# **REVIEW ARTICLE**

# Potential Pathogens Reported in Species of the Family Viverridae and Their Implications for Human and Animal Health

L. V. Wicker<sup>1,2</sup>, P. J. Canfield<sup>1</sup> and D. P. Higgins<sup>1</sup>

<sup>1</sup> Faculty of Veterinary Science, The University of Sydney, Sydney, NSW 2006, Australia

<sup>2</sup> Save Vietnam's Wildlife, Cuc Phuong National Park, Ninh Binh, Vietnam

## Impacts

- First collation of previously published organisms isolated from species of the family Viverridae provides baseline information to assist viverrid population management.
- Summarizes anthropogenic factors (trade, farming, encroachment on viverrid habitat) bringing viverrids into proximity with humans.
- Discusses detected organisms in terms of potential risk for public health given the described anthropogenic factors which facilitate transmission and spillover of organisms between and amongst animals and people.

#### Keywords:

Viverridae; Zoonosis; Wildlife trade Public health; Civet; Genet

#### Correspondence:

L. V. Wicker. Faculty of Veterinary Science, The University of Sydney, Sydney, NSW 2006, Australia and Save Vietnam's Wildlife, Cuc Phuong National Park, Ninh Binh, Vietnam. Tel.: +61 4868828360; E-mail: leannevwicker@gmail.com

Institution/place where work was carried out: Faculty of Veterinary Science, The University of Sydney, 2006, Australia.

Received for publication October 23, 2015

doi: 10.1111/zph.12290

# Introduction

The family Viverridae is a diverse group of small, nocturnal carnivores, including 34 species of civet, genet and African linsang distributed across Southern Europe, Africa and Asia (Wilson and Reeder, 2005). Viverrids are commonly exploited for human consumption, being farmed and hunted for their fur, meat, 'civet' scent, to produce civet coffee, or to be kept as zoo animals or pets (Schreiber et al., 1989; Balakrishnan and Sreedevi, 2007; Shepherd and Shepherd, 2010; D'Cruze et al., 2014). While habitat loss has contributed to historical population declines, hunting for human consumption is considered the most significant

Summary

The Viverridae is a family of nocturnal carnivores including civets, genets and African linsangs. While a list of known organisms isolated from a species is an essential tool for population management, this review represents the first attempt to collate published reports of organisms isolated from viverrids. A wide range of organisms, including 11 viruses, eight bacterial species, one internal arthropod species, representatives from eight genera of protozoan, 21 genera of nematode, seven genera of cestode, eight genera of trematode and six genera of external arthropod (mites, ticks and louse), have been reported in literature spanning over a century of research. Many of these are capable of infecting multiple hosts, including humans. This is of concern given the anthropogenic factors that bring humans and domestic species into close contact with viverrids, facilitating transmission and spillover of organisms between groups. These factors include trade in viverrids for human consumption, captive management in zoos, rescue centres or on commercial breeding farms, and the increasing overlap of free-ranging viverrid distribution and human settlement.

threat to their global conservation (Schreiber et al., 1989; Shepherd and Shepherd, 2010).

An inventory of organisms known to be associated with a particular species is considered essential baseline information for species management (Munson, 1991). This information guides rational development of husbandry protocols for captive populations (Hope and Deem, 2006), facilitates design of surveillance programmes to investigate change in species disease profiles over time (Lonsdorf et al., 2006) and highlights the threatening role infectious diseases might play in endangered species management (Gilbert et al., 2014). Given the potential for transmission of diseases between wildlife, humans and livestock (Jones et al., 2008), a complete list of pathogens and indigenous microflora also enables evidence-based risk assessment of human and animal contact with the species in question (Travis et al., 2006).

No attempt has yet been made to collate the current knowledge of potential pathogens detected from species within the family Viverridae (Shepherd, 2008; Bongiovanni et al., 2014) despite the family's long history of exploitation for human consumption (Abebe, 2003; Shepherd and Shepherd, 2010), the management of threatened viverrids for conservation (Roberton et al., 2002), the peri-urban habitation of many species within the family (King et al., 1993; Ninomiya et al., 2003; Sato et al., 2013) and their susceptibility to a number of important zoonotic pathogens including the novel coronavirus responsible for the outbreak of severe acute respiratory syndrome (SARS) (Guan et al., 2003; Tu, 2004), rabies virus (Matsumoto et al., 2011) and highly pathogenic avian influenza H5N1 (HPAI H5N1) (Roberton et al., 2006). While many organisms have been identified in a very wide range of viverrid species globally, this information is scattered throughout the scientific and grey literature. An accessible list of organisms isolated from viverrids does not currently exist.

This review represents the first collation of currently recognized organisms isolated from the Viverridae, derived from an extensive and intensive assessment of the literature. In doing so, it expands on our understanding of viverrid health and the key epidemiological factors of infectious disease involving free living and captive wildlife. More importantly, this review assesses the significance of isolation of organisms from viverrids in terms of the implications for public health. Anthropogenic factors including wildlife trade, the keeping of viverrids in captivity and land use change all encourage increased contact between viverrids and other species, thereby facilitating the transmission and spillover of these organisms between humans, viverrids and other animals.

## **Methodologies and their Limitations**

A systematic review of the scientific literature resulted in this first collation of all organisms previously reported for species from the carnivorous family Viverridae. All available fields of the databases Google scholar, Web of Science, PubMed and Scopus were searched using all possible combinations of the following key terms: 'viverrid\*' or 'civet' or 'linsang' or 'binturong' or 'genetta' (the scientific name for the genus Genetta was used to reduce the number of papers on 'genetics' returned by the search), AND 'disease' or 'pathogen' or 'vir\*' (to locate both virus and viral) or 'bacteria\*' (to locate both bacteria and bacterial) or 'parasit\*' (to locate parasite or parasitic) or 'fung\*' (to locate both fungus and fungal). No limitations were placed on date of

While this review resulted in important baseline information, a number of limitations are acknowledged. It is undoubtedly incomplete as many more reports are likely to exist in the medical records of zoos and rescue centres that hold viverrids, unavailable to a database literature review. Inaccuracies are also likely included due to the reliance on traditional approaches to identification, such as descriptions of morphology (Nadler and De Leon, 2011). Increased availability of molecular methods has significantly improved accuracy in the detection and identification of organisms (Bhadury et al., 2008; Thompson et al., 2009), resulting in a revision of numerous taxonomic trees (Brown-Elliott et al., 2006; Balajee et al., 2009). Future research may find some organisms listed here no longer considered valid species, and advancing molecular techniques mean that future revision of this list of recognized organisms of Viverridae are inevitable.

## Results

A total of 98 peer-reviewed publications reported the identification of organisms from species within the family Viverridae. These included 10 viruses, eight bacterial species, a single internal arthropod species and representatives from 21 genera of nematode, seven genera of cestode, eight genera of trematode, six genera of external arthropod, and eight genera of protozoan, many of which were not identified to species level. These organisms are presented in detail in Tables 1-7.

Of the ten viruses reported for Viverridae (Table 1), three were zoonoses of considerable public health significance. These were the SARS coronavirus (SARS CoV) (Guan et al., 2003; Poon et al., 2005); HPAI H5N1 (Roberton et al., 2006; Wu et al., 2013) and a number of variants of the rabies virus (Enurah et al., 1988a; Wilde et al., 1991; Tremlett et al., 1994; Nel et al., 2005; Susetya et al., 2008; Pfukenyi et al., 2009; Matsumoto et al., 2011). Three important viruses of domestic carnivores were also reported, including canine distemper virus (CDV) (Machida et al., 1992; Hur et al., 1999; Chandra et al., 2000; López-Peña et al., 2001; Hirama et al., 2004; Chen et al., 2007; Takayama et al., 2009), feline parvovirus (caused by the feline panleukopenia virus, FPV) (Ikeda et al., 1999; Demeter et al., 2009) and canine parvovirus (CP) (Santos et al., 2009; Xiao-Ying et al., 2011; Duarte et al., 2013). In more recent years, the use of advanced molecular techniques has enabled the identification of five novel viruses of uncertain significance. These were an orthoreovirus (mammalian reovirus MPC/04) isolated

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Virus	Viverrid Species affected	Clinical signs in viverrids	Country (source)	References
Family Coronaviridae Severe acute respiratory syndrome coronavirus <sup>2,M</sup>	Masked palm civet (Paguma larvata)	Lethargy, reduced aggression, diarrhoea, conjunctivitis	China (market, farm, restaurant)	(Guan et al., 2003; Tu, 2004; Kan et al., 2005; Wu et al., 2005; Wang and Eaton, 2007)
Family Orthomyxoviridae Highly pathogenic avian influenza virus H5N1 <sup>2,M</sup>	Owston's civet ( <i>Chrotogale owstoni</i> ), Palm civet (species unknown)	Lethargy, neurological signs (circling, ataxia, dysphagia, blindness, deafness), loss of appetite, death	Vietnam, China (rescue centre, unknown)	(Roberton et al., 2006; Wu et al., 2013)
Family Rhabdoviridae Rabies virus <sup>z.M</sup>	African civet ( <i>Civettictis civetta</i> ), Common genet ( <i>Genetta genetta</i> ), Small-toothed palm civet ( <i>Arctogalidia trivirgata</i> ), Small Indian civet ( <i>Viverricula indica</i> ), Golden palm civet ( <i>Paradoxurus zevlonensis</i> )	Neurological signs, loss of appetite	Botswana, Zimbabwe, Namibia, South Africa, Nigeria, Thailand, Indonesia, Sri Lanka (wild, zoo)	(Enurah et al., 1988a; Wilde et al., 1991; Tremlett et al., 1994; Nel et al., 2005; Susetya et al., 2008b; Pfukenyi et al., 2009; Matsumoto et al., 2011)
Ikoma lyssavirus Family Paramyxoviridae	African civet	Neurological signs	Tanzania (wild)	(Marston et al., 2012)
Canine distemper virus <sup>M</sup>	Binturong ( <i>Arctictis binturong</i> ), Masked palm civet, Common palm civet ( <i>Paradoxurus hermaphroditus</i> ), Small Indian civet, Common genet	Depression, dyspnoea, coughing, oculonasal discharge, gastrointestinal signs, dehydration, neurological signs, foot pad hvoerkeratosis	USA, Korea, Taiwan, Japan, Spain, Thailand (wild, farm, zoo)	(Machida et al., 1992; Hur et al., 1999; Chandra et al., 2000; López-Peña et al., 2001; Hirama et al., 2004; Chen et al., 2007; Takayama et al., 2009; Techangamsuwan et al., 2014)
Family Parvoviridae Feline panleukopenia virus <sup>M</sup>	Formosan gem-faced civet ( <i>P. larvata</i> tairana) Common nalm civet	Lethargy, vomiting, diarrhoea	Taiwan, Hungary (farm, zoo)	(lkeda et al., 1999; Demeter et al., 2009)
Canine parvovirus <sup>M</sup>	Common genet, Masked palm civet	Fever, diarrhoea, depression, anorexia, vomiting	Portugal, China (wild)	(Santos et al., 2009; Xiao-Ying et al., 2011; Duarte et al., 2013)
Family Reoviridae Mammalian reovirus MPC/04 Family Picornaviridae	Masked palm civet	Not discussed	China (unknown)	(Shao et al., 2008, 2010)
Genet faecal theilovirus, Novel kobuvirus, genet faecal Dicobirnavirus	Common genet	Not discussed	Spain (wild)	(Bodewes et al., 2014)

Z, zoonotic potential acknowledged; M, virus affects multiple hosts other than Viverridae.

Table 1. Viruses recognized in Viverridae

Bacteria	Viverrid Species affected	Clinical signs in viverrids	Country (source)	References
Family Leptospiraceae				
Leptospira interrogans <sup>Z,M</sup> serovars lcterohemorragiae, Pomona, Sentot, Semarang, Australis, Gryppotyphosa, Panama, Sejroe, Ballum	Common palm civet (Paradoxurus hermaphroditus), Formosan gem-faced civet (Paguma larvata taivana), Common genet (Genetta genetta)	Not discussed	Malaysia, Taiwan, France, Spain (wild)	(Smith et al., 1961; Tsai et al., 1973; Millán et al., 2009; Moinet et al., 2010)
Family Bartonellaceae				
Bartonella henselae <sup>Z,M</sup>	Masked palm civet ( <i>P. larvata)</i>	No clinical signs seen	Japan (wild)	(Sato et al., 2013)
Family Enterobacteriaceae				
Klebsiella pneumonia <sup>Z,M</sup>	African civet ( <i>Civettictis civetta</i> )	Lethargy, respiratory distress, anorexia	Nigeria (zoo)	(Enurah et al., 1988b)
Salmonella enterica <sup>z.M</sup> serovars Glostrup, Enteritidis, Nagoy, 4,12:I	African civet, Masked palm civet	Haemorrhagic diarrhoea, vomiting, lethargy, and anorexia	Nigeria, Japan (zoo, free-ranging peri-urban)	(Falade and Durojaiye, 1976) (Lee et al., 2011)
Escherichia coli <sup>z,M</sup>	Masked palm civet	Not discussed	Japan (zoo)	(Ahmed et al., 2007)
Yersinia pseudotuberculosis <sup>Z,M</sup>	Masked palm civet	No clinical signs seen	Japan (free-ranging peri-urban)	(Lee et al., 2011)
Plesiomonas shigelloides <sup>Z,M</sup>	Binturong (Arctictis binturong)	Sepsis	Czech republic (unknown)	(Bardon, 1999)
Family Campylobacteriaceae				
Campylobacter spp. <sup>Z,M</sup>	Masked palm civet	No clinical signs seen	Japan (free-ranging peri-urban)	(Lee et al., 2011)

Z, zoonotic potential acknowledged (all listed bacteria); M, bacteria affects multiple hosts other than Viverridae.

from Masked palm civet (*Paguma larvata*) in China (Shao et al., 2008, 2010); the ikoma lyssavirus, a novel divergent lyssavirus (Marston et al., 2012); two picornaviruses (genet faecal theilovirus (GFTV) and a kobuvirus genotype); and a picobirnavirus (genet faecal picobirnavirus) (Bodewes et al., 2014;).

Reports of eight bacterial species, all of which are multihost organisms with zoonotic potential, were found (Table 2). Nine serovars of Leptospira interrogans, including some known to cause leptospirosis in humans (Millán et al., 2009), were cultured (Smith et al., 1961; Tsai et al., 1973) or identified on serology (Millán et al., 2009; Moinet et al., 2010), and the gram-negative bacteria Bartonella henselae, responsible for cat scratch fever in humans, was isolated from a wild, peri-urban-dwelling Masked palm civet (Sato et al., 2013). A number of reports also describe isolation of enteric bacteria from viverrids. These include Salmonella enterica serovar Glostrup (Falade and Durojaiye, 1976); Klebsiella pneumoniae (Enurah et al., 1988b); and Plesiomonas shigelloides (Bardon, 1999), an Escherichia coli with a broad antibiotic resistance panel from a captive Masked palm civet (Ahmed et al., 2007), and Salmonella enterica enterica (serovars Enteritidis, Nagoya and 4,12:I), Yersinia pseudotuberculosis and Campylobacter spp. from peri-urban, free-ranging Masked palm civets (Lee et al., 2011).

Of the vectorborne protozoans recognized for viverrids (Table 4), those carried by ticks include *Hepatozoon canis* (Laird, 1959) and six *Babesia* spp. (Léger and Léger, 1920; Heisch, 1952; Peenen et al., 1968; Tolosa and Regassa, 2007). The trypanosomes, *Trypanosoma brucei* and *T. congolense* (Njiokou et al., 2006; Tolosa and Regassa, 2007), and *Leishmania donovani*, the protozoan responsible for Visceral Leishmaniasis in humans, were reported (Hoogstraal and Heyneman, 1969).

Species from four genera of non-vector-borne protozoan were reported (Table 4). These included the zoonotic intracellular protozoan *Toxoplasma gondii* (Janitschke and Werner, 1972; Lopes et al., 2011); the coccidian *Isospora* spp. (Colon and Patton, 2013; Su et al., 2013); *Eimeria* spp. (Colon and Patton, 2013); and three species of *Giardia* including *Giardia dasi* (Abraham, 1962), *G. hegneri* (Chu, 1930) and the zoonotic *G. duodenalis*, one of the few organisms confirmed using molecular (polymerase chain reaction (PCR) on faeces of a captive Common palm civet, *Paradoxurus hermaphroditus*) rather than morphological techniques (Beck et al., 2011).

Some of the earliest papers found during this review reported on nematode (roundworm) parasites. Over two centuries of research has reported on nematodes isolated from a very wide range of viverrid species (Table 5). While many were not identified to species level, nematodes

Protozoan	Vector	Viverrid Species affected	Clinical signs in viverrids	Country (source)	References
Babesia felis <sup>M</sup> , B. herpestedis <sup>M</sup> , B. garnhami, B. genettae, B. civettae	<i>lxodes</i> spp. (lxodid ticks)	African civet ( <i>Civettictis civetta</i> ), Common palm civet ( <i>Paradoxurus</i> <i>hermaphroditus</i> ), Common genet ( <i>Genetta genetta</i> ), Large-spotted genet ( <i>G. tigrina</i> )	Anaemia, death	Ethiopia, Vietnam, Kenya, Senegal (farm, wild)	(Léger and Léger, 1920; Heisch, 1952; Peenen et al., 1968; Penzhorn, 2006; Tolosa and Regassa, 2007)
Hepatozoon canis <sup>M</sup>	Rhipicephalus sanguineus (Dog tick)	Common palm civet	Not discussed	Malaysia (wild)	(Laird, 1959)
Trypanosoma brucei <sup>Z,M</sup> , T. congolense <sup>M</sup>	<i>Glossina</i> spp. (Tsetse fly)	Servaline genet ( <i>G. servalina</i> ), African palm civet ( <i>Nandinia</i> <i>binotata</i> ), African civet	Not discussed	Cameroon, Ethiopia (market, farm)	(Njiokou et al., 2006; Tolosa and Regassa, 2007)
Leishmania donovani <sup>Z,M</sup>	<i>Phlebotomus</i> spp. (Sandflies)	Senegal genet (G. senegalensis)	Not discussed	Sudan (wild)	(Hoogstraal and Heyneman, 1969)

Z, zoonotic potential acknowledged; M, protozoan affects multiple hosts other than Viverridae.

Table 4.	Non-vector-borne	protozoans	recognized in	Viverridae

Protozoan	Viverrid Species affected	Clinical signs in Viverrids	Country (source)	References
Toxoplasma gondii <sup>Z,M</sup>	Masked palm civet ( <i>Paguma larvata</i> ), Large Indian civet ( <i>Viverra zibetha</i> ), Common genet ( <i>Genetta genetta</i> )	Not discussed	Germany India, Thailand, Portugal (wild, zoo)	(Janitschke and Werner, 1972; Lopes et al., 2011)
Isospora felis <sup>Z,M</sup> , Isospora reiota <sup>M</sup> , Isospora sp. <sup>M</sup>	Small Indian civet ( <i>Viverricula indica</i> ), Malayan civet ( <i>Viverra tangalunga</i> )	Not discussed	Taiwan, Borneo (wild)	(Colon and Patton, 2013; Su et al., 2013)
Eimeria sp. <sup>M</sup>	Malayan civet, Common palm civet (Paradoxurus hermaphroditus)	Not discussed	Borneo (wild)	(Colon and Patton, 2013)
Giardia duodenalis <sup>Z,M</sup> , G. dasi <sup>M</sup> , G. hegneri <sup>M</sup>	Common palm civet, Malayan civet	Not discussed	Croatia, India, Philippines	(Chu, 1930; Abraham, 1962; Beck et al., 2011)

Z, zoonotic potential acknowledged; M, protozoan affects multiple hosts other than Viverridae.

representing 21 genera from 16 families have been reported in 25 published papers. These included Toxocara spp. (Warren, 1972; Maung, 1975; Alvarez et al., 1990; Colon and Patton, 2013; Su et al., 2013); Ascaris spp. (Xavier et al., 2000; Ajibade et al., 2010; Pradhan et al., 2011); the hookworms Ancylostoma spp. and Uncinaria longespiculum (Baylis, 1933; Chowdhury and Schad, 1972; Coumaranem and Mohan, 2008; Colon and Patton, 2013; Su et al., 2013); Strongyloides sp. threadworms (Su et al., 2013); Crenosoma sp. lungworms and Viverrostrongylus brauni (Myers and Kuntz, 1969; Asakawa et al., 1986; Colon and Patton, 2013); Mammomonogamus sp. (Colon and Patton, 2013); Trichuris spp. whipworms (Colon and Patton, 2013; Su et al., 2013); Capillaria sp. (Colon and Patton, 2013; Su et al., 2013); Rictularia spp. (Baylis, 1928; Chen, 1937; Schmidt and Kuntz, 1967; Kumar et al., 2005; Mahali et al., 2010), Spirura sp. (Casanova et al., 2000); Spirocera sp. and Cyathospirura seurati (Su et al., 2013); Physaloptera sp. (Casanova et al., 2000); *Gnathostoma sp.* (probably *G. spinigerum*) (Colon and Patton, 2013); *Brugia* spp. and *Dirofilaria* sp. (Edeson and Wilson, 1964; Masbar et al., 1981); and *Trichinella* spp. (Wang et al., 2012). Nematodes were commonly identified by the examination of morphological features of adult worms, eggs, larvae or oocysts under light microscopy. Only a single reference described the use of molecular diagnostic techniques, in this case PCR and genetic sequencing to accurately identify zoonotic *Trichinella spiralis* in infected muscle tissue of a Masked palm civet in China (Wang et al., 2012).

Platyhelminthes (flatworms) from two classes (Cestoda and Trematoda), many of which have zoonotic potential, were also reported (Table 6). Cestode tapeworms from four families included *Echinococcus* sp. and *Taenia* spp. (Mahannop et al., 1984; Ndiaye et al., 2002; Millan and Casanova, 2007; Lahmar et al., 2009); *Diplopylidium* spp. and *Joyeuxiella pasqualei* (Casanova et al., 2000; Millan and Casanova,

Table 5. Nematodes recognized in Viverridae			
Species	Viverrid Species affected	Country (source)	Reference
Family Toxocaridae Toxocara genettae <sup>M</sup> , T. Sprenti <sup>M</sup> , T. Canis <sup>Z.M</sup> , T. Cati <sup>Z.M</sup> , T. Vincenti <sup>M</sup> , T. Paradoxura <sup>M</sup>	Common genet (Genetta genetta), Small Indian civet (Viverricula indica), African civet (Civettictis civetta), Malayan civet (Viverra tangalunga)	South Africa Thailand, Spain, Taiwan, Borneo (wild, zoo)	(Schrank et al., 1788; Warren, 1972; Maung, 1975; Alvarez et al., 1990; Casanova et al., 2000; Colon and Patton, 2013; Su et al., 2013)
Family Ascarididae Ascaris lumbricoides <sup>2,M</sup> , Ascaris sp. <sup>2,M</sup>	Large Indian civet ( <i>Viverra zibetha</i> ), Small Indian civet, Masked palm civet ( <i>Paquma larvata</i> )	Nigeria, India (wild, zoo)	(Xavier et al., 2000; Ajibade et al., 2010; Pradhan et al., 2011)
Family Ancylostomatidae Ancylostoma martinezi <sup>z,M</sup> , A. ceylanicum <sup>z,M</sup> , Ancylostoma sp. <sup>z,M</sup> , Uncinaria longespiculum <sup>z,M</sup>	Common palm civet ( <i>Paradoxurus hermaphroditus</i> ), Common genet, Small Indian civet, Malayan civet	India, Spain, Taiwan, Borneo, USA (wild, cantive)	(Baylis, 1933; Chowdhury and Schad, 1972; Casanova et al., 2000; Coumaranem and Mohan, 2008: Colon and Patton 2013: Su et al. 2013)
Family Strongyloididae Strongyloides sp. <sup>2,M</sup>	Small Indian civet	Taiwan (wild)	500, 500, 5013) (Su et al., 2013)
ouperiarrininy ivietastronigyloudee Crenosoma sp. <sup>z.M</sup> , Viverrostrongylus brauni <sup>M</sup>	Small-toothed palm civet (Arctogalidia trivirgata), Large-spotted civet (G. tigrina), Malayan civet	Malaysia (Borneo) (wild)	(Myers and Kuntz, 1969; Asakawa et al., 1986; Colon and Patton, 2013)
Family Syngamidae Mammomonogamus sp. <sup>2,M</sup> Econity Terebuidae	Malayan civet	Malaysia (Borneo) (wild)	(Colon and Patton, 2013)
rammy muude Trichuris sp. M	Small Indian civet, Malayan civet	Taiwan, Malaysia (Borneo) (wild)	(Colon and Patton, 2013; Su et al., 2013)
Family Capillariidae Ca <i>pillari</i> a sp. <sup>M</sup>	Small Indian civet, Malayan civet, Banded palm civet (Hemigalus derbyanus)	Taiwan, Malaysia (Borneo) (wild)	(Colon and Patton, 2013; Su et al., 2013)
Family Rictulariidae Rictularia paradoxuri <sup>2,M</sup> , Rictularia cahirensis <sup>2,M</sup> , Rictularia mjobergi <sup>2,M</sup> , Pterygodermatites affinis <sup>2,M</sup> , P. leiperi <sup>2,M</sup>	Common palm civet, Small Indian civet, Masked palm civet, Binturong ( <i>Arctictis binturong</i> ), Common genet	Philippines, India, China, Malaysia (Sarawak), Spain (wild, zoo)	(Baylis, 1928; Chen, 1937; Schmidt and Kuntz, 1967; Casanova et al., 2000; Kumar et al., 2005; Mahali et al., 2010)
Family Spiruridae Spirura sp. <sup>M</sup> , Mastophorus muris <sup>M</sup>	Common genet	Spain (wild)	(Casanova et al., 2000)
Family Spirocercidae Spirocerca sp. <sup>M</sup> , <i>Cyathospirura seurati<sup>M</sup></i>	Small Indian civet, Common genet	Taiwan, Spain (wild)	(Casanova et al., 2000; Su et al., 2013)
ramıy rriysalopteridae <i>Physaloptera</i> sp. <sup>2,M</sup>	Common genet	Spain (wild)	(Casanova et al., 2000)

Species	Viverrid Species affected	Country (source)	Reference
Family Gnathostomatidae G <i>nathostoma</i> sp. <sup>2,M</sup> (probably G. <i>spinigerum</i> ) Family Onchocercidae	Malayan civet	Malaysia (Borneo) (wild)	(Colon and Patton, 2013)
<i>Brugia malayi<sup>z,M</sup>, Brugia pahangi<sup>z,M</sup>,</i> Dirofilaria sp. <sup>z,M</sup>	Common palm civet, Small-toothed palm civet, Large Indian civet, Binturong	Malaysia, Indonesia (South Kalimantan) (wild)	Edeson and Wilson, 1964; Masbar et al., 1981)
Family Trichinellidae Trichinella spiralis <sup>2,M</sup> , Trichinella sp. <sup>2,M</sup>	Masked palm civet, Common genet	China, Spain (wild)	(Casanova et al., 2000; Wang et al., 2012)
Z, zoonotic potential acknowledged; M, nematode aff Clinical signs were not discussed for any Nematode sp	ects multiple hosts other than Viverridae. ecies recognized in Viverridae.		

Table 5. (Continued)

2007); Mesocestoides spp. (Casanova et al., 2000; Su et al., 2013); and Spirometra erinaceieuropaei and Diplobothrium sp. (Uchida et al., 2000; Xavier et al., 2000).
Flukes from the class Trematoda reported for viverrids included species from eight genera, in six families. These were as follows: Echinochasmus hangzhouensis and

were as follows: Echinochasmus hangzhouensis and Artyfechinostomum sp. (Xida, 1990; Varadharajan and Kandasamy, 2000); Metagonimus yokagawai (Uchida et al., 2000); Opisthorchis viverrine and Metorchis albidus (Nicoll, 1927; Casanova et al., 2000); Schistosoma japonicum (Carney et al., 1978; He et al., 2001); Brachylaema spp. (Baugh, 1962; Casanova et al., 2000); and Paragonimus spp. in a wide range of civet species (Chen, 1959; Dissanaike and Paramananthan, 1961; Sachs et al., 1986; Gang et al., 1999; Aka et al., 2009; Colon and Patton, 2013; Su et al., 2013). The vast majority of platyhelminthes reported for viverrids were identified by examining morphology of different stages within the parasite's life cycle. Only one paper cited the use of a molecular biochemical test, an enzyme-linked immunosorbent assay (ELISA), to identify Echinococcus sp. antigen in Common genet (Genetta genetta) faecal samples from Tunisia (Lahmar et al., 2009).

Both external and internal arthropods from seven genera, in four families - Sarcoptidae (mites), Ixodidae (ticks), Trichodectidae (chewing lice) and Porocephalidae (pentostomes) - were reported for viverrids (Table 7). The sarcoptid mite, Notoedres cati, a common parasite of domestic and wild felids, was reported for urban-dwelling Masked palm civet in Japan (Ninomiya et al., 2003). Many species of ixodid tick, most of which are themselves carriers of zoonotic pathogens, were also reported, including Amblyomma testudinarium (Grassman et al., 2004); Ixodes ovatus (Tanskul et al., 1983; Robbins et al., 1997); a number of Haemaphysalis spp. (Hoogstraal and Trapido, 1966; Hoogstraal, 1971; Tanskul et al., 1983; Tolosa and Regassa, 2007; Mediannikov et al., 2012); Rhipicephalus spp. (Grassman et al., 2004; Tolosa and Regassa, 2007); Dermacentor tawianensis (Hoogstraal et al., 1986) and D. auratus (Hoogstraal and Wassef, 1985). The chewing louse, Felicola bengalensis was collected from a wild civet (Changbunjong et al., 2011), and one internal arthropod parasite, the pentostome Armillifer moniliformis, was reported for a range of civet species (Stabler and Self, 1967; Krishnasamy et al., 1981). Identification of arthropods was based on morphology of varying life cycle stages of the organisms collected from viverrids.

## Discussion

While previous authors have suggested that very little is known about the pathogens of viverrids (Williams and Thorne, 1996; Shepherd, 2008; Bongiovanni et al., 2014), this review identified a wide range of viral, bacterial, Metorchis albidus<sup>Z,M</sup>

Family Brachylaimidae Brachylaemus paradoxuri <sup>M</sup>

Brachylaema sp.<sup>M</sup>

Family Paragonimidae

Paragonimus sp.<sup>Z,M</sup>

Paragonimus uterobilateralis<sup>Z,M</sup>,

P. skrjabini<sup>Z,M</sup>, P. compactus<sup>Z,M</sup>,

Family Schistosomatidae Schistosoma japonicum<sup>Z,M</sup>

Platyhelminth	Viverrid Species affected	Clinical signs in viverridae	Country (source)	References
Class Cestoda (Tapeworms)				
Family Taeniidae				
Echinococcus sp. <sup>Z,M</sup> Taenia parva <sup>Z,M</sup> Taenia sp. <sup>Z,M</sup>	Common genet ( <i>Genetta genetta</i> ), Common palm civet ( <i>Paradoxurus hermaphroditus</i> )	Patent infection <i>T. parva</i> asymptomatic or mild gastritis	Tunisia, Spain, Thailand (wild, zoo)	(Mahannop et al., 1984; Ndiaye et al., 2002; Millan and Casanova, 2007; Lahmar et al., 2009)
Family Dipylidiidae				
Diplopylidium monoophorum <sup>M</sup> D. triseriale <sup>M</sup> Joyeuxiella pasqualei <sup>M</sup>	Common genet	Not discussed	Spain (wild)	(Casanova et al., 2000; Millan and Casanova, 2007)
Family Mesocestoididae				
Mesocestoides litteratus <sup>Z,M</sup>	Small Indian civet ( <i>Viverricula</i> <i>indica</i> ), Common genet	Not discussed	Taiwan, Spain (wild)	(Casanova et al., 2000; Su et al., 2013)
Family Diphyllobothriidae				
Spirometra erinaceieuropaei <sup>Z,M</sup> Diplobothrium sp. <sup>Z,M</sup> Class Trematoda (Flukes)	Masked palm civet ( <i>Paguma</i> <i>larvata</i> ), Small Indian civet	Not discussed	Japan, India (wild)	(Uchida et al., 2000; Xavier et al., 2000)
Family Echinostomatidae				
Echinochasmus hangzhouensi s <sup>z</sup> Artyfechinostomum sp. <sup>z,m</sup>	Small Indian civet, other civet species (not identified)	Not discussed	China, India (wild)	(Xida, 1990; Varadharajan and Kandasamy, 2000)
Family Heterophyidae				
Metagonimus yokagawai <sup>z,m</sup>	Masked palm civet	Not discussed	Japan (wild)	(Uchida et al., 2000)
Family Opistorchiidae				
Opisthorchis viverrine <sup>Z,M</sup>	Common genet, Civet	Not discussed	Thailand Spain (wild)	(Nicoll, 1927; Casanova

Not discussed

Not discussed

Not discussed

Z, zoonotic potential acknowledged; M, platyhelminth affects multiple hosts other than Viverridae.

(Species not identified)

Small Indian civet, Malayan

civet (Viverra tangalunga)

Common palm civet,

Masked palm civet, Small

African civet (Civettictis

Indian civet, Malayan civet,

Common genet

civetta)

unicellular and multicellular parasites reported for species within this family, the result of research spanning over two centuries. All published records were for species of civet or genet, with no reports found for the two viverrid linsang species - African linsang (Poiana richardsonii) and Leighton's linsang (Poiana leightoni) - revealing a paucity of knowledge on this group. Although the Viverridae gained widespread media attention as a result of the role the Masked palm civet played in the outbreak of the SARS epidemic in Southern China in 2003, this review highlights a role for genets and civets as hosts for a wide variety of many more, lesser known organisms.

#### Significance for animal health

China, Malaysia (wild)

India, Spain (wild)

China, Taiwan,

Malaysia (Borneo),

Liberia, Nigeria, Sri

unknown sources)

Lanka (wild, market,

Knowledge of the significance of isolation of an organism for animal health builds on the baseline information provided by a simple inventory of organisms for the species. Observation of clinical signs in infected individuals contributes to our understanding of pathogenicity. Detailed descriptions of clinical signs seen in viverrids were included in a small number of reports, including an investigation into morbidity or mortality in Viverridae (Roberton et al., 2006), and the documentation of experimental infection of viverrids with SARS CoV (Wu et al., 2005). However, most

et al., 2000)

(He et al., 2001)

et al., 2000)

Baugh, 1962; Casanova

(Chen, 1959; Dissanaike and

Paramananthan, 1961;

Sachs et al., 1986; Gang

et al., 1999; Aka et al.,

2009; Colon and Patton, 2013; Su et al., 2013)

Table 7. Arthropods recognized in Viv	erridae				
Arthropod	Zoonotic pathogens carried by organism	Viverrid Species affected	Clinical signs in Viverridae	Country	References
Family Sarcoptidae (Mites) Notoedres cati <sup>Z,M</sup>	None reported	Masked palm civet ( <i>Paguma larvata</i> )	Alopecia, crusting dermatitis	Japan (free-ranging – urban)	(Ninomiya et al., 2003)
Family Ixodidae (Ticks) Amblyomma testudinarium <sup>z,M</sup>	Rickettsia japonica, Rickettsia tamurae, Ehrichis ch-ffonoric	Large Indian civet ( <i>Viverra zibetha</i> )	Not discussed	Thailand (wild)	(Grassman et al., 2004)
Ixodes ovatus <sup>z,M</sup>	Erimuna charteensis R. japonica, Ehrlichia sp., Tick Borne Encephalitis Virus, Borrelia burgdorferi	Owston's civet (Chrotogale owston), Large Indian civet, Common palm civet (Paradoxurus hermaphroditus)	Not discussed	Laos, Thailand, Ethiopia (market, wild, farm)	(Tanskul et al., 1983; Robbins et al., 1997)
Haemaphysalis leach <sub>i</sub> <sup>M</sup> , H. punctaleach <sup>Z,M</sup> , H. bispinosa <sup>Z,M</sup> , H. koningsberger <sup>iZ,M</sup> H. asiaticus <sup>Z,M</sup> , H. canestrinii <sup>Z,M</sup>	R. conorii, Borrelia burgdorferi	African civet ( <i>Civettictis civetta</i> ), Binturong ( <i>Arctictis binturong</i> ), Large Indian civet, Small Indian civet ( <i>Viverricula indica</i> ), Common palm civet	Not discussed	Ethiopia, Democratic Republic of Congo, Thailand, Taiwan, India, Myanmar (wild, farm)	(Hoogstraal and Trapido, 1966; Hoogstraal, 1971; Tanskul et al., 1983; Tolosa and Regassa, 2007; Mediannikov et al., 2012)
Rhipicephalus haemaphysaolides <sup>z.M</sup> , Rhipicephalus sp. <sup>z.M</sup> . M	None reported	African civet, Binturong	Not discussed	Ethiopia, Thailand (wild, farm)	(Grassman et al., 2004; Tolosa and Regassa, 2007)
Dermacentor talwanensis <sup>w</sup> , D. auratus <sup>z, M</sup>	R. japonica, Kyasanur Forest disease, Flavivirus, Toxoplasma sp.	Formosan gem-faced civet ( <i>Paguma</i> <i>larvata taivana</i> ), Small-toothed palm civet ( <i>Arctogalidia trivirgata</i> ), Masked palm civet, Common palm civet, Small Indian civet	Not discussed	Taiwan, Malaysia, India, Vietnam, Myanmar (wild)	(Hoogstraal and Wasset, 1985; Hoogstraal et al., 1986)
Family Trichodectidae (Chewing lice) Felicola bengalensis Family Porocephalidae (Pentostome)	None reported	Common palm civet	Not discussed	Thailand (wild)	(Changbunjong et al., 2011)
Armillifer moniliformis <sup>2.M</sup>	None reported	Binturong, Small-toothed palm civet, Masked palm civet, Common palm civet, Otter civet (C <i>ynogale bennetti</i> i	Infection fatal, pre-mortem signs not described	Malaysia, USA (wild, zoo)	(Stabler and Self, 1967; Krishnasamy et al., 1981)

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Z, zoonotic potential acknowledged; M, arthropod affects multiple hosts other than Viverridae.

reports listed here provide no information on the presence or absence of clinical signs associated with infection, as many document researches carried out on stored biological samples (Moinet et al., 2010), on samples collected at necropsy (Santos et al., 2009; Duarte et al., 2013), or on samples, such as faeces, collected opportunistically without seeing the individual animal (Colon and Patton, 2013; Su et al., 2013). In other reports, including all reported nematodes in viverrids (Table 3), clinical signs were simply not discussed. In these cases, it is not possible to elucidate whether isolation of these organisms from clinically unwell Viverridae explains the presence of disease, or whether it is simply an incidental finding.

Knowledge of the role a host plays in the life cycle of an organism provides further understanding of the significance of its isolation, and assists in the prevention or management of outbreaks of disease caused by the organism. Viverrids are understood to be infective hosts, capable of transmitting disease, for a small number of organisms. These include the SARS CoV, for which Masked palm civets were important amplification and transmission hosts in the epidemic of respiratory disease caused by the organism in southern China in 2003 (Guan et al., 2003). Viverrids also transmit the infective life cycle stage of a number of macroparasites including the Sarcoptid mite, Notoedres cati (Ninomiya et al., 2003) and helminthes Toxocara genettae (Sanmartin et al., 1992), Ancylostoma sp. (Coumaranem and Mohan, 2008), Rictularia sp. (Schmidt and Kuntz, 1967; Kumar et al., 2005), Taenia sp. (Mahannop et al., 1984; Millan and Casanova, 2007) and Diplopylidium monoophorum (Millan and Casanova, 2007). However, for many more, the significance of viverrids as hosts is probably insignificant. For example, wild Common genets are dead end hosts for Leptospira interrogans serovars (Icterohemorragiae and Ballum) (Millán et al., 2009); and Binturong (Arctictus binturong), Small-toothed palm civet (Arctogalidia trivirgata), Masked palm civet, Common palm civet and Otter civet (Cynogale bennettii) are believed to be accidental hosts for the pentostome Armillifer moniliformis (Stabler and Self, 1967; Krishnasamy et al., 1981;). In many other cases, the opportunistic identification of organisms from a small sample size, a recognized impediment to disease surveillance in wild species (Stitt et al., 2007), hampers our ability to understand the role of Viverridae in the organism's life cycle. The amount of useful epidemiological information obtained is particularly limited where a multihost organism, such as the ixodid tick Amblyomma testudinarium, is identified from just one individual viverrid (Grassman et al., 2004). Positive results obtained through opportunistic sampling of small numbers of individuals remain useful in that they provide information on the presence of potential new carriers for an organism, but further research is required to understand the role that viverrids play in the organism's life cycle, or their significance in the epidemiology of the diseases which they cause.

Some of the organisms listed in this review may be of significance for the conservation of threatened populations of viverrid or other wild carnivores. Canine distemper virus (CDV), feline panleukopenia virus (FPV) and canine parvovirus (CP) (Table 1) are all highly contagious and cause significant morbidity and mortality in susceptible carnivore species. Infected carnivores shed a high viral load in faeces and other bodily secretions (Deem et al., 2000; Steinel et al., 2001), facilitating environmental contamination and rapid spread of disease. Infection of susceptible animals does not require direct contact as transmission may be via inhalation of aerosolized respiratory secretions or ingestion of contaminated material from the environment (Deem et al., 2000; Steinel et al., 2001). Spillover of canine distemper virus from the domestic dog has already impacted several wild carnivore populations, including African wild dogs (Lycaon pictus) (Fanshawe et al., 1991), Santa Catalina Island foxes (Urocyon littoralis catalinae) (Timm et al., 2009), Black-footed ferrets (Mustela nigripes) (Williams et al., 1988) and Lions (Panthera leo) (Roelke-Parker et al., 1996), and has been implicated as a significant concern for the conservation of Amur tiger (Panthera tigris altaica) in Russia (Gilbert et al., 2014). Multihost viruses such as those listed for Viverridae may pose a threat to the conservation of threatened wild viverrids where their distribution overlaps areas inhabited by unvaccinated domestic carnivores, and must be considered in population management, preventative health measures or in case of disease outbreak. Conversely, viverrids themselves may contribute to the maintenance and cycling of pathogens in an environment which, in turn, could threaten the conservation of other endangered species.

#### Significance for human health

In addition to the potential significance for viverrid and other animal health, many of the organisms listed for Viverridae raise concerns for human health. Wild species are a common source or carrier of zoonotic pathogens (Wolfe et al., 2005; Jones et al., 2008), and there is a growing interest in understanding the host, pathogen and external (environmental and anthropogenic) factors that facilitate their transmission from wild animals to people and other animals (Bengis et al., 2004; Woolhouse and Gowtage-Sequeria, 2005; Greger, 2007; Chomel, 2008; Rhyan and Spraker, 2010). The vast majority of organisms reported here for viverrids have the capacity to infect a wide range of species a characteristic which, while common amongst pathogens in general - 91% of all domestic carnivore pathogens infect more than one host (Cleaveland et al., 2001) - is of concern as it is a significant risk factor for outbreak of disease (Cleaveland et al., 2001; Greger, 2007). Given the prevalence of multihost organisms reported for viverrids, particularly those with zoonotic potential, an examination of the factors bringing these forest dwelling mammals into unnaturally close proximity with humans is warranted. For the Viverridae, these include the trades (legal and illegal) in wildlife for human consumption, keeping of viverrids in captivity (wildlife farms, zoos or rescue centres), and human contact with free-ranging viverrids in areas where human and viverrid habitation overlap, or from human incursion into wild spaces.

The global wildlife trade is widely regarded as an interface where close contact between humans and wild animals creates an ecosystem favouring disease emergence and expression (Bengis et al., 2004; Kuiken et al., 2005; Karesh et al., 2007; Pavlin et al., 2009; Cutler et al., 2010; Bausch and Schwarz, 2014). Stressed, sick and injured animals are transported in mixed-species shipments (Bell et al., 2004) to wet markets or other trade nodes where animals are kept in crowded, unhygienic conditions, exposed to both a wide range of other wild and domestic animals for sale (Kan et al., 2005; Woo et al., 2006), and to potentially immunologically naïve, urban-dwelling wildlife consumers (Swift et al., 2007). This combination of conditions facilitates emergence, transmission and amplification of pathogens (Greger, 2007).

Viverrids are frequently encountered in the wildlife trade in Africa and Asia (Shepherd, 2008; Nijman, 2009; Shepherd and Shepherd, 2010) where they are consumed for their meat (Bell et al., 2004; Yang et al., 2007; Van Song, 2008) or utilized in traditional medicines (Kumara and Singh, 2007; Ashwell and Walston, 2008; Tsegave et al., 2008). While the number of organisms reported for this animal source (refer to 'Country (source)' column, Tables 1-7) is low compared to other animal sources, this is likely due to the paucity of research in this area rather than a reliable indication of the health of viverrids in the trade, or the potential significance of this source as a concern for public health. In fact, although few in number, all organisms reported for viverrids sourced from the wildlife trade - the SARS coronavirus (Table 1) (Tu, 2004), an ixodid tick (Table 7) (Robbins et al., 1997), a Giardia sp. protozoan (Table 4) (Abraham, 1962), the vectorborne parasite responsible for African sleeping sickness Trypanosoma brucei (Table 3) (Njiokou et al., 2006) and a trematode fluke of genus Paragonimus (Table 6) (Chen, 1959) - are zoonotic, multihost organisms with the potential to cause considerable socio-economic impact (Liu et al., 2008; Chan et al., 2013). In fact, a viverrid played a central role in the pandemic of human respiratory disease caused by one of the most significant diseases to emerge from the wildlife trade system to date - the SARS CoV

(Table 1). Masked palm civets in this crowded, multispecies wet market in southern China were implicated as the main source of infection in humans via exposure to viral particles in bodily fluids aerosolized during slaughter and preparation for human consumption (Guan et al., 2003; WHO, 2004; Li, 2008; Chan et al., 2013). The socioeconomic impact of this outbreak, which resulted in over 8000 human cases and a fatality rate of 10%, was considerable (Dong et al., 2007; Chan et al., 2013).

This process of preparation of carcasses for human consumption presents a considerable risk for transmission of disease to and from viverrids (Wang, 2005; Woo et al., 2006), a risk which is amplified by the illegal nature of much of the wildlife trade, meaning that slaughter and preparation for human consumption frequently occur outside government-regulated slaughterhouses, unbound by official hygiene standards (WCS, 2008). Any one of the zoonotic pathogens reported for viverrids in this review may be transmitted to humans during this process, but the rabies virus, another significant viral zoonosis commonly reported for viverrids, is one for which this process is a documented transmission risk (Table 1). The broad tissue tropism of rabies (Carey and McLean, 1978) facilitates aerosolization and environmental contamination during the butchering of rabid animals, resulting in confirmed cases of transmission to people following slaughter of domestic dog and cat in China and Vietnam (Kureishi et al., 1992; Wertheim et al., 2009; Nguyen et al., 2011). Given the conditions in which the wildlife trade currently operates, the considerable scale of trade in viverrids and their susceptibility to such a wide range of multihost organisms, it is likely that species from this family could again play a central role in the emergence, amplification and transmission of disease to people within this system (Dong et al., 2007).

Maintenance of wild species in captivity provides another opportunity for unnatural human-wildlife proximity, facilitating interspecies sharing of organisms (Daszak et al., 2001). Viverrids are kept in captivity in zoos (Cosson et al., 2007), conservation breeding programmes for threatened species (Roberton et al., 2002) and, in far greater numbers, on commercial wildlife farms. Civets have traditionally been farmed for their fur (Shi and Hu, 2008) and to supply the demand for 'civet' scent (used in the production of perfume), a practice which drives farming of civets in Ethiopia (Tolosa and Regassa, 2007) and India (Balakrishnan and Sreedevi, 2007). More recently, farming of civet in Asia has expanded to supply a growing demand for their meat in wildlife restaurants and markets (Patou et al., 2009). While published data on wildlife farming are scant, the number of individual civets on farms is likely to be large - by 2003, 40,000 individual civets were registered on farms in China (Patou et al., 2009). Another growing industry is the production of civet coffee, where coffee beans are fed to civets and subsequently harvested, undigested, from their faeces. Traditionally collected from the faeces of free-ranging animals in the vicinity of coffee farms, coffee producers are increasingly turning to caged production to satisfy demand for this product, which has the dubious distinction of being the 'world's most expensive coffee' (D'Cruze et al., 2014; Techangamsuwan et al., 2014).

A wide variety of zoonoses have been reported for captive viverrids (refer to 'Country (source)' columns, Tables 1-7), including the very high profile zoonotic virus HPAI H5N1 (Table 1). This was confirmed on PCR and serology from a number of Owston's civets (Chrotogale owstoni) which died following an outbreak of respiratory and neurological diseases in a conservation breeding programme in Vietnam (Roberton et al., 2006). While no evidence of viverrid-to-human transmission of HPAI H5N1 exists, isolation of pathogens with pandemic potential from any mammalian host is significant as it may provide conditions suitable for the virus to adapt to mammalian respiratory epithelial receptors, enabling efficient mammalto-human, and possibly also human-to-human, transmission, paving the way for a potentially devastating pandemic (Rimmelzwaan et al., 2006; Peiris et al., 2007). Isolation of this virus from captive civets is also significant in that some countries with the highest number of human cases and fatalities due to HPAI H5N1, such as Indonesia, China and Vietnam (WHO, 2015), overlap with those where civets are also farmed in the greatest numbers (Patou et al., 2009; D'Cruze et al., 2014), a risk compounded by the poor standards of husbandry and lack of veterinary care reported for wildlife farms (WSPA, 1998; WCS, 2008). Knowledge of susceptibility to zoonotic pathogens guides the development of appropriate quarantine and biosecurity protocols in captive institutions required to safeguard both human and animal health.

Understanding transmission routes of reported organisms also assists in identifying the practices associated with keeping viverrids in captivity which pose the greatest risk to public health. For many of the organisms reported here for captive civets, including the enterobacteriaceae Klebsiella pneumoniae and Salmonella enterica serovar Glostrup in Nigerian zoos (Falade and Durojaiye, 1976; Enurah et al., 1988b) and Escherichia coli in a Japanese zoo (Ahmed et al., 2007), the faecal-oral transmission route is common. Appropriate hygiene and husbandry standards can reduce the spread of these organisms amongst animals, and between animals and humans, in captive environments. However, for those workers tasked with the collection of undigested coffee beans from civet faeces in the production of civet coffee (D'Cruze et al., 2014), they present a significant, ongoing occupational hazard which must be addressed.

Captive viverrids have also been reported as hosts for a number of diseases listed by the World Health Organization (WHO) as 'neglected tropical diseases' (NTD), including rabies in an African civet which displayed neurological signs prior to death (Table 1) (Enurah et al., 1988a), soiltransmitted helminthiasis (ascarid roundworms in Large Indian civet and Masked palm civets and ancylostome hookworms in Common palm civet and Small Indian civet, Table 5) (Baylis, 1933; Ajibade et al., 2010; Pradhan et al., 2011) and human African trypanosomiasis in a farmed African civet (Table 3) (Njiokou et al., 2006). These pathogens are considered 'neglected' because they are poorly studied and commonly ignored by donors, policy makers and public health officials (Maudlin et al., 2009); however, they continue to cause widespread morbidity and mortality in the poorer regions of the world (Hotez et al., 2007; WHO, 2010). Identification of the pathogens responsible for NTDs in captive viverrids contributes to our understanding of potential animal reservoirs for these diseases, knowledge which is vital to the development of interventions aimed at their control or elimination (Zinsstag et al., 2007).

Ecotourism is a further anthropogenic factor which brings people into contact with free-ranging viverrids, facilitating the cycling of organisms between these groups. As ecotourism, and hence visitation to national parks, expands globally, an increase in human-wildlife contact has led to a corresponding increase in the risk of transmission of disease (Muehlenbein et al., 2008), a risk which was illustrated in the Serengeti National Park in 2009 when an African civet, showing clinical signs consistent with rabies, bit a child in an unprovoked attack. A novel lyssavirus, the ikoma lyssavirus, was subsequently isolated from the civet (Marston et al., 2012). Although the pathogenicity of Ikoma Lyssavirus to humans is unknown, and further research is required to understand its prevalence and distribution (Marston et al., 2012), this case highlighted the risk of disease emergence when immunologically naïve people come into close and unnatural proximity with wild animals.

As human populations expand, and wild spaces are lost, there is an increasing overlap between human habitation and the distribution of wild species, particularly for species which have adapted well to human settlement (Campbell, 2009). Tolerance of human presence by some viverrids has led to high density urban and peri-urban populations, where they are frequently seen as pests, scavenging food from garbage bins, gardens and orchards, and living in the roofs and wall spaces of houses (Ninomiya et al., 2003; Campbell, 2009). Direct contact between viverrids and people in an urban environment leading to disease transmission was reported in Japan, where cat scratch fever (caused by the gram-negative bacteria *Bartonella henselae*) was transmitted to a man via a scratch from a free-ranging Masked palm civet (Table 2) (Sato et al., 2013). Peri-urban wildlife may also serve as sylvatic reservoirs for zoonotic disease (Weiss and McMichael, 2004), as reported for African civet, believed to contribute to the maintenance and cycling of the mongoose biotype of the rabies virus (Sabeta et al., 2008), and Masked palm civet, considered a maintenance host of the enteric pathogens *Salmonella, Campylobacter* spp. and *Yersinia* (Table 2) in Japan (Lee et al., 2011).

While the list of known organisms for viverrids will grow as future work incorporates improved methodology and advanced molecular techniques, this review provides an important baseline inventory of organisms reported for species from the family Viverridae. A number of these have clear and serious implications for viverrid health, and as such, this information facilitates sensible health management of both wild and captive viverrids, and provides a knowledge base from which future research, surveillance programmes and disease outbreak investigations can be developed. As the vast majority of organisms listed here are also capable of infecting a wide range of hosts, including humans, many may also pose a risk to public health. This is of concern given the anthropogenic factors, including trade of viverrids for human consumption, keeping of viverrids in captivity, and land use changes which bring people and other animals into closer contact with the Viverridae than would naturally occur, facilitating transmission and spillover of organisms within and between these groups.

However, gaps remain in our understanding of the significance of isolation for many of the organisms reported for viverrids. Whether due to small sample numbers, or a failure to investigate factors which help to explain the epidemiology of the diseases they cause, we have very little appreciation of the importance of many of these organisms for viverrid, human and other animal health. Future research should utilize larger host sample sizes in a range of environmental settings (wild and captive), investigate the role of viverrids in the life cycle of the organism in question, and consider the significance of known and novel organisms for both human and animal health, rather than simply reporting their presence.

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