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Wild animals as source of zoonotic diseases-a review

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ABSTRACT

Wildlife is a study of nondomesticated animal and noncultivated plants. Total 1415 human pathogens have been calculated till now, out of total, 62 percent are of zoonotic origin. Wildlife plays a vital role in human being life and it also helpful for human in cultural, medicinal, esthetic values and act as bioindicators. Human interactions with wildlife can create a threat and can be transferred diseases to human being. People who have close contact with animals in home, zoo and nature can be at threat for zoonotic diseases. Zoonotic pathogen can be transmitted from wild animal to human and human to human with contact, sexual contact, infected droplet, aerosol, vector and oral. Adaptation and Mutation have driven the co-evolution of coronaviruses and animals for thousands of years. Two coronaviruses i.e. severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) were recognized to cause mild disease, like common cold, before 2003. At the end of 2019, the appearance of SARS-CoV-2 in China has originated with high transmissibility and low pathogenicity as compared to SARS-CoV. Analysis showed that SARS-CoV-2 may be evolved from the bat, but later analysis of SARS-CoV-2 demonstrated that recombination actions were probable to happen either in human or animals (i.e. bat or pangolin).

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INTRODUCTION

Wildlife is a study of nondomesticated animal (fish, amphibians, reptiles, mammals and birds) and noncultivated plants. Total 1415 human pathogens have been calculated till now, out of total, 62 percent are of zoonotic origin (Taylor *et al.*, 2001). Wildlife plays a vital role in human being life (Alves, 2011) and it also helpful for human in cultural (Altaf *et al.*, 2017), medicinal uses (Altaf *et al.*, 2018b), esthetic values (Parson, 2007) and act as bioindicators (Altaf, 2016; Altaf *et al.*, 2018a). Human interactions with wildlife can create a threat for zoonoses (Lowry and Smith, 2007; Kazwala, 2016) and can be transferred to human being, leading to infection and disease (Kruse *et al.*, 2004). People who have close contact with animals in home, zoo and nature, can be at threat for zoonotic diseases (Chomel *et al.*, 2007; Chethan *et al.*, 2013). Furthermore, persons with weakened immune systems, like the aged people (Stull *et al.*, 2015), children (Landrigan, 2004; Salmon and Halsey, 2012), pregnant women (Sauteur *et al.*, 2013), diabetic and cancer patient (Sauteur *et al.*, 2013), having more vulnerable to disease. Fortunately, most zoonotic ailments can be shunned with proper maintenance and prevention measures of best health in fauna and humans (Leeflang *et al.*, 2008; Shiferaw *et al.*, 2017).

Zoonoses with wild animal reservoir are characteristically caused by different parasites, viruses and bacteria, while fungi are of negligible significance (Belay *et al.*, 2004; Kruse *et al.*, 2004). The overall frequency of transmission of disease-producing sources from fish to human is very low. However, number of sources that are present in fish and water have the chances to be transmitted to humans (EHS, 2016b).

ZOONOTIC ORIGINS

Zoonotic infections have long been deemed a significant type of novel diseases, with fauna reservoirs providing a cause of novel infections for human being in whole time of evolutionary record (Kruse *et al.*, 2004). Pathogens have developed in wild animal and jumped from wild animal to human and after that transmitted from human to human (Childs *et al.*, 2007).

HISTORY ZOONOTIC DISEASES

Leprosy was pandemic disease, due to *Mycobacterium leprae*. The leprosy outbreaks occurred in ancient Greek, India and Middle East since 23 AD (McLeod and Yates, 1981). *M. leprae* is a main cause of chronic disease leprosy. Probably, this pathogen is transmitted to human by armadillos species i.e. *Dasypus novemcinctus* (da Silva *et al.*, 2018).

Tuberculosis is an infectious and contagious disease, due to *Mycobacterium tuberculosis* that has always been a challenge over the human life history, because of its harsh social implications. The disease was recognized in France and England as "king's evil". In 1720, for the first time, the infectious source of tuberculosis was recognized and the first victorious medicine against tuberculosis was the beginning of the treatment. (Barberis *et al.*, 2017). Probably, *M. tuberculosis* is transmitted to human by elephants (Michalak *et al.*, 1998).

Spanish influenza was pandemic and caused almost 50 million worldwide deaths, in 1918 (Taubenberger and Morens, 2006), due to H1N1 virus. It spread worldwide during 1918-1919. It was originated from United States of America, one-third of the world's population infected and 50 million death were calculated (CDC, 2019). Swine influenza was originate on 2009 and spread worldwide. Swine influenza viruses also can cause disease in all ages of human beings. The WHO declared an H1N1 pandemic on 2009 and it was recorded more than seventy countries documented almost thirty thousand cases of H1N1 infection.

(Rewar *et al.*, 2015). Avian influenza virus was pandemics in1957 and 1968. It was caused by an H5N1 virus with avian origin (Peiris *et al.*, 2007).

Ebola virus disease (EVD) outbreak origin from Africa in 1976 and caused Ebola hemorrhagic fever. EVD is often lethal for human and fatality rate is around 50% (WHO, 2020a).

MERS-CoV is transferred from Arabian camel in 2012, from direct or indirect contact. Infection with this virus can source harsh ailment resulting in high death rate. MERS-CoV has confirmed the ability to transmit between humans (WHO, 2020b). In 2003, SARS-CoV was originated from China. After that almost 8000 cases and almost 800 deaths were noted. SARS-CoV was finally controlled by means of quick isolation of patients, syndromic observation, strict enforcement of quarantine of all suspected, and in some areas top to down enforcement of society quarantine. By disrupting all human being to human being transmission, SARS-CoV was effectively eliminated. In start of 2020, coronavirus disease 2019 (COVID-19) was also originated from China, COVID-19 varies from SARS in terms of transmissibility, clinical severity, infectious period, and extent of community spread (Wilder-Smith *et al.*, 2020).

EVOLUTION OF SARS-COV-2

Adaptation and Mutation have driven the co-evolution of coronaviruses and animals, for thousands of years (Woo *et al.*, 2012). Two coronaviruses i.e. severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) were recognized to reason mild disease, like common cold, before 2003. At the end of 2019, the appearance of SARS-CoV-2 in China has originated, high transmissibility and low pathogenicity as compared to SARS-CoV. Research showed that SARS-CoV-2 may be evolved from the bat (Paraskevis *et al.*, 2020), but later analysis of SARS-CoV-2 demonstrated that recombination actions were probable to happen in pangolin and bat origin coronaviruses either in human or animals (i.e. bat or pangolin) (Zhang *et al.*, 2020).

MODE OF TRANSMISSION

Wildlife reservoirs represent a wide range of modes of transmission e.g. contact, bite, vectors, aerosol and oral (Table 1). Zoonotic pathogen can be transmitted from wild animal to human and human to human with contact, e.g. *Leptospira species* (Health.vic, 2020)*, Chlamydophila psittaci* (Marrie, 2020)*, H5N1* (Imai *et al.*, 2013), *Staphylococcus aureus* (Knox *et al.,* 2015) and *Streptococcus agalactiae* (Botelho *et al.,* 2018); with sexual contact and infected droplet e.g. *Lentivirus* (Schlimgen *et al.*, 2016); with bites *Rabies lyssavirus* (Rupprecht, 1996); with aerosol e.g. *Orthopoxvirus* (Martinez *et al*., 2000), *COVID-19* (Shereen *et al*., 2020), *SARS-CoV* (Shereen *et al.,* 2020), *Ebolavirus* (Mekibib and Ariën, 2016), *Marburgvirus* (Ewers *et al*., 2016), *H1N1* (Cowling *et al*., 2013), *Mycobacterium tuberculosis* (Shiloh, 2016), *Mycobacterium leprae (McDermott-Lancaster and McDougall, 1990), Avian coronavirus* (Cavanagh, 2007) and *Murine coronavirus* (Weiss and Navas-Martin, 2005); with vector e.g. *Rickettsia rickettsi* (Moraes-Filho *et al.,* 2018)*, Bartonella henselae* (Moraes-Filho *et al.,* 2018), *Leishmania* spp. (Schaut *et al*., 2015), *Yersinia pestis* (Eisen *et al*., 2015*)* and *Trypanosoma brucei (WHO, 2012); and with* oral e.g. *Campylobacter jejuni, C. fetus, C. coli* (WHO, 2018), *Ascaris lumbricoides* (Hlaing *et al*., 1984), *Moniliformis moniliformis* (Berenji *et al*., 2007)*, Toxoplasma gondii* (Hill and Dubey, 2002)*, Strongyle ova* (CDC, 2018)*, Trichinella britovi* (Gottstein *et al*., 2009)*, Capillaria bursata* (Qamar *et al*., 2017), *Spirometra* spp. (Kuchta *et al*., 2015), *Escherichia coli* (Anthony, 2017), *Edwardsiella tarda* (Hirai *et al*., 2015)*, Armillifer armillatus* and *A. grandis, Mycobacterium marinum* (Ortega *et al*., 2014; Hashish *et al*., 2018)*, Aeromonas* spp. (Igbinosa *et al*., 2012; Batra *et al*., 2016)*, BatCoV-1* (Li *et al.,* 2019)*, FrCoV* (Li *et al*., 2019), *Salmonella* spp. (Baron *et al*., 1996), *Baylisascaris procyonis* (Gavin *et al*., 2005) and *Trichuris* spp. (CFSPH, 2019).

CONCLUSION

Wildlife is uses as of food, medicine and pet and these sources lead to Zoonotic diseases. Wildlife reservoir represent a wide range of modes of transmission e.g. aerosol, oral, contact, vectors and bite. Adaptation and Mutation have driven the co-evolution of coronaviruses and animals, for thousands of years. Two coronaviruses i.e. severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS) were recognized to reason mild disease, like common cold, before 2003. At the end of 2019, the appearance of SARS-CoV-2 in China has originated with high transmissibility and low pathogenicity as compared to SARS-CoV. Analysis showed that SARS-CoV-2 may be evolved from the bat, but later analysis of SARS-CoV-2 demonstrated that recombination actions were probable to happen either in human or animals (i.e. bat or pangolin).

Table 1: Wild animal as source of zoonotic diseases.

Zoonotic animal	**Pathogens**	**Mode transmission**	**Diseases**	**References**
Mammals				
Bats	*SARS-CoV-2*	Aerosol	COVID-19	(Michalak *et al*., 1998; Hendriksen *et al*., 2004; Leroy *et al*., 2004; Pozio *et al*., 2005; Liégeois *et al*., 2009; Pourrut *et al*., 2009; Lussac,
	SARS-CoV	Aerosol	Severe acute respiratory disease	
	BatCoV	Oral	Porcine epidemic diarrhea	
	Zaire ebolavirus	Aerosol	Ebola virus disease	

	Marburgvirus	Aerosol	Marburg virus disease	2010; Peeters *et al.*, 2010; Adejinmi and Emikpe, 2011; Tidona and Darai, 2011; CDC, 2013; CFSPH, 2013; Foni *et al.*, 2013; Saey, 2013; da Silva *et al.*, 2018)
Wild boar	*H1N1*	Aerosol	swine influenza	
	Salmonella typhimurium	Oral	Typhoid fever	
Panthers, cheetahs	*Bartonella henselae*	Vector (i.e. fleas, body lice, and sand flies)	Cat Scratch Fever	
Ferrets	*FrCoV*	Oral	Ferret epizootic catarrhal enteritis	
Mice and rats	*Murine coronavirus*	Likely aerosol	Puffinosis	
Non-human primates	*Orthopoxvirus*	Aerosol	Monkeypox	
Non-human primates	*Trichuris suis, T. trichiura, T. vulpis*	Oral	Trichuriasis	
All mammals	*Rabies lyssavirus*	Bite	Rabies	
Non-human Primates	*Campylobacter jejuni, C. fetus, C. coli*	Oral	Campylobacteriosis	
Sea lions and seals	*Leptospira species*	Contact with blood, tissue or urine from an infected animal	Leptospirosis	
Deer, opossums and raccoons	*Borrelia burgdorferi*	Vector (i.e. ticks)	Lyme Disease	
Prairie dogs, rock and ground squirrels	*Yersinia pestis*	Vector (i.e. fleas)	Plague	
Opossums, Rodents and rabbits,	*Rickettsia rickettsi*	Vector (i.e. tick)	Rocky Mountain Spotted Fever	
Hedgehogs	*Salmonella* spp.	Oral	Salmonellosis	
Raccoons and kinkajous	*Baylisascaris procyonis*	Oral	Baylisascariasis	
Bats, marsupials, opossums, anteaters, armadillos and non-human primates	*Trypanosoma brucei*	Vector (i.e. tsetse fly)	Chagas Disease	
Marsupials and non-human primates	*Leishmania* spp.	Vector (i.e. sandflies)	Leishmaniasis	
Striped land squirrels (*Xenus*	*Ascaris lumbricoides,*	Oral	Gastroenteritis	

erythropus)	*Trichuris trichiura, Moniliformis moniliformis*			
Brush tailed porcupine	*Toxoplasma gondii*	Oral	Toxoplasmosis	
Cane rats (*Thryonomys swinderianus*)	*Strongyle ova*	Oral	Gastroenteritis	
Civets	*Trichinella britovi*	Oral	Trichinosis	
Rodents	*Hantaviruses*	Contact	Hantavirus Pulmonary Syndrome	
Chimpanzees	*Ebolavirus*	Aerosol	Ebola virus disease	
Monkeys, lemurs, rabbits and ferrets	*Lentivirus*	Sexual contact	AIDS	
Nine-banded armadillos (*Dasypus novemcinctus*)	*Mycobacterium leprae*	Aerosol	Leprosy	
Elephant	*Mycobacterium tuberculosis*	Aerosol	Tuberculosis	
Arabian Camel	*MERS-CoV*	Aerosol	Middle East respiratory syndrome	
Birds				
Wild birds	*Avian coronavirus*	Aerosol, Oral	Infectious bronchitis, fever and kidney disease	(Whitworth *et al.*, 2007; Lussac, 2010; Tidona and Darai, 2011; Lawson *et al.*, 2014)
Love birds and parakeets	*Chlamydophila psittaci*	Contact	Psittacosis	
Guinea fowls and Bush fowls	*Ascaris lumbricoides, Capillaria bursata*	Oral	Gastroenteritis	
Senegal Coucal (*Centropus senegalensis*)	*Toxoplasma gondii*	Oral	Toxoplasmosis	
Bar-headed Goose, Brown-headed Gull, Great Cormorant, Greater Flamingo, Pallas's Gull and Ruddy Shelduck,	*H5N1*	Contact	Avian influenza	
Bullfinch,	*Salmonella*	Oral	Salmonellosis	

Chaffinch, Goldfinch, Greenfinch, House sparrow and Siskin	*enteric*			
Amphibians				
Frog	*Salmonella* spp.	Oral	Salmonellosis	(CFSPH, 2013; EHS, 2016a)
Amphibians	*Spirometra* spp.	Oral	Sparganosis	
Amphibians	*Escherichia coli*	Oral	Nausea, vomiting, and diarrhea	
Amphibians	*Edwardsiella tarda*	Oral	Nausea, vomiting, and diarrhea	
Reptiles				
Turtles	*Staphylococcus aureus*	Contact	Methicillin-Resistant	(CFSPH, 2013; Okoye *et al*., 2015; Tappe *et al*., 2016)
Reptiles	*Mycobacterium marinum*	Oral	Mycobacteriosis	
Reptiles	*Salmonella* spp.	Oral	Salmonellosis	
Python	*Armillifer armillatus* and *A. grandis*	Oral	Snakeborne Armillifer pentastomiasis	
Ornate monitor lizards African savannah monitor lizards	*Ascaris lumbricoides*	Oral	Gastroenteritis	
Fishes				
All species of fishes	*Mycobacterium marinum*	Oral	Mycobacteriosis	(Verner-Jeffreys *et al*., 2012; CFSPH, 2013; EHS, 2016b)
All species of fishes	*Aeromonas* spp.	Oral	Gastroenteritis	
All species of fishes	*Escherichia coli*	Oral	Nausea, vomiting, and diarrhea	
Doctor fish (*Garra rufa*)	*Streptococcus agalactiae*	Contact	Infection	

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