation (B) and Law enforcement/judicial/forensic (L).

- (2) seizures of all live, unlicensed specimens of species included in the CITES Appendices and/or UK Wildlife Trade Regulations made at the United Kingdom border, 2013–2021, as recorded in the UK national seizure database (hereafter referred to as UK seizure data);
- (3) seizures and instances of smuggling/illegal trade of live specimens<sup>7</sup> recorded in TRAFFIC International's Wildlife Trade Portal, 2013–2021.

As with the legal trade analysis, a CITES family was considered to be associated with a priority disease if it contained at least one association at the species, genus or family level, regardless of whether the particular association was with a CITES-listed taxon. Taxa were considered to be 'present' in illegal trade if there were one or more incidences recorded in the relevant dataset. It is important to note that, while the United States and UK seizure data comprise data on seizures at each country's border (and are thus likely to represent seizures of animals being traded internationally), seizures and instances of smuggling/illegal trade held in the TRAFFIC International Wildlife Trade Portal are drawn from a variety of sources, and do not necessarily indicate that each species was about to or had entered *international* illegal trade.

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<sup>7</sup> Seizures are classified as specific events in which wildlife or wildlife products were seized; smuggling/illegal trade is defined as any specific event in which people have illegally traded or smuggled wildlife or wildlife products, but no direct seizure or poaching incident has been mentioned or reported.

### 3| CITES-listed taxa associated with WHO R&D Blueprint priority diseases

Our literature search identified 282 taxa that have been directly associated with one or more priority diseases<sup>8</sup>. The majority of these taxon-disease associations (200) were documented at the species or subspecies level (see Addendum Annex C); an additional 60 associations were documented at genus level, and 22 associations were documented at the family level (Table 1). The overall number of unique taxon-disease associations was 398, as some taxa were associated with more than one priority disease.

Of the 282 taxa that were directly associated with one or more priority diseases, 104 taxa were either a CITES-listed species or contained a CITES-listed species or subspecies. In total, 633 CITES-listed species are included within the families in which at least one association with a priority disease has been identified.

**Table 1:** Number of taxa directly associated with at least one WHO R&D Blueprint priority disease based on source papers (n = 70) identified through the literature search. For a family or genus to be considered a 'CITES-taxon' it must contain at least one species in the CITES Appendices.

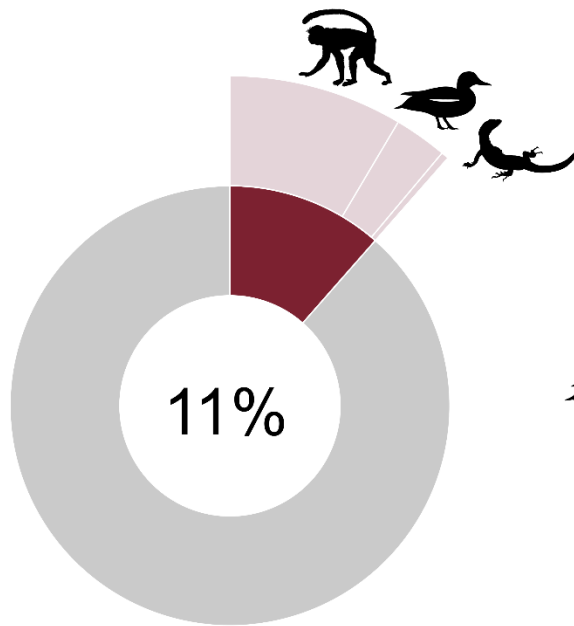
| Taxonomic level   | CITES taxa | Non-CITES taxa | All taxa |
|-------------------|------------|----------------|----------|
| <b>Family</b>     | 13         | 9              | 22       |
| <b>Genus</b>      | 29         | 31             | 60       |
| <b>Species</b>    | 62         | 137            | 199      |
| <b>Subspecies</b> | –          | 1              | 1        |
| <b>Total taxa</b> | 104        | 178            | 282      |

Of the 270 animal families that include at least one species in the CITES Appendices (henceforth referred to as 'CITES families'), 31 families (11.5%) included at least one taxon associated with a priority disease (Figure 1; Addendum Annex Table B lists the 53 taxonomic families associated with at least one WHO R&D Blueprint priority disease based on the source papers identified through the literature search, including 31 CITES families and 22 non-CITES families). Mammals were the class containing the highest proportion of CITES families associated with at least one priority disease, with nearly one third (29.5%) of CITES mammal families (23) associated with one or more diseases (Figure 1). Within the mammals, CITES families associated with one or more priority diseases were concentrated within the Artiodactyla (even-toed ungulates; six families), Carnivora (four families) and Primates (four families). The Passeriformes were the single avian order containing more than one CITES family associated with a priority disease (two families), and only one order of reptiles (Sauria) contained any CITES families associated with the priority diseases.

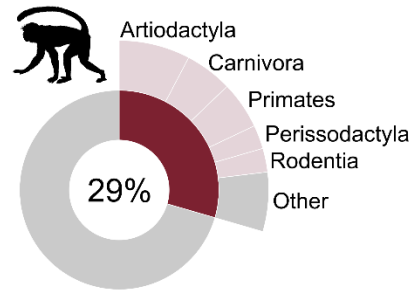
<sup>8</sup> Note that associations between taxa and SARS-CoV, MERS-CoV and SARS-CoV-2 outlined in Anderson *et al.* (2020); Chan *et al.* 2015; Haider *et al.* (2020); Jo *et al.* (2020); Latif and Mukaratirwa (2020); Mackensie and Smith (2020); Tsan-Yuk *et al.* (2020); Ye *et al.* (2020) and Zhang *et al.* (2020) are based on percentage similarities between animal coronaviruses and human SARS-CoV, MERS-CoV and SARS CoV-2 isolates.



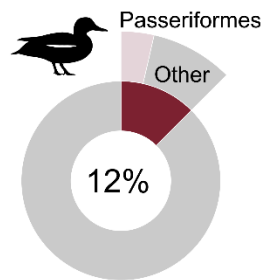
All CITES animal families:



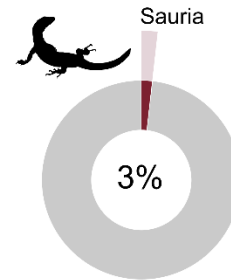
Mammals:



Birds:



Reptiles:

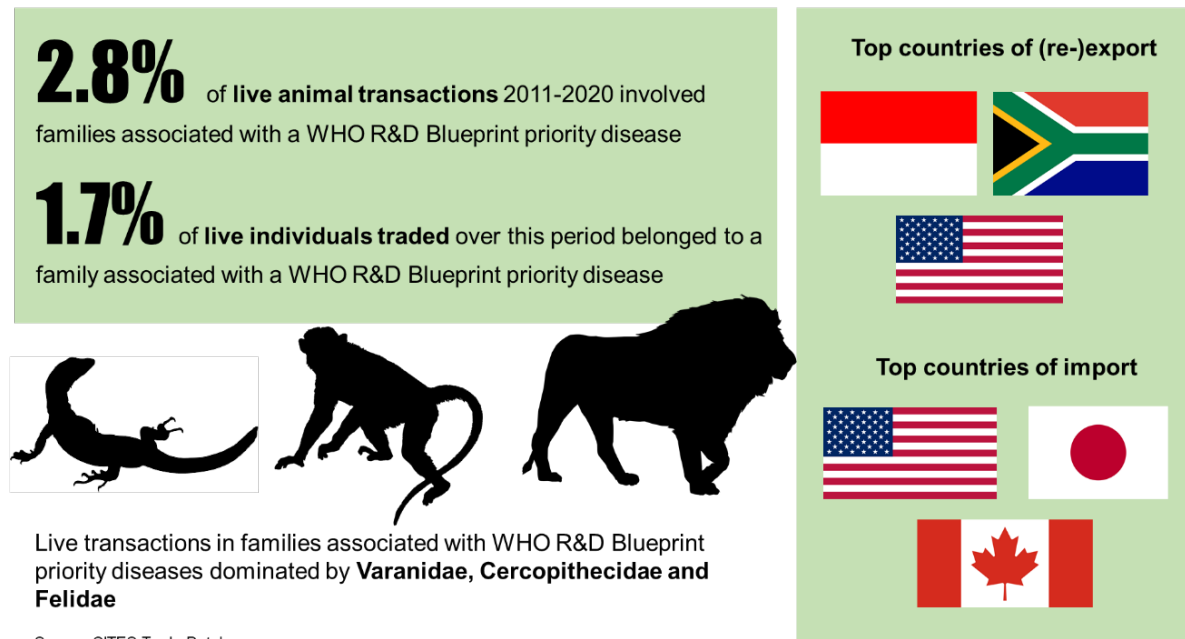


**Figure 1:** Proportion of CITES animal ( $n = 270$ ), mammal ( $n = 78$ ), bird ( $n = 62$ ) and reptile ( $n = 38$ ) families associated with at least one WHO R&D Blueprint priority disease (inner ring). The outer rings show the proportion of these families that belong to each taxonomic class or order. Bird and mammal orders containing only one family associated with a priority disease are included within 'Other'. No taxa within any of the CITES amphibian families ( $n = 13$ ) were associated with a priority disease. 'CITES families' are those that contain at least one species listed in the CITES Appendices.

## 4| Prevalence of taxa associated with WHO R&D Blueprint priority diseases in CITES trade

### 4.1 Analysis of trade at the family level

Figure 2 shows the percentage of live animal transactions at the family level associated with WHO R&D Blueprint diseases and the top countries of (re-)export and import.



**Figure 2:** Analysis of live transactions at the family level associated with WHO R&D Blueprint priority diseases. Source: CITES Trade Database.

Taxa belonging to 29 of the 31 CITES families associated with one or more priority diseases were present in legal international trade reported in the CITES Trade Database between 2011 and 2020 (the two families that were not recorded were the Scolopacidae (sandpipers) and Muridae (murids)). Over this period, approximately 1.2 million (re-)exporter-reported live animal transactions were recorded in the CITES Trade Database. Of these, 33,974 (re-)exporter-reported transactions (2.8% of all (re-)exporter-reported transactions featuring live animals) involved families associated with at least one priority disease. These transactions were dominated by mammals (55.4% of transactions) and reptiles (42.0%), with birds accounting for the remaining 2.6%.

Gross exports (based on direct trade only) indicate that international trade in live individuals over this period involved 68.8 million animals reported by number of specimens, as well as an additional 17.1 million kg of live animals reported by weight. Of the 68.8 million animals reported by number of specimens, 1.12 million individuals belonged to a family associated with at least one priority disease (1.65% of all live individuals reported by number over this period).

The largest (re-)exporters of families associated with at least one priority disease by number of transactions were Indonesia (31.3%, mainly reptiles), South Africa (8.9%, mainly mammals) and the United States (5.6%, mainly mammals). The largest countries of import for families associated with priority diseases by number of transactions were the United States (30.6%, primarily reptiles but also mammals), Japan (8.4%, primarily reptiles but also mammals) and Canada (5.2%, primarily mammals but also reptiles).

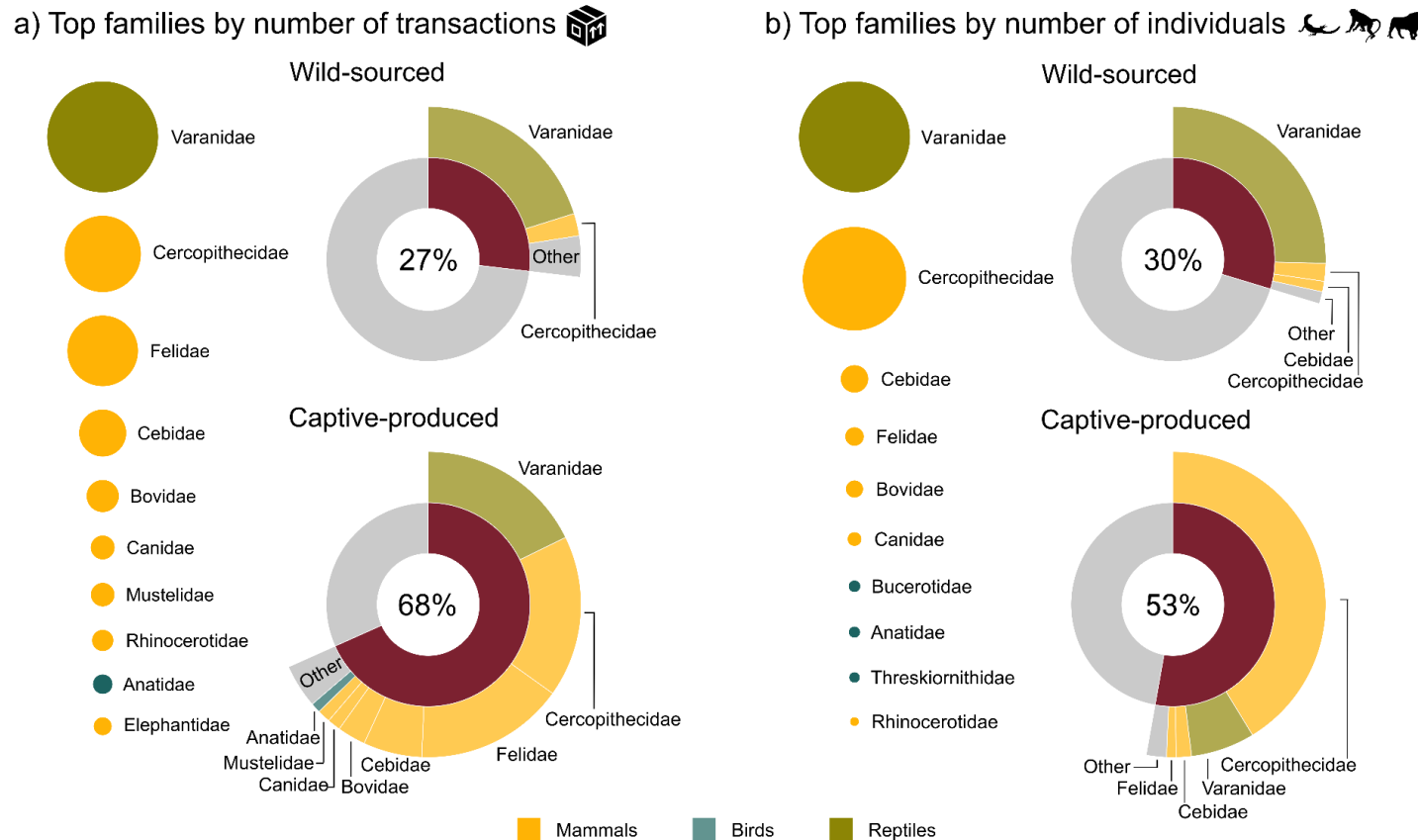
Whilst all eleven priority diseases were associated with at least one CITES family, only ten diseases were associated with CITES families found in international trade as live commodities (all priority diseases with the exception of Lassa fever). Of the ten most traded families associated with a priority disease (by both number of (re-)exporter reported transactions and number of individuals), the Cercopithecidae (Old World monkeys) and Felidae (cats) were associated with the highest number of priority diseases (eight and six priority diseases respectively) (Table 2).

**Table 2:** Matrix showing the WHO R&D Blueprint priority diseases associated with the most highly traded priority disease associated CITES families. Highly traded families are those in the top ten most-traded families, as determined by the **number of (re-)exporter-reported transactions** or the **quantity of individuals traded** 2011–2020. Eight families were included in both of the top ten lists; families appearing only in the top ten most-traded families by the number of (re-)exporter-reported transactions are indicated by an asterisk (\*), whereas those included only within the top ten by the quantity of individuals traded are indicated by (†). Note that associations between taxa and SARS-CoV, MERS-CoV and SARS-CoV-2 in a number of source papers are based on percentage similarities between animal coronaviruses and human SARS-CoV, MERS-CoV and SARS CoV-2 isolates (see methodology).

|                                     |   | Highly traded CITES families      |                  |                          |                  |   |                                     |                           |                |                         |                         |  |                             |
|-------------------------------------|---|-----------------------------------|------------------|--------------------------|------------------|---|-------------------------------------|---------------------------|----------------|-------------------------|-------------------------|--|-----------------------------|
|                                     |   | Anatidae (ducks, swans and geese) | Bovidae (bovids) | Bucerotidae† (hornbills) | Canidae (canids) | Cebidae (capuchin and squirrel monkeys) | Cercopithecidae (Old World monkeys) | Elephantidae* (elephants) | Felidae (cats) | Mustelidae* (mustelids) | Rhinocerotidae (rhinos) | Threskiornithidae† (ibis and spoonbills) | Varanidae (monitor lizards) |
| WHO R&D Blueprint priority diseases | COVID-19  |                                   |                  |                          |                  |   | +                                   |                           | +              | +                       |                         |  |                             |
|                                     | Crimean-Congo haemorrhagic fever                        |                                   | +                | +                        | +                |   |                                     | +                         | +              |                         | +                       |  |                             |
|                                     | Ebola virus disease (EVD)                               |                                   | +                |                          |                  |   | +                                   |                           |                |                         |                         |  |                             |
|                                     | Hendra virus  |                                   |                  |                          |                  |   |                                     |                           |                |                         |                         |  |                             |
|                                     | Lassa fever   |                                   |                  |                          |                  |   |                                     |                           |                |                         |                         |  |                             |
|                                     | Marburg virus disease                                   |                                   |                  |                          |                  |   | +                                   |                           |                |                         |                         |  |                             |
|                                     | Middle East respiratory syndrome coronavirus (MERS-CoV) |                                   |                  |                          |                  | +                                       | +                                   |                           |                |                         |                         |  |                             |
|                                     | Nipah virus   |                                   |                  |                          | +                | +                                       | +                                   |                           | +              |                         |                         |  |                             |
|                                     | Rift Valley fever                                       |                                   | +                |                          | +                |   | +                                   | +                         | +              |                         | +                       |  |                             |
|                                     | Severe Acute Respiratory Syndrome (SARS)                |                                   |                  |                          | +                | +                                       | +                                   |                           | +              | +                       |                         |  |                             |
|                                     | Zika virus  | +                                 | +                |                          |                  | +                                       | +                                   | +                         | +              |                         |                         | +  | +                           |

The family with the highest number of **transactions** involving live animals associated with one or more priority diseases was the Varanidae (monitor lizards), which accounted for 42.0% of (re-)exporter-reported transactions in priority-disease associated families over the ten-year period (Figure 3). However, it should be noted that this family was associated with only one of the eleven priority diseases (Zika virus; Table2), and that the role of this species in zoonotic spillover is unclear (Gutiérrez-Bugallo *et al.* 2019). Taxa within the Cercopithecidae and Felidae accounted for a further 19.6% and 16.7% of live transactions in families associated with priority diseases respectively. CITES trade transactions involving live animals belonging to families associated with one or more priority diseases were mostly in captive-produced animals (68.3% of all transactions) (Figure 3); this was particularly the case for birds (with captive-produced animals accounting for 94.8% of all transactions in priority disease-associated families) and mammals (with captive-produced animals accounting 86.8% of all transactions in priority disease-associated families). Transactions of live reptiles belonging to priority disease-associated families were almost evenly split between wild-sourced (48.0%) and captive-produced (42.3%) animals.

When viewed by the **quantity** of individuals traded, the trade in live animals from families associated with one or more priority diseases was also dominated by the Varanidae and Cercopithecidae (Figure 3). These two families accounted for 92.6% of the individuals in live trade belonging to families associated with priority diseases (49.4% and 43.2%, respectively), with all the remaining families representing less than 1% of this trade. Approximately half (53%) of the individuals in trade belonging to families associated with priority diseases were reported to be captive-produced; this proportion was higher when looking at trade in priority disease-associated families that were birds or mammals (67.8% and 91.5% of the number of individuals associated with priority diseases in trade, respectively). For reptiles, however, a higher proportion of the live individuals belonging to families associated with priority diseases traded were wild-sourced (51.4%) compared to captive-produced (13.7%).



**Figure 3:** Summary of trade in live animals belonging to the top-10 families associated with WHO R&D Blueprint priority diseases 2011–2020, by (a) **number of (re-)exporter-reported transactions**, and (b) **quantity of individuals traded** (all families accounting for > 1% of trade by source are shown). Pie charts show the proportion of trade in priority disease associated families that was wild-sourced (27% of transactions; 30% of the live individuals in trade) or captive-produced (68% of transactions; 53% of the live individuals in trade). The source of the remaining trade in priority disease associated families was ranched (4% of transactions; 17% of the live individuals in trade) or other (< 1% of transactions; < 1% of the live individuals in trade). Note that quantity of individuals is based on gross exports of direct trade only.



## 4.2 Trade in species with direct associations with WHO R&D Blueprint priority diseases

Of the 2005 CITES-listed animal species reported in live, international trade 2011–2020, 310 (15.5%) belonged to families associated with a priority disease (Table 3). Within this subset, 49 CITES-listed species were directly associated with a priority disease in the literature, representing 2.4% of all CITES-listed animal species traded as live individuals during this period (Table 3). Trade in these species accounted for 1.5% of all live animal transactions reported over this period and involved approximately 575,000 individual animals.

Figure 4 shows the top ten CITES-listed species in live international trade belonging to families associated with at least one priority disease, by the number of (re-)exporter-reported transactions recorded in the CITES Trade Database and the quantity of individuals in direct trade. Of the top 10 species according to number of transactions, three species (*Macaca fascicularis*, *Panthera leo* and *Panthera tigris*) were directly associated with at least one priority disease (Figure 4), whereas five of the top ten species by quantity of individuals traded were directly associated with at least one priority disease (*Macaca fascicularis*, *Varanus niloticus*, *Macaca mulatta*, *Saimiri sciureus* and *Callithrix jacchus*).

**Table 3:** Overview of the number of CITES-listed species, number of live animal transactions and quantity of live animals traded over the period 2011–2020, for all species in live trade and for all species in live trade directly associated with at least one WHO R&D Blueprint priority disease. The data presented excludes trade reported at higher taxonomic levels.

|  | Total for all species                        | Total for species in families associated with WHO R&D Blueprint priority diseases | Total for species directly associated with WHO R&D Blueprint priority diseases |
|--|--|---|--|
| Number of CITES-listed animal species in live international trade                  | 2,005  | 310   | 49   |
| Number of transactions recorded in the CITES Trade Database involving live animals | 769,279                                      | 33,907  | 11,721   |
| Quantity of CITES-listed live animals in direct international trade                | 50.3 million individuals and 12.8 million kg | 1.2 million individuals and 1,658 kg  | 575,075 individuals and 14.2 kg  |

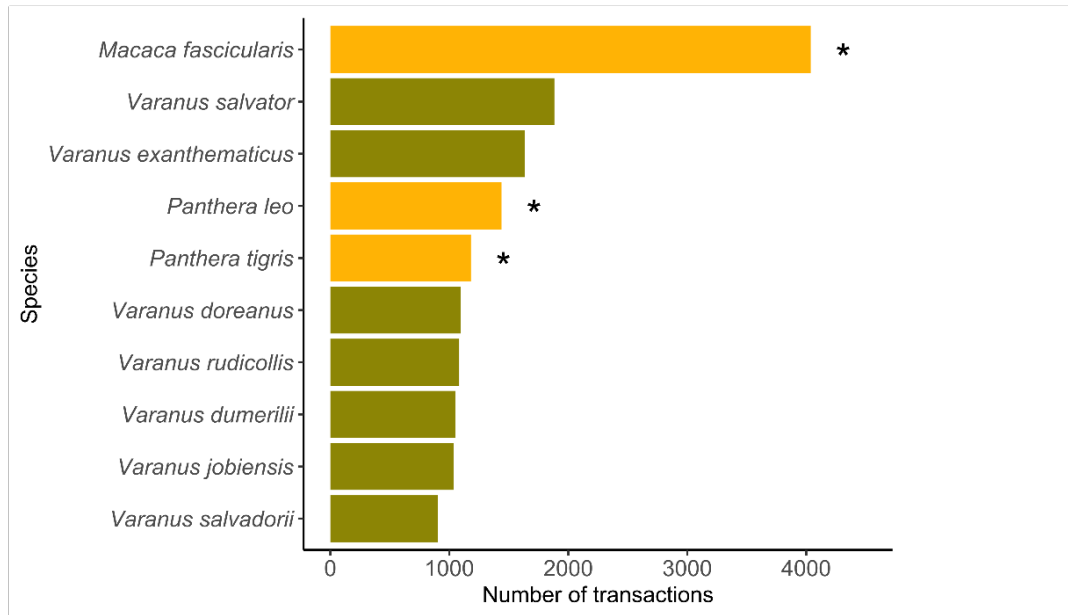
**Table 4:** CITES-listed species which were directly associated with WHO R&D Blueprint priority diseases and reported in live international trade over the period 2011–2020 (n = 49).

| Class    | Order            | Family          | Species   |
|----------|------------------|-----------------|---|
| Mammals  | Artiodactyla     | Bovidae         | <i>Damaliscus pygargus</i> *, <i>Hippotragus niger</i> *  |
|          |                  | Cervidae        | <i>Dama dama</i> *  |
|          |                  | Giraffidae      | <i>Giraffa camelopardalis</i>   |
|          |                  | Hippopotamidae  | <i>Hippopotamus amphibius</i>   |
|          | Carnivora        | Canidae         | <i>Canis lupus</i>  |
|          |                  | Felidae         | <i>Acinonyx jubatus</i> , <i>Otocolobus manul</i> ,<br><i>Panthera leo</i><br><i>Panthera tigris</i>  |
|          | Chiroptera       | Pteropodidae    | <i>Pteropus giganteus</i> , <i>Pteropus lylei</i> ,<br><i>Pteropus poliocephalus</i> , <i>Pteropus vampyrus</i>   |
|          | Perissodactyla   | Equidae         | <i>Equus africanus</i> , <i>Equus grevyi</i> , <i>Equus zebra</i> *   |
|          |                  | Rhinocerotidae  | <i>Ceratotherium simum</i> , <i>Diceros bicornis</i>  |
|          | Pholidota        | Manidae         | <i>Manis javanica</i>   |
|          | Primates         | Aotidae         | <i>Aotus nancymae</i>   |
|          |                  | Cebidae         | <i>Callithrix jacchus</i> , <i>Cebus libidinosus</i> ,<br><i>Saimiri boliviensis</i> , <i>Saimiri sciureus</i>  |
|          |                  | Cercopithecidae | <i>Cercocebus torquatus</i> , <i>Cercopithecus ascanius</i> , <i>Cercopithecus mona</i> ,<br><i>Cercopithecus neglectus</i> , <i>Cercopithecus nictitans</i> , <i>Chlorocebus aethiops</i> ,<br><i>Chlorocebus sabaeus</i> , <i>Colobus guereza</i> , <i>Erythrocebus patas</i> , <i>Lophocebus albigena</i> ,<br><i>Macaca fascicularis</i> , <i>Macaca mulatta</i> , <i>Macaca nemestrina</i> , <i>Mandrillus leucophaeus</i> ,<br><i>Mandrillus sphinx</i> , <i>Papio anubis</i> , <i>Papio cynocephalus</i> |
|          |                  | Hominidae       | <i>Gorilla gorilla</i> , <i>Pan troglodytes</i> , <i>Pongo abelii</i> , <i>Pongo pygmaeus</i>   |
|          | Proboscidea      | Elephantidae    | <i>Loxodonta africana</i>   |
| Birds    | Struthioniformes | Struthionidae   | <i>Struthio camelus</i> †   |
| Reptiles | Sauria           | Varanidae       | <i>Varanus niloticus</i>  |

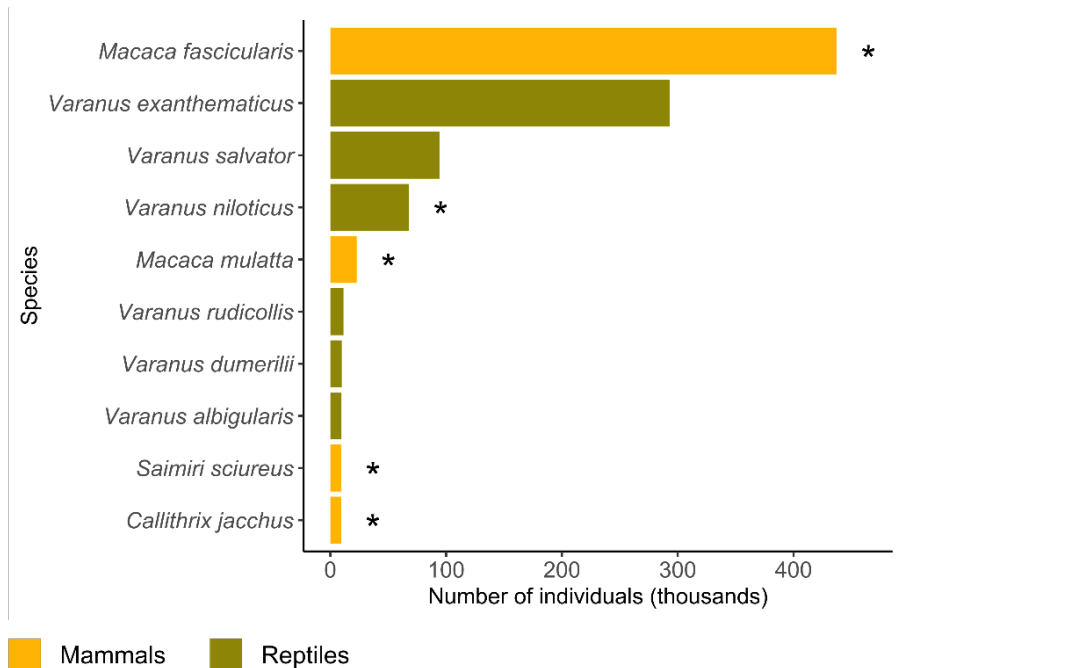
\* Taxa where only specific subspecies are included in the CITES Appendices

† Taxa where only specific populations are included in the CITES Appendices

## Top species in live trade by number of transactions



## Top species in live trade by quantity



**Figure 4:** The top ten CITES-listed species from families associated with at least one WHO R&D Blueprint priority disease, based on the number of (re-)exporter-reported transactions recorded in the CITES Trade Database involving live specimens and the quantity of live individuals in direct trade, 2011–2020. Species directly associated with a WHO R&D Blueprint priority disease are indicated by asterisks (\*). Note that the quantity of individuals is based on gross exports of direct trade only.

## 5| Presence of taxa associated with WHO R&D Blueprint priority diseases in illegal trade

### 5.1 Analysis of illegal trade at the family level

CITES-listed taxa belonging to 30 of the 31 CITES families associated with one or more priority diseases were present in the three datasets of live seizures used in our analysis (Table 5); the only family not identified was Rhinocerotidae. Data from the TRAFFIC International Wildlife Trade Portal identified seizures in far more priority disease-associated families (30) than US seizure data (8) and UK seizure data (3). Associations were documented for all eleven priority diseases. [Note, however, that taxa belonging to the Muridae were not identified at the species- or genus-level within the illegal trade datasets analysed, so it is unclear whether the only known animal reservoir of Lassa fever (*Mastomys* spp.) was present.]

Seizures and smuggling/illegal trade records of species belonging to families associated with priority diseases from the TRAFFIC International Wildlife Trade Portal predominantly involved mammals (22/30 total families associated with priority diseases), but also birds (seven families) and reptiles (one family). In the United States and UK seizure data, all seizures of live specimens of species belonging to families associated with priority diseases involved mammals, with the exception of one reptile family (Varanidae).

Cercopithecidae (Old World Monkeys) was the family with the highest diversity of species recorded in the seizure datasets of live specimens used in this analysis, with 42 species recorded in seizure data over the time periods specified, followed by the Varanidae (29 species) and the Felidae (25 species excluding hybrids).

### 5.2 Analysis of illegal trade at the species level

Thirty-three of the CITES-listed species identified in the illegal trade datasets had a direct association with a priority disease; the majority of these species were primates belonging to the Cebidae (two species), Cercopithecidae (13 species) and Hominidae (3 species). According to the source papers returned by the literature search, these primate species were together directly associated with eight of the 11 priority diseases (Table 6): COVID-19, Ebola virus disease, Marburg virus disease, Middle East respiratory syndrome coronavirus (MERS-CoV), Nipah virus, Rift Valley fever, Severe Acute Respiratory Syndrome (SARS) and Zika virus. In contrast, all priority disease-associated bird and reptile families that were present in illegal trade were associated with a single priority disease at most (Crimean-Congo haemorrhagic fever or Zika virus).

Within the mammal orders identified as being present in illegal trade, a relatively high number of the carnivore and artiodactyl species were also directly associated with a priority disease (five species-specific associations each).

**Table 5:** CITES-listed species (or taxa including a CITES-listed species, subspecies or population) belonging to families associated with one or more WHO R&D Blueprint priority diseases recorded in illegal trade (live individuals only). Evidence for presence in illegal trade was based on United States (2009–2018), UK (2013–2021) and TRAFFIC International Wildlife Trade Portal (2013–2021) seizure data. Species directly associated with a WHO R&D Blueprint priority disease are indicated by asterisks (\*).

| Class   | CITES families associated with one or more WHO R&D Blueprint Priority Diseases | Data source   |   |  |
|---------|--|---|---|--|
|         |  | United States seizures of live specimens (2009–2018)  | UK seizures of live specimens (2013–2021) | Seizures and smuggling/illegal trade incidents involving live individuals recorded in the TRAFFIC International Wildlife Trade Portal (2013–2021)  |
| Mammals | Aotidae  |   |   | <i>Aotus</i> spp., <i>Aotus lemurinus</i>  |
|         | Bovidae  | <i>Ammotragus lervia</i> , <i>Antilope cervicapra</i> |   | Bovidae spp., <i>Ammotragus lervia</i> , <i>Antilope cervicapra</i> , <i>Bubalus depressicornis</i> , <i>Bubalus quarlesi</i> , <i>Capricornis</i> spp., <i>Capricornis milneedwardsii</i> , <i>Gazella bennettii</i> , <i>Hippotragus niger</i> *, <i>Oryx dammah</i> , <i>Ovis</i> spp., <i>Pseudois nayaur</i>  |
|         | Camelidae  |   |   | <i>Lama guanicoe</i>   |
|         | Canidae  | <i>Speothos venaticus</i> , <i>Vulpes zerda</i>       |   | Canidae spp., <i>Canis</i> spp., <i>Canis lupus</i> *, <i>Lycalopex culpaeus</i> , <i>Vulpes</i> spp., <i>Vulpes vulpes</i> *, <i>Vulpes zerda</i>   |
|         | Cebidae  | <i>Cebus capucinus</i>                                |   | Cebidae spp., <i>Callithrix</i> spp., <i>Callithrix jacchus</i> *, <i>Callithrix penicillata</i> , <i>Callithrix pygmaea</i> , <i>Cebus</i> spp., <i>Cebus apella</i> , <i>Cebus capucinus</i> , <i>Cebus olivaceus</i> , <i>Leontopithecus chrysomelas</i> , <i>Leontopithecus rosalia</i> , <i>Saguinus</i> spp., <i>Saguinus geoffroyi</i> , <i>Saguinus imperator</i> , <i>Saguinus midas</i> , <i>Saguinus oedipus</i> , <i>Saimiri</i> spp., <i>Saimiri sciureus</i> * |



| Class   | CITES families associated with one or more WHO R&D Blueprint Priority Diseases | Data source  |   |  |
|---------|--|--|---|--|
|         |  | United States seizures of live specimens (2009–2018) | UK seizures of live specimens (2013–2021) | Seizures and smuggling/illegal trade incidents involving live individuals recorded in the TRAFFIC International Wildlife Trade Portal (2013–2021)  |
| Mammals | Cercopithecidae  | <i>Macaca fascicularis</i> *                         |   | Cercopithecidae spp., <i>Cercocebus torquatus</i> *, <i>Cercopithecus ascanius</i> *, <i>Cercopithecus erythrogaster</i> , <i>Cercopithecus erythrotis</i> , <i>Cercopithecus hamlyni</i> , <i>Cercopithecus lhoesti</i> , <i>Cercopithecus mitis</i> , <i>Cercopithecus neglectus</i> *, <i>Cercopithecus nictitans</i> *, <i>Chlorocebus aethiops</i> *, <i>Chlorocebus pygerythrus</i> , <i>Chlorocebus sabaeus</i> *, <i>Colobus</i> spp., <i>Erythrocebus patas</i> *, <i>Lophocebus aterrimus</i> , <i>Macaca</i> spp., <i>Macaca arctoides</i> , <i>Macaca assamensis</i> , <i>Macaca fascicularis</i> *, <i>Macaca fuscata</i> , <i>Macaca hecki</i> , <i>Macaca leonina</i> , <i>Macaca mulatta</i> *, <i>Macaca nemestrina</i> *, <i>Macaca nigra</i> , <i>Macaca nigrescens</i> , <i>Macaca silenus</i> , <i>Macaca sylvanus</i> , <i>Mandrillus</i> spp., <i>Mandrillus leucophaeus</i> *, <i>Mandrillus sphinx</i> *, <i>Miopithecus talapoin</i> , <i>Nasalis larvatus</i> , <i>Papio</i> spp., <i>Papio anubis</i> *, <i>Papio hamadryas</i> , <i>Presbytis comata</i> , <i>Presbytis melalophos</i> , <i>Presbytis rubicunda</i> , <i>Pygathrix</i> spp., <i>Pygathrix cinerea</i> , <i>Pygathrix nemaeus</i> , <i>Pygathrix nigripes</i> , <i>Semnopithecus</i> spp., <i>Trachypithecus</i> spp., <i>Trachypithecus auratus</i> , <i>Trachypithecus germaini</i> , <i>Trachypithecus hatinhensis</i> , <i>Trachypithecus obscurus</i> |
|         | Cervidae   | <i>Rucervus eldii</i>                                |   | Cervidae spp., <i>Axis porcinus</i> , <i>Cervus elaphus</i> , <i>Dama dama</i> *, <i>Mazama americana</i> , <i>Muntiacus</i> spp., <i>Odocoileus virginianus</i> *   |
|         | Dasypodidae  |  |   | <i>Chaetophractus nationi</i>  |
|         | Elephantidae   |  |   | Elephantidae spp., <i>Elephas maximus</i> , <i>Loxodonta</i> spp.  |
|         | Equidae  |  |   | Equidae spp., <i>Equus</i> spp., <i>Equus zebra</i> *  |

| Class   | CITES families associated with one or more WHO R&D Blueprint Priority Diseases | Data source  |   |   |
|---------|--|--|---|---|
|         |  | United States seizures of live specimens (2009–2018)   | UK seizures of live specimens (2013–2021) | Seizures and smuggling/illegal trade incidents involving live individuals recorded in the TRAFFIC International Wildlife Trade Portal (2013–2021)   |
| Mammals | Felidae  | Felidae spp., <i>Felis</i> spp., <i>Felis margarita</i> , <i>Felis</i> spp., <i>Leptailurus serval</i> , <i>Lynx canadensis</i> , <i>Panthera tigris</i> *, <i>Prionailurus rubiginosus</i> , <i>Puma concolor</i> | <i>Panthera pardus</i>                    | <i>Felidae</i> spp., <i>Acinonyx jubatus</i> *, <i>Caracal caracal</i> , <i>Catopuma badia</i> , <i>Catopuma temminckii</i> , <i>Felis</i> spp., <i>Felis chaus</i> , <i>Felis silvestris</i> , <i>Herpailurus yagouaroundi</i> , <i>Leopardus pardalis</i> , <i>Leopardus tigrinus</i> , <i>Leopardus wiedii</i> , <i>Leptailurus serval</i> , <i>Lynx</i> spp., <i>Lynx rufus</i> , <i>Neofelis nebulosa</i> , <i>Panthera leo</i> *, <i>Panthera onca</i> , <i>Panthera pardus</i> , <i>Panthera tigris</i> *, <i>Pardofelis marmorata</i> , <i>Prionailurus</i> spp., <i>Prionailurus bengalensis</i> , <i>Prionailurus planiceps</i> , <i>Prionailurus viverrinus</i> , <i>Puma concolor</i> |
|         | Giraffidae   |  |   | <i>Giraffa</i> spp.   |
|         | Hippopotamidae   |  |   | <i>Hippopotamus amphibius</i> *   |
|         | Hominidae  |  |   | Hominidae spp., <i>Gorilla</i> spp., <i>Pan</i> spp., <i>Pan paniscus</i> , <i>Pan troglodytes</i> *, <i>Pongo</i> spp., <i>Pongo abelii</i> *, <i>Pongo pygmaeus</i> *   |
|         | Leporidae  |  |   | Leporidae spp.  |
|         | Manidae  |  |   | Manidae spp., <i>Manis</i> spp., <i>Manis crassicaudata</i> , <i>Manis culionensis</i> , <i>Manis gigantea</i> , <i>Manis javanica</i> *, <i>Manis pentadactyla</i> , <i>Manis temminckii</i> , <i>Manis tricuspis</i>  |
|         | Muridae  |  |   | Muridae spp.  |
|         | Mustelidae   | <i>Eira barbara</i> , <i>Mustela sibirica</i>  | <i>Eira barbara</i>                       | Mustelidae spp., <i>Aonyx cinerea</i> , <i>Lontra longicaudis</i> , <i>Lutra</i> spp., <i>Lutra lutra</i> , <i>Lutra sumatrana</i> , <i>Lutrogale perspicillata</i> , <i>Martes flavigula</i> , <i>Mustela</i> spp., <i>Mustela kathiah</i>   |
|         | Pteropodidae   |  |   | <i>Pteropus lylei</i> *   |
|         | Sciuridae  |  |   | Sciuridae spp., <i>Cynomys</i> spp., <i>Marmota</i> spp., <i>Ratufa affinis</i> , <i>Ratufa bicolor</i>   |
|         | Suidae   |  |   | <i>Babryrousa celebensis</i> , <i>Sus</i> spp.  |

| Class   | CITES families associated with one or more WHO R&D Blueprint Priority Diseases | Data source  |   |   |
|---------|--|--|---|---|
|         |  | United States seizures of live specimens (2009–2018) | UK seizures of live specimens (2013–2021) | Seizures and smuggling/illegal trade incidents involving live individuals recorded in the TRAFFIC International Wildlife Trade Portal (2013–2021)   |
| Mammals | Viverridae   |  |   | Viverridae spp., <i>Arctictis binturong</i> , <i>Civettictis</i> spp., <i>Cynogale bennettii</i> , <i>Paguma larvata</i> *, <i>Paradoxurus</i> spp., <i>Paradoxurus hermaphroditus</i> , <i>Prionodon linsang</i> , <i>Prionodon pardicolor</i> , <i>Viverra</i> spp., <i>Viverra zibetha</i> , <i>Viverricula indica</i>   |
| Birds   | Anatidae   |  |   | Anatidae spp., <i>Dendrocygna</i> spp., <i>Dendrocygna autumnalis</i>   |
|         | Bucerotidae  |  |   | Bucerotidae spp., <i>Aceros cassidix</i> , <i>Aceros corrugatus</i> , <i>Anorrhinus galeritus</i> , <i>Anorrhinus tickelli</i> , <i>Anthracoceros albirostris</i> , <i>Anthracoceros malayanus</i> , <i>Anthracoceros marchei</i> , <i>Berenicornis comatus</i> , <i>Buceros bicornis</i> , <i>Buceros hydrocorax</i> , <i>Buceros rhinoceros</i> , <i>Penelopides panini</i> , <i>Rhinoplax vigil</i> , <i>Rhyticeros plicatus</i> , <i>Rhyticeros undulatus</i> |
|         | Muscicapidae   |  |   | Muscicapidae spp., <i>Cyornis</i> spp., <i>Leiothrix argentauris</i> , <i>Leiothrix lutea</i> , <i>Turdus</i> spp.  |
|         | Pycnonotidae   |  |   | Pycnonotidae spp., <i>Pycnonotus</i> spp., <i>Pycnonotus zeylanicus</i>   |
|         | Scolopacidae   |  |   | Scolopacidae spp.   |
|         | Struthionidae  |  |   | <i>Struthio</i> spp., <i>Struthio camelus</i> *   |
|         | Threskiornithidae  |  |   | Threskiornithidae spp.  |

| Class    | CITES families associated with one or more WHO R&D Blueprint Priority Diseases | Data source  |  |   |
|----------|--|--|--|---|
|          |  | United States seizures of live specimens (2009–2018)   | UK seizures of live specimens (2013–2021)          | Seizures and smuggling/illegal trade incidents involving live individuals recorded in the TRAFFIC International Wildlife Trade Portal (2013–2021)   |
| Reptiles | Varanidae  | <i>Varanus acanthurus</i> ,<br><i>Varanus albigularis</i> ,<br><i>Varanus beccarii</i> ,<br><i>Varanus cumingi</i> ,<br><i>Varanus doreanus</i> ,<br><i>Varanus exanthematicus</i> ,<br><i>Varanus gouldii</i> ,<br><i>Varanus indicus</i> ,<br><i>Varanus jobiensis</i> ,<br><i>Varanus kordensis</i> ,<br><i>Varanus macraei</i> ,<br><i>Varanus melinus</i> ,<br><i>Varanus niloticus*</i> ,<br><i>Varanus prasinus</i> ,<br><i>Varanus reisingeri</i> ,<br><i>Varanus rudicollis</i> ,<br><i>Varanus salvadorii</i> ,<br><i>Varanus salvator</i> ,<br><i>Varanus similis</i> ,<br><i>Varanus spinulosus</i> ,<br><i>Varanus timorensis</i> | <i>Varanus</i> spp.,<br><i>Varanus bengalensis</i> | <i>Varanidae</i> spp., <i>Varanus</i> spp., <i>Varanus albigularis</i> , <i>Varanus beccarii</i> , <i>Varanus bengalensis</i> , <i>Varanus exanthematicus</i> , <i>Varanus flavescens</i> , <i>Varanus jobiensis</i> , <i>Varanus komodoensis</i> , <i>Varanus macraei</i> , <i>Varanus marmoratus</i> , <i>Varanus nebulosus</i> , <i>Varanus niloticus*</i> , <i>Varanus olivaceus</i> , <i>Varanus palawanensis</i> , <i>Varanus prasinus</i> , <i>Varanus rainerguentheri</i> , <i>Varanus reisingeri</i> , <i>Varanus rudicollis</i> , <i>Varanus salvadorii</i> , <i>Varanus salvator</i> |

**Table 6:** Matrix showing the WHO R&D Blueprint priority diseases associated with CITES families found in illegal trade as live animals. Note that associations between taxa and SARS-CoV, MERS-CoV and SARS-CoV-2 in a number of source papers are based on percentage similarities between animal coronaviruses and human SARS-CoV, MERS-CoV and SARS CoV-2 isolates (see methodology).

|                 |                   | WHO R&D Blueprint priority diseases |                                  |                           |              |             |               |  |             |                   |  |            |
|-----------------|-------------------|-------------------------------------|----------------------------------|---------------------------|--------------|-------------|---------------|--|-------------|-------------------|--|------------|
|                 |                   | COVID-19                            | Crimean-Congo haemorrhagic fever | Ebola virus disease (EVD) | Hendra virus | Lassa fever | Marburg virus | Middle East respiratory syndrome coronavirus | Nipah virus | Rift Valley fever | Severe Acute Respiratory Syndrome (SARS) | Zika virus |
| <b>Mammals</b>  | Aotidae           |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Bovidae           |                                     | +                                | +                         |              |             |               |  |             | +                 |  | +          |
|                 | Camelidae         |                                     | +                                |                           |              |             |               |  |             | +                 |  |            |
|                 | Canidae           |                                     | +                                |                           |              |             |               |  | +           | +                 | +  |            |
|                 | Cebidae           |                                     |                                  |                           |              |             |               | +  | +           |                   | +  | +          |
|                 | Cercopithecidae   | +                                   |                                  | +                         |              |             | +             | +  | +           | +                 | +  | +          |
|                 | Cervidae          |                                     |                                  |                           |              |             |               |  |             | +                 |  |            |
|                 | Dasypodidae       |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Elephantidae      |                                     | +                                |                           |              |             |               |  |             | +                 |  | +          |
|                 | Equidae           |                                     | +                                |                           |              |             |               |  |             | +                 |  | +          |
|                 | Felidae           | +                                   | +                                |                           |              |             |               |  | +           | +                 | +  | +          |
|                 | Giraffidae        |                                     | +                                |                           |              |             |               |  |             | +                 |  |            |
|                 | Hippopotamidae    |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Hominidae         |                                     |                                  | +                         |              |             |               |  |             |                   |  | +          |
|                 | Leporidae         |                                     | +                                |                           |              |             |               | +  |             |                   |  | +          |
|                 | Manidae           | +                                   |                                  |                           |              |             |               |  |             |                   |  |            |
|                 | Muridae           |                                     | +                                | +                         |              | +           |               |  | +           | +                 | +  | +          |
|                 | Mustelidae        | +                                   |                                  |                           |              |             |               |  |             |                   | +  |            |
|                 | Pteropodidae      | +                                   |                                  | +                         | +            |             | +             |  | +           | +                 | +  | +          |
|                 | Sciuridae         |                                     | +                                |                           |              |             |               |  |             | +                 |  |            |
|                 | Suidae            |                                     | +                                | +                         |              |             |               |  | +           | +                 | +  | +          |
|                 | Viverridae        |                                     | +                                |                           |              |             |               |  |             |                   | +  |            |
| <b>Birds</b>    | Anatidae          |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Bucerotidae       |                                     | +                                |                           |              |             |               |  |             |                   |  |            |
|                 | Muscicapidae      |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Pycnonotidae      |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Scolopacidae      |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
|                 | Struthionidae     |                                     | +                                |                           |              |             |               |  |             |                   |  |            |
|                 | Threskiornithidae |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |
| <b>Reptiles</b> | Varanidae         |                                     |                                  |                           |              |             |               |  |             |                   |  | +          |



## 6| Discussion

### 6.1 Associations of CITES-listed taxa with WHO R&D Blueprint priority diseases

Overall, a smaller number of CITES families were associated with the subset of diseases that make up the WHO R&D Blueprint priority list than were associated with the wider disease list used in UNEP-WCMC and JNCC (2021). The proportion of CITES families in which a disease association was recorded decreased across all four classes in which associations were detected in UNEP-WCMC and JNCC (2021). However, the implications of restricting the disease list were most pronounced in relation to the proportion of bird and reptile families in which associations were recorded (68% of bird families contained at least one species associated with a zoonotic disease in UNEP-WCMC and JNCC (2021), but only 12% of bird families contained one or more species associated with a priority disease; 58% versus 3% of reptile families for each type of association, respectively). This is likely due to the absence from the priority disease list of a small number of zoonoses that have been found in a wide number of bird and reptile species, such as Chlamydiosis and Salmonellosis.

The differences emphasise that any 'shortlist' of species that carry spillover risk can be heavily impacted by the initial list of zoonotic diseases deemed to be of importance; what is consistent, however, is the prominent role of the orders Primates, Carnivora and Artiodactyla as potential sources of spill over.

### 6.2 Prevalence of families associated with WHO R&D Blueprint priority diseases in legal CITES trade

Our analysis shows that only a small proportion of international trade in live specimens of CITES-listed taxa involves species belonging to a family that has been associated with at least one priority disease (2.8% of all (re-)exporter-reported transactions featuring live animals 2011–2020, and 1.65% of all live individuals reported by number over this period). Looking only at transactions involving a live animal where a direct association with a priority disease has been recorded in the literature, this proportion falls to 1.5% of live animal transactions recorded in the CITES Trade Database between 2011 and 2020, and 1.1% of individual live animals traded over this period.

While the proportions remain small, and the number of individuals belonging to families associated with priority diseases traded over a ten-year period (1.12 million) is lower than the c. 26.5 million individuals traded as live animals over a ten-year period that were identified as being associated with the much broader range of zoonotic diseases identified in UNEP-WCMC and JNCC (2021), this may still be considered to equate to a substantial quantity of trade potentially associated with risk. The ten-year total of 1.12 million individuals equates to an average of 112,000 individuals being traded each year belonging to a family that may carry zoonotic risk in the context of this specific list of diseases, and an average of approximately 57,500 live animals being traded each year belonging to species that have been directly associated with a priority disease in the literature.

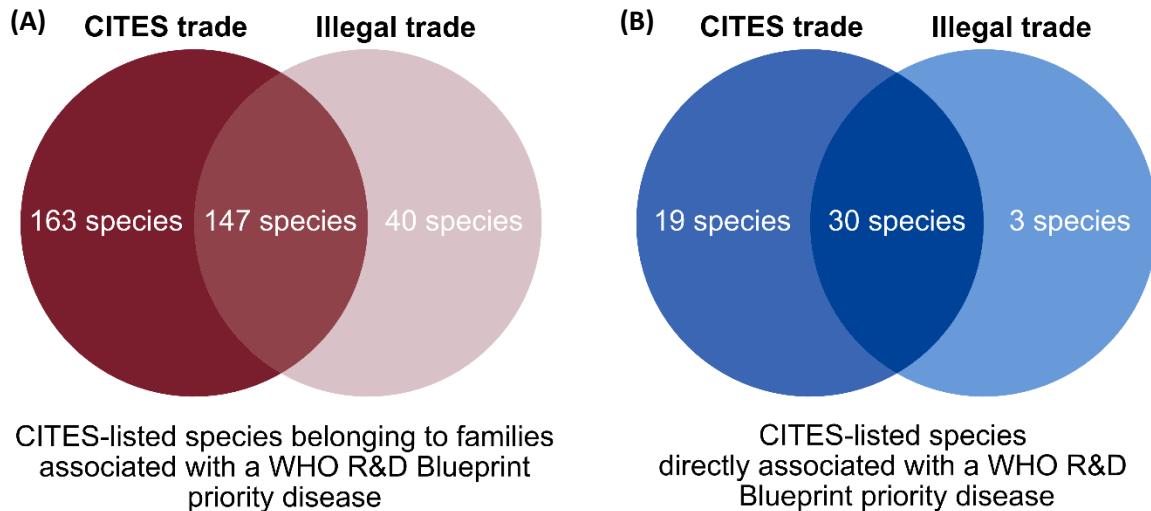
While Varanidae was the top family traded associated with the priority diseases by transactions as well as by number, it should be noted that this family contained only one species with a direct association with a priority disease (*Varanus niloticus* and Zika virus) and that the role that this species could potentially play in zoonotic spillover of this disease is unclear (Gutiérrez-Bugallo *et al.* 2019). In contrast, the second and third most traded families associated with priority diseases, the Cercopithecidae (Old World monkeys) and Felidae (cats), have been associated with eight and six of the eleven priority diseases, respectively. These families may generally be better candidates to prioritise when considering the

measures to be taken to reduce spillover risk of priority diseases in the context of international trade, but nevertheless it is also important to consider the origin and circumstances in which the majority of individuals in these families are traded. For example, most trade in Cercopithecidae over the ten-year period was in *Macaca fascicularis*, which was directly associated with five priority diseases; but the vast majority of trade in this species was in captive-bred specimens. The IUCN's situation analysis on the roles and risks of wildlife in the emergence of human infectious diseases (Kock & Caceres-Escobar 2022) notes that captivity, if for extended periods or breeding, "usually leads to a filtering out of many original pathogenic the importance of this trade in this family as a potential source of zoonotic spillover. It should also be remembered that our analysis does not take into account differing conditions in rearing, housing, or the preparation and transport of wildlife products, which are all known to influence animal health and spillover risk (see Greatorex *et al.* 2016; Webster 2004; Woo *et al.* 2006; Van Vliet *et al.* 2017; Huong *et al.* 2020).

### 6.3 CITES families associated with WHO R&D Blueprint priority diseases in illegal trade

Our preliminary analysis of illegal trade showed that live individuals have been seized belonging to 30 of the 31 families that our literature search identified as having at least one species listed in the CITES Appendices and an association with a priority disease. This is a similar proportion to the number of priority disease-associated families detected in international CITES legal trade (29/31), showing that, at the family level at least, both legal and illegal trade that potentially carries this particular type of zoonotic risk involves similar taxa.

A higher number of CITES-listed species belonging to priority disease-associated families were documented in legal international trade in live animals (310) than in illegal trade in live animals across the three seizure datasets (187) (Figure 5). However, there was a high degree of overlap between both groups of species; 42% (147 species) of all CITES-listed species belonging to a priority-disease associated family were detected in both legal and illegal trade of live specimens. A similar pattern was evident when considering only CITES-listed species that have a direct association with a priority disease (Figure 5), although a higher proportion (58%) of the species in this subset were documented in both legal and illegal trade of live animals (30 species). Of these 30 species, the majority (60%) were Primates, including 13 Cercopithecidae species, reinforcing the status of this taxonomic group as a possible candidate for prioritisation.



**Figure 5:** Venn diagrams showing the degree of overlap in legal and illegal trade among (A) CITES-listed species belonging to families associated with one or more WHO R&D Blueprint priority diseases (n = 350), and (B) CITES-listed species with a direct association with one or more WHO R&D Blueprint priority diseases (n = 52), according to the source papers used in our analyses.

It should be remembered that the three datasets of live seizures used in our analysis draw from different data sources and that each is subject to its own caveats, as well as the general caveats outlined in Sas-Rolfes *et al.* (2019) around detection of illegal trade and reporting biases. In particular it should be noted that, while the United States and UK datasets represent seizures made at country borders (and thus are highly likely to represent species that are entering or are about to enter illegal international trade), data on live seizures from the TRAFFIC International Wildlife Trade Portal may also include seizures of animals that were traded, or were about to be traded, domestically. Sixty-six percent of the species recorded across the three datasets that are included in the CITES Appendices have been recorded in the CITES Trade Database between 2011 and 2020, indicating that in around two-thirds of cases at least there is documented international demand.

#### 6.4 Additional key caveats

The caveats outlined in UNEP-WCMC and JNCC (2021) also apply to the analyses in this addendum, which in the case of the CITES legal trade analysis principally measure risk in terms of trade volumes and consider disease risk at the family level. These include sampling and reporting biases for both species and pathogens, and the fact that zoonotic spillover may not have been confirmed in all species/disease associations included in our dataset (see the Methods section for a full justification of chosen approach).

In addition, we emphasise that our list of taxon/disease associations should not be considered exhaustive. New taxon/disease associations are being characterised all the time, particularly for emerging diseases such as COVID-19 (a full list of the disease/taxon associations documented can be found in Addendum Annexes B and C), and as such our analysis should be interpreted within the context of the limitations imposed by the literature review approach. Similarly, part of the potential risk posed by wildlife trade is that it may bring together species that would not otherwise be in close contact during the selling and transportation process, thus creating novel opportunities for disease transmission across species and the creation of new animal reservoirs (Glidden *et al.* 2021). This aspect of spillover risk is not accounted for in our analyses but should be a key consideration when designing approaches to minimise risk.

## 6.5 Impact on recommendations in UNEP-WCMC and JNCC (2021)

While this analysis goes partway towards fulfilling the recommendations in UNEP-WCMC and JNCC (2021), it does not address them in full. Several avenues for refining an analysis of risk entailed by legal international CITES trade in priority disease-associated taxa remain unexplored, including analyses that consider the effect of weighting risk measurements by the **number of diseases** associated with individual taxa, and the effect of incorporating the degree of **range overlaps** between potential hosts, pathogens and their vectors. Similarly, it will be valuable to conduct analyses that focus on the potential prevalence in trade of **pathogens that are known to remain infectious in products for a long period of time**, and which may therefore pose an infection risk through all stages of the supply chain and end consumption.

For analyses of the risk posed by illegal trade in priority disease-associated species, the **incorporation of additional sources of illegal trade data** will help to create a more complete picture of potential risk across a wider geographical area. Ideally future analyses would be able to consider **volumes of illegal trade and key illegal trade routes**, but such research would have to account for reporting biases and other uncertainties such as whether seizure records truly reflect the composition of illegal trade as a whole. Analyses should also be expanded to explore illegal trade in other high risk commodity types, such as meat.

Finally, additional input from health experts could allow future analyses to take into account the impact of particular hygiene and quarantine protocols on spillover risk, and, for illegal trade, the impact on spillover risk of factors such as concealment methods.

Given the caveat surrounding the continual characterisation of novel associations between diseases and animal hosts, the recommendation in UNEP-WCMC and JNCC (2021) for the creation and maintenance of a **central repository of disease/species associations covering the full range of zoonotic pathogens and their associated diseases** (rather than just viruses, for example) remains particularly pertinent. Work to identify and collate available data on disease/taxon associations was highlighted by the CITES working group on *the role of CITES in reducing risk of future zoonotic disease emergence associated with international wildlife trade* as a potential future area of work for CITES to jointly undertake with the World Organisation for Animal Health (OIE) (SC74 Doc. 16), highlighting the recognised need for such datasets. Additional potential avenues of joint work between CITES and OIE suggested by the working group include conducting analyses of trade to identify species, origins (e.g. wild, captive), and activities that present the most likely risk of zoonotic disease transmission and pathogen spillover along the international trade supply chain (SC74 Doc. 16). It is hoped that this addendum, alongside UNEP-WCMC and JNCC (2021), could be helpful in providing a foundation for this work.

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## Addendum Annex A

List of papers (referred to as 'source papers') used to build the dataset of taxon disease associations (\* – Papers added as a result of the supplementary search conducted for this addendum).

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## Addendum Annex B: CITES families and species associated with at least one WHO R&D Blueprint priority diseases

**Addendum Table B:** Taxonomic families (n = 53, including 31 CITES families (a taxonomic family that contains one or more CITES-listed species) and 22 non-CITES families) associated with at least one WHO R&D Blueprint priority disease according to the source papers identified through the literature search. Within each taxonomic order, families are ranked by the number of associated Blueprint diseases identified. The percentage of the total number of WHO R&D Blueprint priority diseases (n = 11) associated with each family is shown in parentheses.

|          | Order        | Family         | No. of CITES-listed species | No. of diseases | Diseases  |
|----------|--------------|----------------|-----------------------------|-----------------|---|
| Mammalia | Artiodactyla | Suidae         | 5                           | 6 (55%)         | Crimean-Congo haemorrhagic fever; Ebola virus disease (EVD); Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS); Zika virus |
|          |              | Bovidae        | 60                          | 4 (37%)         | Crimean-Congo haemorrhagic fever; Ebola virus disease (EVD); Rift Valley fever; Zika virus  |
|          |              | Camelidae      | 2                           | 2 (19%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever   |
|          |              | Giraffidae     | 1                           | 2 (19%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever   |
|          |              | Cervidae       | 13                          | 1 (10%)         | Rift Valley fever   |
|          |              | Hippopotamidae | 2                           | 1 (10%)         | Zika virus  |
|          | Carnivora    | Felidae        | 40                          | 6 (55%)         | COVID-19*; Crimean-Congo haemorrhagic fever; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS); Zika virus                 |
|          |              | Canidae        | 13                          | 4 (37%)         | Crimean-Congo haemorrhagic fever; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS)*                                       |
|          |              | Mustelidae     | 21                          | 2 (19%)         | COVID-19*; Severe Acute Respiratory Syndrome (SARS)*  |
|          |              | Viverridae     | 12                          | 2 (19%)         | Crimean-Congo haemorrhagic fever; Severe Acute Respiratory Syndrome (SARS)*   |

|                         | Order          | Family           | No. of CITES-listed species | No. of diseases | Diseases   |
|-------------------------|----------------|------------------|-----------------------------|-----------------|--|
| Mammalia<br>(continued) | Chiroptera     | Pteropodidae     | 69                          | 8 (73%)         | COVID-19*; Ebola virus disease (EVD); Hendra virus; Marburg virus disease; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS)*; Zika virus |
|                         |                | Vespertilionidae | 0                           | 6 (55%)         | Crimean-Congo haemorrhagic fever; Marburg virus disease; Middle East respiratory syndrome coronavirus (MERS-CoV)*; Nipah virus; Rift Valley fever; Zika virus    |
|                         |                | Rhinolophidae    | 0                           | 5 (46%)         | COVID-19*; Marburg virus disease; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS)*  |
|                         |                | Hipposideridae   | 0                           | 4 (37%)         | Ebola virus disease (EVD); Marburg virus disease; Nipah virus; Rift Valley fever   |
|                         |                | Molossidae       | 0                           | 3 (28%)         | Ebola virus disease (EVD); Middle East respiratory syndrome coronavirus (MERS-CoV); Zika virus   |
|                         |                | Emballonuridae   | 0                           | 1 (10%)         | Middle East respiratory syndrome coronavirus (MERS-CoV)  |
|                         |                | Nycteridae       | 0                           | 1 (10%)         | Middle East respiratory syndrome coronavirus (MERS-CoV)  |
|                         | Cingulata      | Dasypodidae      | 3                           | 1 (10%)         | Zika virus   |
|                         | Erinaceomorpha | Erinaceidae      | 0                           | 1 (10%)         | Crimean-Congo haemorrhagic fever   |
|                         | Erinaceomorpha | Soricidae        | 0                           | 1 (10%)         | Zika virus   |
|                         | Lagomorpha     | Leporidae        | 2                           | 3 (28%)         | Crimean-Congo haemorrhagic fever; Middle East respiratory syndrome coronavirus (MERS-CoV); Zika virus  |
|                         | Perissodactyla | Equidae          | 5                           | 3 (28%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever; Zika virus  |
|                         |                | Rhinocerotidae   | 5                           | 2 (19%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever  |
|                         | Pholidota      | Manidae          | 8                           | 1 (10%)         | COVID-19*  |

|                         | Order           | Family          | No. of CITES-listed species | No. of diseases | Diseases   |
|-------------------------|-----------------|-----------------|-----------------------------|-----------------|--|
| Mammalia<br>(continued) | Primates        | Cercopithecidae | 136                         | 8 (73%)         | COVID-19*; Ebola virus disease (EVD); Marburg virus disease; Middle East respiratory syndrome coronavirus (MERS-CoV)*; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS)*; Zika virus |
|                         |                 | Cebidae         | 60                          | 4 (37%)         | Middle East respiratory syndrome coronavirus (MERS-CoV)*; Nipah virus; Severe Acute Respiratory Syndrome (SARS)*; Zika virus   |
|                         |                 | Hominidae       | 6                           | 2 (19%)         | Ebola virus disease (EVD); Zika virus  |
|                         |                 | Aotidae         | 9                           | 1 (10%)         | Zika virus   |
|                         | Proboscidea     | Elephantidae    | 2                           | 3 (28%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever; Zika virus  |
|                         | Rodentia        | Muridae         | 4                           | 7 (64%)         | Crimean-Congo haemorrhagic fever; Ebola virus disease (EVD); Lassa fever; Nipah virus; Rift Valley fever; Severe Acute Respiratory Syndrome (SARS)*; Zika virus  |
|                         |                 | Cricetidae      | 0                           | 4 (37%)         | COVID-19*; Middle East respiratory syndrome coronavirus (MERS-CoV); Nipah virus; Severe Acute Respiratory Syndrome (SARS)*   |
|                         |                 | Sciuridae       | 7                           | 2 (19%)         | Crimean-Congo haemorrhagic fever; Rift Valley fever  |
|                         |                 | Anomaluridae    | 0                           | 1 (10%)         | Ebola virus disease (EVD)  |
|                         |                 | Dipodidae       | 0                           | 1 (10%)         | Crimean-Congo haemorrhagic fever   |
|                         |                 | Hystriidae      | 0                           | 1 (10%)         | Crimean-Congo haemorrhagic fever   |
|                         |                 | Nesomyidae      | 0                           | 1 (10%)         | Crimean-Congo haemorrhagic fever   |
|                         |                 | Pedetidae       | 0                           | 1 (10%)         | Crimean-Congo haemorrhagic fever   |
| Aves                    | Anseriformes    | Anatidae        | 17                          | 1 (10%)         | Zika virus   |
|                         | Charadriiformes | Scolopacidae    | 3                           | 1 (10%)         | Zika virus   |



|                     | Order            | Family            | No. of CITES-listed species | No. of diseases | Diseases                         |
|---------------------|------------------|-------------------|-----------------------------|-----------------|----------------------------------|
| Aves<br>(continued) | Ciconiiformes    | Ardeidae          | 0                           | 1 (10%)         | Zika virus                       |
|                     |                  | Threskiornithidae | 5                           | 1 (10%)         | Zika virus                       |
|                     | Coraciiformes    | Bucerotidae       | 24                          | 1 (10%)         | Crimean-Congo haemorrhagic fever |
|                     |                  | Meropidae         | 0                           | 1 (10%)         | Zika virus                       |
|                     | Passeriformes    | Cisticolidae      | 0                           | 1 (10%)         | Zika virus                       |
|                     |                  | Malaconotidae     | 0                           | 1 (10%)         | Zika virus                       |
|                     |                  | Muscicapidae      | 19                          | 1 (10%)         | Zika virus                       |
|                     |                  | Nectariniidae     | 0                           | 1 (10%)         | Zika virus                       |
|                     |                  | Ploceidae         | 0                           | 1 (10%)         | Zika virus                       |
|                     |                  | Pycnonotidae      | 1                           | 1 (10%)         | Zika virus                       |
|                     | Struthioniformes | Struthionidae     | 1                           | 1 (10%)         | Crimean-Congo haemorrhagic fever |
| Reptilia            | Sauria           | Varanidae         | 78                          | 1 (10%)         | Zika virus                       |
|                     | Squamata         | Lamprophiidae     | 0                           | 1 (10%)         | Zika virus                       |
| Amphibia            | Anura            | Ranidae           | 0                           | 1 (10%)         | Zika virus                       |

\* Note that associations between taxa and SARS-CoV, MERS-CoV and SARS-CoV-2 outlined in Anderson *et al.* (2020); Chan *et al.* 2015; Haider *et al.* (2020); Jo *et al.* (2020); Latif and Mukaratirwa (2020); Mackensie and Smith (2020); Tsan-Yuk *et al.* (2020); Ye *et al.* (2020) and Zhang *et al.* (2020) are based on percentage similarities between animal coronaviruses and human SARS-CoV, MERS-CoV and SARS CoV-2 isolates.

## Addendum Annex C. CITES-listed species directly associated with at least one WHO R&D Blueprint priority disease, according to the source papers identified by the literature search.

**Addendum Table C:** CITES-listed species directly associated with at least one WHO R&D Blueprint priority disease, according to the source papers identified by the literature search. Note that this table is not intended as a comprehensive summary of *all* CITES-listed species and their associations with WHO R&D Blueprint priority diseases, since the 70 source papers (see Addendum A) comprise a subset of the complete literature on this subject and are likely to be influenced by levels of research effort, which vary markedly between specific taxa and diseases. “✓” symbols denote whether a taxon was present in live CITES trade over the period 2011–2020, or whether live specimens were detected in illegal trade, based on the TRAFFIC, US and UK seizure datasets which were analysed.

| Group    | Order        | Family         | Taxon                         | Common name          | No. of diseases | Diseases  | CITES legal trade | Illegal trade |
|----------|--------------|----------------|-------------------------------|----------------------|-----------------|---|-------------------|---------------|
| Mammalia | Artiodactyla | Bovidae        | <i>Bubalus arnee</i>          | Wild Asiatic Buffalo | 3               | Crimean-Congo haemorrhagic fever; Rift Valley fever; Zika virus             |                   |               |
|          |              |                | <i>Cephalophus dorsalis</i>   | Bay Duiker           | 1               | Ebola virus disease (EVD)   |                   |               |
|          |              |                | <i>Damaliscus pygargus</i>    | Blesbok              | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever                         | ✓                 |               |
|          |              |                | <i>Hippotragus niger</i>      | Sable Antelope       | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever                         | ✓                 | ✓             |
|          |              | Cervidae       | <i>Dama dama</i>              | Fallow Deer          | 1               | Rift Valley fever   | ✓                 | ✓             |
|          |              |                | <i>Odocoileus virginianus</i> | White-tailed deer    | 1               | Rift Valley fever   |                   | ✓             |
|          |              | Giraffidae     | <i>Giraffa camelopardalis</i> | Giraffe              | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever                         | ✓                 |               |
|          |              | Hippopotamidae | <i>Hippopotamus amphibius</i> | Hippopotamus         | 1               | Zika virus  | ✓                 | ✓             |
|          | Carnivora    | Canidae        | <i>Canis lupus</i>            | Common Wolf          | 1               | Crimean-Congo haemorrhagic fever  | ✓                 | ✓             |
|          |              |                | <i>Vulpes vulpes</i>          | Red Fox              | 2               | Crimean-Congo haemorrhagic fever; Severe Acute Respiratory Syndrome (SARS)* |                   | ✓             |
|          |              | Felidae        | <i>Acinonyx jubatus</i>       | Cheetah              | 1               | Rift Valley fever   | ✓                 | ✓             |

| Group                | Order                 | Family              | Taxon                          | Common name                | No. of diseases | Diseases                                  | CITES legal trade | Illegal trade |
|----------------------|-----------------------|---------------------|--------------------------------|----------------------------|-----------------|---|-------------------|---------------|
| Mammalia (continued) | Carnivora (continued) | Felidae (continued) | <i>Otocolobus manul</i>        | Pallas's Cat               | 1               | Crimean-Congo haemorrhagic fever          | ✓                 |               |
|                      |                       |                     | <i>Panthera leo</i>            | Lion                       | 3               | COVID-19*; Rift Valley fever; Zika virus  | ✓                 | ✓             |
|                      |                       |                     | <i>Panthera tigris</i>         | Tiger                      | 1               | COVID-19*                                 | ✓                 | ✓             |
|                      |                       | Viverridae          | <i>Paguma larvata</i>          | Masked Palm Civet          | 1               | Severe Acute Respiratory Syndrome (SARS)* |                   | ✓             |
|                      | Chiroptera            | Pteropodidae        | <i>Pteropus admiralitatum</i>  | Admiralty Flying-fox       | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus alecto</i>         | Black Flying-fox           | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus capistratus</i>    | Bismarck Masked Flying-fox | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus conspicillatus</i> | Spectacled Flying-fox      | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus giganteus</i>      | Indian Flying-fox          | 1               | Nipah virus                               | ✓                 |               |
|                      |                       |                     | <i>Pteropus hypomelanus</i>    | Small Flying-fox           | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus lylei</i>          | Lyle's Flying-fox          | 1               | Nipah virus                               | ✓                 | ✓             |
|                      |                       |                     | <i>Pteropus neohibernicus</i>  | Bismarck Flying-fox        | 2               | Hendra virus; Nipah virus                 |                   |               |
|                      |                       |                     | <i>Pteropus poliocephalus</i>  | Grey-headed Flying-fox     | 2               | Hendra virus; Nipah virus                 | ✓                 |               |
|                      |                       |                     | <i>Pteropus rufus</i>          | Madagascar Flying-fox      | 2               | Hendra virus; Nipah virus                 |                   |               |

| Group                | Order                  | Family                   | Taxon                      | Common name                   | No. of diseases | Diseases  | CITES legal trade | Illegal trade |
|----------------------|------------------------|--------------------------|----------------------------|-------------------------------|-----------------|---|-------------------|---------------|
| Mammalia (continued) | Chiroptera (continued) | Pteropodidae (continued) | <i>Pteropus scapulatus</i> | Little Red Flying-fox         | 1               | Hendra virus  |                   |               |
|                      |                        |                          | <i>Pteropus vampyrus</i>   | Large Flying-fox              | 1               | Nipah virus   | ✓                 |               |
|                      | Perissodactyla         | Equidae                  | <i>Equus africanus</i>     | African Ass                   | 1               | Crimean-Congo haemorrhagic fever  | ✓                 |               |
|                      |                        |                          | <i>Equus grevyi</i>        | Grevy's Zebra                 | 1               | Zika virus  | ✓                 |               |
|                      |                        |                          | <i>Equus zebra</i>         | Mountain zebra                | 1               | Zika virus  | ✓                 | ✓             |
|                      |                        | Rhinocerotidae           | <i>Ceratotherium simum</i> | White Rhinoceros              | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever   | ✓                 |               |
|                      |                        |                          | <i>Diceros bicornis</i>    | Black Rhinoceros              | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever   | ✓                 |               |
|                      | Pholidota              | Manidae                  | <i>Manis javanica</i>      | Malayan Pangolin              | 1               | COVID-19*   | ✓                 | ✓             |
|                      | Primates               | Aotidae                  | <i>Aotus nancymae</i>      | Ma's Night Monkey             | 1               | Zika virus  | ✓                 |               |
|                      |                        | Cebidae                  | <i>Callithrix jacchus</i>  | Common Marmoset               | 3               | Middle East respiratory syndrome coronavirus (MERS-CoV)*; Severe Acute Respiratory Syndrome (SARS)*; Zika virus | ✓                 | ✓             |
|                      |                        |                          | <i>Cebus libidinosus</i>   | Black-striped Tufted Capuchin | 1               | Zika virus  | ✓                 |               |
|                      |                        |                          | <i>Saimiri boliviensis</i> | Black-headed Squirrel Monkey  | 1               | Zika virus  | ✓                 |               |
|                      |                        |                          | <i>Saimiri sciureus</i>    | Common Squirrel Monkey        | 1               | Nipah virus   | ✓                 | ✓             |

| Group                | Order                | Family          | Taxon                          | Common name                      | No. of diseases | Diseases  | CITES legal trade | Illegal trade |
|----------------------|----------------------|-----------------|--------------------------------|----------------------------------|-----------------|---|-------------------|---------------|
| Mammalia (continued) | Primates (continued) | Cercopithecidae | <i>Cercocebus torquatus</i>    | Collared Mangabey                | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Cercopithecus ascanius</i>  | Black-cheeked White-nosed Monkey | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Cercopithecus mona</i>      | Mona Monkey                      | 1               | Zika virus  | ✓                 |               |
|                      |                      |                 | <i>Cercopithecus neglectus</i> | De Brazza's Monkey               | 1               | Ebola virus disease (EVD)   | ✓                 | ✓             |
|                      |                      |                 | <i>Cercopithecus nictitans</i> | Greater White-nosed Monkey       | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Chlorocebus aethiops</i>    | Grivet Monkey                    | 3               | Marburg virus disease; Nipah virus; Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Chlorocebus sabaeus</i>     | Green Monkey                     | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Colobus guereza</i>         | Eastern Black-and-white Colobus  | 1               | Zika virus  | ✓                 |               |
|                      |                      |                 | <i>Erythrocebus patas</i>      | Patas Monkey                     | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                 | <i>Lophocebus albigena</i>     | Grey-cheeked Mangabey            | 1               | Zika virus  | ✓                 |               |
|                      |                      |                 | <i>Macaca fascicularis</i>     | Crab-eating Macaque              | 5               | COVID-19*; Ebola virus disease (EVD); Middle East respiratory syndrome coronavirus (MERS-CoV)*; Severe Acute Respiratory Syndrome (SARS)*; Zika virus | ✓                 | ✓             |
|                      |                      |                 | <i>Macaca mulatta</i>          | Rhesus Macaque                   | 4               | COVID-19*; Middle East respiratory syndrome coronavirus (MERS-CoV)*; Rift Valley fever; Zika virus  | ✓                 | ✓             |

| Group                | Order                | Family                      | Taxon                         | Common name                | No. of diseases | Diseases  | CITES legal trade | Illegal trade |
|----------------------|----------------------|-----------------------------|-------------------------------|----------------------------|-----------------|---|-------------------|---------------|
| Mammalia (continued) | Primates (continued) | Cercopithecidae (continued) | <i>Macaca nemestrina</i>      | Pig-tailed Macaque         | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                             | <i>Mandrillus leucophaeus</i> | Drill                      | 1               | Ebola virus disease (EVD)                           | ✓                 | ✓             |
|                      |                      |                             | <i>Mandrillus sphinx</i>      | Mandrill                   | 1               | Ebola virus disease (EVD)                           | ✓                 | ✓             |
|                      |                      |                             | <i>Papio anubis</i>           | Anubis Baboon              | 2               | Ebola virus disease (EVD); Zika virus               | ✓                 | ✓             |
|                      |                      |                             | <i>Papio cynocephalus</i>     | Yellow Baboon              | 1               | Zika virus  | ✓                 |               |
|                      |                      | Hominidae                   | <i>Gorilla gorilla</i>        | Gorilla                    | 1               | Ebola virus disease (EVD)                           | ✓                 |               |
|                      |                      |                             | <i>Pan troglodytes</i>        | Chimpanzee                 | 1               | Ebola virus disease (EVD)                           | ✓                 | ✓             |
|                      |                      |                             | <i>Pongo abelii</i>           | Sumatran Orangutan         | 1               | Zika virus  | ✓                 | ✓             |
|                      |                      |                             | <i>Pongo pygmaeus</i>         | Bornean Orangutan          | 1               | Zika virus  | ✓                 | ✓             |
|                      | Proboscidea          | Elephantidae                | <i>Loxodonta africana</i>     | African Elephant           | 2               | Crimean-Congo haemorrhagic fever; Rift Valley fever | ✓                 |               |
| Aves                 | Struthioniformes     | Struthionidae               | <i>Struthio camelus</i>       | Ostrich                    | 1               | Crimean-Congo haemorrhagic fever                    | ✓                 | ✓             |
| Reptilia             | Sauria               | Varanidae                   | <i>Varanus niloticus</i>      | African Small-grain Lizard | 1               | Zika virus  | ✓                 | ✓             |

\* Note that associations between taxa and SARS-CoV, MERS-CoV and SARS-CoV-2 outlined in Anderson *et al.* (2020); Chan *et al.* 2015; Haider *et al.* (2020); Jo *et al.* (2020); Latif and Mukaratirwa (2020); Mackensie and Smith (2020); Tsan-Yuk *et al.* (2020); Ye *et al.* (2020) and Zhang *et al.* (2020) are based on percentage similarities between animal coronaviruses and human SARS-CoV, MERS-CoV and SARS CoV-2 isolates.

## Addendum Annex D: Overview of live trade in CITES families associated with at least one WHO R&D Blueprint priority disease.

**Addendum Table D1:** Overview of live trade in CITES families (defined as a taxonomic family that contains one or more CITES-listed species) associated with at least one WHO R&D Blueprint priority disease. The number of transactions encompasses the total number of live animal shipments reported by (re-)exporters between 2011–2020 regardless of unit; while the vast majority of trade was reported in terms of the number of individuals or items that can be equated to one individual, a small amount of trade in live animals was reported in terms of weight. Details for trade in live animals reported by weight are shown in table D2. Families are ranked in order of the overall quantity of live individuals in trade. Trading partners are denoted by ISO 3166-1 alpha-2 codes and are only included when they account for > 5% trade. Source code definitions are given in table D3.

| Group    | Order     | Family          | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source  | Exporters   | Importers   | Taxa  |
|----------|-----------|-----------------|-----------------|-----------------------------|---|---|---|---|---|
| Reptiles | Sauria    | Varanidae       | 1               | 14,275                      | 551,826   | W (49.9%);<br>R (34.9%);<br>C (8.2%);<br>F (5.5%) | TG (28.4%);<br>ID (24.1%);<br>GH (22.3%);<br>BJ (14.6%) | US (56.4%);<br>JP (8.7%)  | <i>Varanus exanthematicus</i> (53.1%);<br><i>Varanus salvator</i> (17.1%) |
| Mammals  | Primates  | Cercopithecidae | 8               | 6,659                       | 482,406   | C (70.2%);<br>F (25.3%)                           | CN (39.4%);<br>KH (21.8%);<br>MU (19.7%);<br>VN (11.4%) | US (55.9%);<br>JP (12.4%);<br>CN (7.4%);<br>ES (5.1%);<br>FR (5.1%) | <i>Macaca fascicularis</i> (90.6%);<br><i>Macaca mulatta</i> (4.7%)       |
| Mammals  | Primates  | Cebidae         | 4               | 2,433                       | 30,279  | C (57.3%);<br>W (40.4%)                           | ZA (49.2%);<br>GY (32.2%);<br>SR (8.5%)                 | CN (32.3%);<br>TH (15.7%);<br>BD (11.4%);<br>US (11.3%)             | <i>Saimiri sciureus</i> (31.3%);<br><i>Callithrix jacchus</i> (30.9%)     |
| Mammals  | Carnivora | Felidae         | 6               | 5,662                       | 12,707  | C (83.6%);<br>W (7.9%);<br>F (5.1%)               | ZA (43.3%);<br>US (9.5%);<br>RU (5.1%)                  | CN (14%);<br>US (8.7%);<br>CA (7.1%)                                | <i>Panthera leo</i> (30.1%);<br><i>Panthera tigris</i> (15.2%)            |



| Group   | Order          | Family            | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source                              | Exporters   | Importers  | Taxa  |
|---------|----------------|-------------------|-----------------|-----------------------------|---|-------------------------------------|---|--|---|
| Mammals | Artiodactyla   | Bovidae           | 4               | 1,094                       | 10,670  | C (39.8%);<br>F (33%);<br>W (23.1%) | ZA (44.3%);<br>AE (28.7%);<br>SD (8.2%)             | NA (41.9%);<br>QA (16.4%);<br>SA (8.1%);<br>AE (5.7%)                              | <i>Kobus leche</i> (43.7%);<br><i>Oryx leucoryx</i> (23.4%)                     |
| Mammals | Carnivora      | Canidae           | 4               | 575                         | 6,247   | C (55.4%);<br>W (41.9%)             | SD (83.8%)  | CN (24.8%);<br>TH (15.7%);<br>AE (10.5%);<br>US (9.9%);<br>KR (5.6%);<br>MY (5.1%) | <i>Vulpes zerda</i> (90.5%);<br><i>Canis lupus</i> (7.9%)                       |
| Birds   | Coraciiformes  | Bucerotidae       | 1               | 184                         | 4,135   | I (60.6%);<br>W (24.9%);<br>C (12%) | MY (62.2%);<br>SB (23.9%);<br>PH (5.5%)             | ID (60.6%);<br>Various (9.8%);<br>OM (6.1%)  | <i>Rhyticeros plicatus</i> (85.3%);<br><i>Buceros hydrocorax</i> (2.5%)         |
| Birds   | Anseriformes   | Anatidae          | 1               | 363                         | 3,731   | C (93.8%);<br>Unspecified (5.5%)    | NL (75.9%);<br>BE (10.8%);<br>ML (5.4%)             | CN (22.2%);<br>AE (13.7%);<br>MY (10.6%);<br>BD (8.1%);<br>TH (7.5%)               | <i>Cygnus melancoryphus</i> (63.5%);<br><i>Branta ruficollis</i> (16.3%)        |
| Birds   | Ciconiiformes  | Threskiornithidae | 1               | 291                         | 3,236   | C (84.2%);<br>Unspecified (12.8%)   | NL (55.8%);<br>ML (10.4%);<br>BE (7.8%);<br>ZA (7%) | CN (29.9%);<br>ML (11.5%);<br>AE (11.5%);<br>TH (7.4%)                             | <i>Eudocimus ruber</i> (91.8%);<br><i>Geronticus eremita</i> (6.8%)             |
| Mammals | Perissodactyla | Rhinocerotidae    | 2               | 443                         | 2,012   | W (77.2%);<br>C (12.3%)             | ZA (83.6%)  | NA (42.8%);<br>BW (11.2%);<br>CN (10.8%)   | <i>Ceratotherium simum simum</i> (50.1%);<br><i>Ceratotherium simum</i> (36.6%) |

| Group   | Order         | Family       | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source                                | Exporters  | Importers  | Taxa  |
|---------|---------------|--------------|-----------------|-----------------------------|---|---------------------------------------|--|--|---|
| Birds   | Passeriformes | Muscicapidae | 1               | 40                          | 1,839   | C (99.3%)                             | MY (87.5%)   | ID (87%)   | <i>Garrulax canorus</i> (88.2%);<br><i>Leiothrix lutea</i> (7.2%)       |
| Mammals | Chiroptera    | Pteropodidae | 8               | 114                         | 1,590   | W (87.2%);<br>C (11.5%)               | ID (86.2%)   | CN (26.4%);<br>NL (16.8%);<br>IT (14.7%);<br>US (12.5%);<br>KO (5.4%)            | <i>Pteropus vampyrus</i> (86.5%);<br><i>Pteropus rodricensis</i> (3.8%) |
| Mammals | Carnivora     | Mustelidae   | 2               | 559                         | 1,320   | C (59.1%);<br>F (19.7%);<br>W (16.6%) | US (17.8%);<br>CA (9.7%);<br>GY (8.2%);<br>ID (7.7%);<br>TZ (7.6%);<br>RU (6.3%);<br>NL (6%) | US (18.6%);<br>CA (12.1%);<br>JP (11.4%);<br>CN (9%);<br>UZ (7.8%);<br>KR (7.3%) | <i>Aonyx cinerea</i> (46.1%);<br><i>Mustela nigripes</i> (19.5%)        |
| Mammals | Pholidota     | Manidae      | 1               | 54                          | 1,276   | W (98.9%)                             | TG (57.7%);<br>NG (39.2%)  | CN (40%);<br>LA (23.5%);<br>VN (15.7%);<br>US (9.8%)                             | <i>Manis tricuspis</i> (67.6%);<br><i>Manis tetradactyla</i> (17.2%)    |
| Mammals | Proboscidea   | Elephantidae | 3               | 303                         | 918   | W (66.3%);<br>C (24.9%)               | ZW (24.8%);<br>ZA (15.8%);<br>LA (13.9%);<br>CN (8.8%);<br>Unknown (8.4%)                    | MZ (28.6%);<br>CN (27.1%);<br>AE (9.2%)  | <i>Loxodonta africana</i> (62.1%);<br><i>Elephas maximus</i> (29%)      |

| Group   | Order            | Family         | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source  | Exporters  | Importers  | Taxa   |
|---------|------------------|----------------|-----------------|-----------------------------|---|---|--|--|--|
| Mammals | Carnivora        | Viverridae     | 2               | 135                         | 875   | W (57.1%);<br>Unspecified (20.2%);<br>C (19.2%)   | ID (51%);<br>TG (22.4%)  | KO (17.1%);<br>IT (15%);<br>NL (14.5%);<br>JP (10.7%);<br>US (10.6%);<br>GH (6.9%);<br>GB (6.6%) | <i>Paradoxurus hermaphroditus</i> (42.2%);<br><i>Civettictis civetta</i> (36.5%) |
| Mammals | Primates         | Hominidae      | 2               | 271                         | 503   | C (73.2%);<br>F (12.7%);<br>W (6.2%);<br>I (5.4%) | SY(10.3%);<br>US (7.4%);<br>DE (6.6%);<br>ZA (5.8%);<br>RU (5.8%)                  | CN (20.3%);<br>UA (6.6%);<br>RU (5.4%)   | <i>Pan troglodytes</i> (61.4%);<br><i>Pongo pygmaeus</i> (16.1%)                 |
| Birds   | Struthioniformes | Struthionidae  | 1               | 13                          | 481   | C (74%);<br>W (9.1%);<br>R (7.3%);<br>I (5.2%)    | Unknown (70.3%);<br>NG (8.3%);<br>US (6.2%);<br>NE (5.6%)                          | SD (66.5%);<br>NE (13.7%);<br>TT (6.4%)  | <i>Struthio camelus</i> (96%);<br><i>Struthio</i> spp. (4%)                      |
| Mammals | Perissodactyla   | Equidae        | 3               | 145                         | 297   | C (71.7%);<br>F (12.8%);<br>W (11.1%)             | US (22.2%);<br>CH (14.8%);<br>HU (13.1%);<br>ZA (9.8%);<br>CZ (9.4%);<br>FR (5.4%) | RU (20.2%);<br>MX (14.5%);<br>MN (6.7%);<br>CN (6.1%);<br>FR (5.4%)                              | <i>Equus przewalskii</i> (39.7%);<br><i>Equus grevyi</i> (26.6%)                 |
| Mammals | Artiodactyla     | Hippopotamidae | 1               | 126                         | 270   | W (47.8%);<br>C (43.3%);<br>R (7.4%)              | ZA (42.6%);<br>SZ (13.3%);<br>BJ (6.7%)  | NA (24.8%);<br>FR (8.1%);<br>Unknown (7.4%);<br>CN (7%);<br>ZA (5.9%)                            | <i>Hippopotamus amphibius</i> (80%);<br><i>Hexaprotodon liberiensis</i> (17.8%)  |

| Group   | Order         | Family       | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source                              | Exporters  | Importers  | Taxa  |
|---------|---------------|--------------|-----------------|-----------------------------|---|-------------------------------------|--|--|---|
| Mammals | Artiodactyla  | Cervidae     | 1               | 40                          | 227   | C (90.3%);<br>F (5.7%)              | AZ (42.3%);<br>CL (9.7%);<br>KW (8.8%);<br>EE (7.5%);<br>DE (6.2%);<br>SG (5.3%)                 | UZ (41.9%);<br>IL (9.7%);<br>KO (8.8%);<br>CH (7%);<br>AR (7%);<br>PH (5.3%)                   | <i>Dama dama</i> (33%);<br><i>Cervus elaphus</i> (22.5%)          |
| Mammals | Primates      | Aotidae      | 1               | 101                         | 150   | C (90.7%);<br>F (9.3%)              | PE (72%);<br>CH (18.7%);<br>ZA (5.3%)  | CN (38.7%);<br>TH (16.7%);<br>NL (11.3%);<br>GB (6.7%);<br>MY (6%);<br>BG (5.3%);<br>ID (5.3%) | <i>Aotus vociferans</i> (35.3%);<br><i>Aotus nancymae</i> (33.3%) |
| Mammals | Artiodactyla  | Giraffidae   | 2               | 3                           | 129   | W (98.4%)                           | ZA (95.3%)   | TH (60.5%);<br>US (34.9%)  | <i>Giraffa camelopardalis</i> (100%)                              |
| Mammals | Artiodactyla  | Camelidae    | 2               | 74                          | 126   | C (80.2%);<br>I (9.5%);<br>F (6.3%) | CH (17.5%);<br>CA (15.9%);<br>RU (11.1%);<br>DE (9.5%);<br>FR (6.3%);<br>CZ (6.3%);<br>GR (5.6%) | US (11.1%);<br>TT (9.5%);<br>TR (8.7%);<br>UA (7.9%);<br>RU (7.1%);<br>DE (7.1%);<br>SA (5.6%) | <i>Vicugna vicugna</i> (51.6%);<br><i>Lama guanicoe</i> (46.8%)   |
| Mammals | Rodentia      | Sciuridae    | 2               | 6                           | 52  | C (59.6%);<br>F (40.4%)             | ID (86.5%);<br>LK (13.5%)  | AE (63.5%);<br>CZ (11.5%);<br>DE (11.5%);<br>SK (11.5%)  | <i>Ratufa affinis</i> (86.5%);<br><i>Ratufa macroura</i> (13.5%)  |
| Birds   | Passeriformes | Pycnonotidae | 1               | 2                           | 46  | W (93.5%);<br>C (6.5%)              | MY (100%)  | KW (100%)  | <i>Pycnonotus zeylanicus</i> (100%)                               |

| Group   | Order        | Family      | No. of diseases | No. of exp-rep transactions | No. individuals / items that can be equated to one individual | Source                  | Exporters                 | Importers  | Taxa                                 |
|---------|--------------|-------------|-----------------|-----------------------------|---|-------------------------|---------------------------|--|--------------------------------------|
| Mammals | Lagomorpha   | Leporidae   | 3               | 4                           | 20  | C (100%)                | MX (100%)                 | JP (100%)  | <i>Romerolagus diazi</i> (100%)      |
| Mammals | Artiodactyla | Suidae      | 6               | 5                           | 17  | F (64.7%);<br>C (35.3%) | US (88.2%);<br>CA (11.8%) | MX (35.3%);<br>CA (23.5%);<br>DE (11.8%);<br>GB (11.8%);<br>US (11.8%);<br>CZ (5.9%) | <i>Babyrousa celebensis</i> (100%)   |
| Mammals | Cingulata    | Dasypodidae | 1               | -                           | 3   | W (100%)                | Unknown (100%)            | BO (100%)  | <i>Chaetophractus nationi</i> (100%) |

**Addendum Table D2:** Overview of live trade in CITES families associated with at least one WHO R&D Blueprint priority disease, for trade reported by weight (in kg), 2011–2020. Families are ranked in order of the overall quantity by weight (kg). Trading partners are denoted by ISO 3166-1 alpha-2 codes.

| Group   | Order       | Family          | No. of diseases | Quantity (kg) | Source   | Exporters | Importers  | Taxa                              |
|---------|-------------|-----------------|-----------------|---------------|----------|-----------|------------|-----------------------------------|
| Mammals | Carnivora   | Mustelidae      | 2               | 24            | U (100%) | CN (100%) | DE (100%)  | <i>Mustela sibirica</i> (100%)    |
| Mammals | Primates    | Cercopithecidae | 8               | 14            | C (100%) | CN (100%) | US (90.9%) | <i>Macaca fascicularis</i> (100%) |
| Mammals | Carnivora   | Viverridae      | 2               | 2             | C (100%) | CU (100%) | NL (100%)  | <i>Arctictis binturong</i> (100%) |
| Mammals | Carnivora   | Felidae         | 6               | 0             | C (100%) | BR (100%) | AR (100%)  | <i>Panthera onca</i> (100%)       |
| Mammals | Proboscidea | Elephantidae    | 3               | 0             | W (100%) | KE (100%) | US (100%)  | <i>Loxodonta africana</i> (100%)  |

**Addendum Table D3:** CITES source code definitions.

| Code | Description   |
|------|---|
| W    | Specimens taken from the wild   |
| R    | Ranched specimens: specimens of animals reared in a controlled environment, taken as eggs or juveniles from the wild, where they would otherwise have had a very low probability of surviving to adulthood  |
| D    | Appendix-I animals bred in captivity for commercial purposes in operations included in the Secretariat's Register, in accordance with Resolution Conf. 12.10 (Rev. CoP15), and Appendix-I plants artificially propagated for commercial purposes, as well as parts and derivatives thereof, exported under the provisions of Article VII, paragraph 4, of the Convention        |
| A    | Plants that are artificially propagated in accordance with Resolution Conf. 11.11 (Rev. CoP18), as well as parts and derivatives thereof, exported under the provisions of Article VII, paragraph 5 (specimens of species included in Appendix I that have been propagated artificially for non-commercial purposes and specimens of species included in Appendices II and III) |
| C    | Animals bred in captivity in accordance with Resolution Conf. 10.16 (Rev.), as well as parts and derivatives thereof, exported under the provisions of Article VII, paragraph 5   |
| F    | Animals born in captivity (F1 or subsequent generations) that do not fulfil the definition of 'bred in captivity' in Resolution Conf. 10.16 (Rev.), as well as parts and derivatives thereof  |
| I    | Confiscated or seized specimens (may be used with another code)   |
| O    | Pre-Convention specimens  |
| U    | Source unknown  |
| X    | Specimens taken in "the marine environment not under the jurisdiction of any State"   |
| Y    | Specimens of plants that fulfil the definition for 'assisted production' in Resolution Conf. 11.11 (Rev. CoP18) as well as parts and derivatives thereof  |