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CHAPTER 12

Zoonotic wildlife pathogens in Malaysia and the effects of anthropogenic landscape alteration on transmission dynamics: Implications for One Health

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Abstract: Zoonotic diseases associated with wildlife represent an increasing public health concern, particularly in biodiversity-rich tropical regions experiencing rapid anthropogenic landscape modification. Malaysia harbours a diverse array of zoonotic wildlife pathogens, while deforestation, agricultural expansion, forest fragmentation and urbanisation are progressively altering ecological interactions among wildlife, domestic animals, vectors and humans. This review synthesises available evidence on the diversity, reservoir hosts and transmission pathways of wildlife-associated zoonotic pathogens in Malaysia, examines the influence of habitat degradation on disease spillover and highlights the importance of incorporating zoonotic disease risks into Environmental Impact Assessment (EIA) and Health Impact Assessment (HIA) frameworks. Anthropogenic habitat modification may amplify transmission risks by disrupting wildlife habitats, altering reservoir and vector dynamics, and creating ecological transition zones (ecotones) that increase opportunities for interspecific contact. The emergence and spread of zoonotic pathogens including the Nipah virus and malaria parasite (*Plasmodium knowlesi*) exemplify the complex relationships between land-use change and pathogen spillover in Malaysia. Despite these established ecological associations, wildlife-associated zoonotic spillover is not explicitly incorporated as a routine risk-assessment component within existing Malaysian EIA and HIA frameworks. This review advocates integrating wildlife reservoir and vector surveillance, ecological interface mapping, and pathogen exposure pathways into environmental assessment procedures, particularly for developments involving forest conversion, agricultural intensification and habitat disturbance. Adopting a multidisciplinary One Health approach involving environmental, veterinary, wildlife and public-health authorities would strengthen preventive surveillance, improve development-related risk mitigation and support more sustainable land-use planning while safeguarding ecosystem, animal and human health.

INTRODUCTION

Zoonotic diseases (caused by pathogens transmitted from animals to humans) present a significant threat to global public health and exert a substantial socio-economic burden, especially among developing nations (Budke *et al*. 2011; Torgerson and Macpherson 2011; Lv *et al.* 2024). The implementation of control and prevention strategies for zoonotic diseases are often challenging because their emergence is shaped by complex interactions among humans, domestic animals, wildlife, vectors, and rapidly changing environments. Wildlife populations constitute natural reservoirs for a diverse array of zoonotic pathogens including viruses, bacteria, protozoa and helminths; many of which can cross species barriers when ecological conditions facilitate contact with humans or domestic animals. Such spillover events are rarely determined by pathogen presence alone. Rather, they emerge from interacting ecological, environmental and socioeconomic processes that influence reservoir abundance, host behaviour, vector distribution and opportunities for interspecific transmission (Patz *et al*. 2004; Gibb *et al*. 2020; Plowright *et al*. 2021). Understanding zoonotic

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disease emergence therefore requires an integrated perspective that considers pathogen diversity together with host ecology, transmission pathways and anthropogenic modification of natural environments.

Malaysia provides a compelling setting in which to examine these dynamic interactions. The country supports a diverse array of wild flora and fauna while simultaneously experiencing extensive agricultural development, urbanisation, infrastructure expansion and modification of forested landscapes (Ma *et al.* 2024). Wild animals in Malaysian are known to be carriers of numerous zoonotic pathogens which may be transmitted through direct contact, aerosols, arthropod vectors, contaminated water and soil, and ingestion of infective stages (Nguyen *et al.* 2025). These sylvatic reservoir hosts include bats, non-human primates, rodents, wild pigs, birds, reptiles and other vertebrates, while mosquitoes, ticks, mites, fleas and other haematophagous arthropods may act as vectors connecting wildlife -associated transmission cycles with humans and domestic animals.

Several Malaysian examples demonstrate that the epidemiological significance of these pathogens is strongly influenced by ecological interfaces. The local Nipah virus outbreak (Chua *et al.* 2002a) and the emerging threat of zoonotic malaria (Johnson *et al.* 2024) illustrate clearly the detrimental effects of anthropogenic landscape alteration and habitat destruction on pathogen transmission dynamics. In addition, environmental modification can intensify these risks by restructuring the spatial relationships among the wildlife reservoirs, vectors, livestock and human populations. Deforestation, forest fragmentation, plantation expansion, mining, road construction, wetland modification and urban encroachment create ecotones between forests, farms, plantations and settlements. Such transition zones may increase opportunities for contact among species that previously interacted less frequently, thereby functioning as epidemiological interfaces for pathogen spillover (Shah *et al.* 2019; Gibb *et al.* 2020; Plowright *et al.* 2021).

Zoonotic disease spillover and transmission have important implications for environmental governance. Environmental Impact Assessment (EIA) is intended to anticipate the environmental consequences of development before implementation, while Health Impact Assessment (HIA) provides a framework for identifying potential effects on human health. In Malaysia, prescribed development activities are regulated under the Environmental Quality (Prescribed Activities) (Environmental Impact Assessment) Order 2015 (Department of Environment Malaysia 2015), and national guidance also recognises HIA within the EIA process. However, wildlife-associated pathogen spillover is not explicitly established as a routine risk pathway, despite the capacity of development projects to alter wildlife movement, vector ecology, livestock contact and human exposure.

Against this background, this review synthesises current knowledge on the diversity, wildlife hosts and transmission pathways of major zoonotic pathogens reported in Malaysia and examines how anthropogenic habitat degradation may modify their spillover risk. Data was gathered from published literature curated in public databases (PubMed, Scopus, Web of Science) as well as publications archived at the Faculty of Veterinary Medicine, Universiti Putra Malaysia. Particular attention was given to ecological interfaces created by land-use change, and to representative zoonoses illustrating wildlife–vector–domestic animal–human connectivity. Finally, the review evaluates the need to incorporate zoonotic spillover risk identification and assessment into Malaysian EIA and HIA processes within a One Health framework. Integrating wildlife ecology, veterinary health, environmental management and public-health surveillance into development planning may provide a more preventive approach to zoonotic disease emergence while simultaneously strengthening environmental, human and wildlife health protection.

DIVERSITY, TRANSMISSION PATHWAYS AND HOST OF ZOONOTIC WILDLIFE PATHOGENS IN MALAYSIA

Viruses

Transmission by direct contact/aerosols

Malaysia has experienced several zoonotic viral threats involving domestic animals, wildlife reservoirs, vectors, and human–animal interfaces. Documented examples include Nipah virus infection, mosquito-borne *Orthoflavivirus*, primate-associated *Simplexvirus* and *Alphavirus* infections, as well as bat-associated viruses such as *Paramyxovirus* and *Orthoreovirus*. The Nipah virus (*Henipavirus nipahense*) caused one of the most significant wildlife-related zoonotic disease spillovers in the country. The virus was first recognised during the 1998 – 1999 outbreak associated with pig-farming communities, where domestic pigs acted as amplifying hosts and facilitated transmission to humans. Evidence from Peninsular Malaysia indicate that frugivorous bats (*Pteropus vampyrus* and *P. hypomelanus*) are the natural sylvatic reservoir hosts (Chua *et al.* 2000, 2002b, 2010; Field *et al.* 2001; Rahman *et al.* 2010, 2013) that shed the virus in their saliva, urine, and partially eaten fruits, contaminating pig farms located near fruit orchards. Deforestation, slash-and-burn practices, and the severe 1997 – 1998 El Niño-driven drought significantly reduced fruit bats' forest habitats and the availability of food, resulting in the movement of these bats into cultivated fruit orchards (Chua *et al.* 2002a). Pigs likely became infected after consuming contaminated fruit or contacting contaminated surfaces, after which the virus spread efficiently through respiratory secretions and close contact (Chua *et al.* 2000). Epidemiological and virological investigations demonstrated that pigs acted as amplifying hosts, increasing viral transmission and facilitating subsequent infection of humans who had close contact with the infected swine (Parashar *et al.* 2000; Field 2009). This bat–pig–human transmission pathway is considered the primary mechanism responsible for the Malaysian Nipah virus outbreak and remains a classic example of zoonotic spillover involving wildlife, livestock, and humans.

Wildlife disease surveillance in Malaysia has identified several additional bat-associated viruses with zoonotic potential. The Tioman virus (*Tioman pararubulavirus*), a paramyxovirus, was isolated from fruit bats in Malaysia, specifically *P. hypomelanus* from Tioman Island (Chua *et al.* 2001; Yaiw *et al.* 2007). The Pulau virus (PRV2P, *Pteropine orthoreovirus* group) isolated from *P. hypomelanus* inhabiting Tioman Island is closely related to the Nelson Bay virus isolated in Australia (Chua 2003; Pritchard *et al.* 2006). The Melaka virus (PRV3M), Kampar Virus (PRV4K), and Sikamat virus (PRV7S) that belong to the *P. orthoreovirus* group have all been linked to acute respiratory disease in humans, although the exact bat reservoir host species and transmission route to humans remains undetermined (Chua*et al.* 2007, 2008, 2011). More recently, pathogen surveillance among bats detected alphacoronavirus and betacoronavirus in guano samples from the dusky fruit bats (*Penthetor lucasi*) in Sarawak (Habeebur-Rahman *et al.* 2023), and coronavirus in insectivorous bats (*Rhinolophus* spp.) from Pahang (Siew *et al.* 2023).

Non-human primates (hereinafter: primates) are also important reservoirs of zoonotic viruses which may be transmitted by direct contact or aerosols. These include the Herpes B virus [*Simplexvirus macacinealpha* or *Macacine alphaherpesvirus* 1 (MaHV1; B virus)] which has been detected in local populations of free-ranging long-tailed macaques (*Macaca fascicularis*) (Lee *et al.* 2015). The macaques exhibit substantial viral DNA shedding, highlighting occupational risk for personnel handling macaques during capture, transport, or conflict-management activities. Transmission risk is associated with bites, scratches, mucosal exposure, saliva, or direct contact with infected body fluids.

Transmission by arthropod vectors

The *Aedes*-borne Arboviruses of primates in Malaysia include Chikungunya (*Alphavirus chikungunya*) and Dengue (*Orthoflavivirus dengue*) viruses. In Sabah, serological titres of Arboviruses have been demonstrated in wild and semi-captive Orangutans (*Pongo pygmaeus morio*) as well as local human populations, strongly suggesting the existence of sylvatic transmission cycles (Wolfe *et al*. 2001). Chikungunya virus infection has been documented in local populations of *M. fascicularis*, supporting possible sylvatic primate–mosquito–human transmission (Marchette *et al*. 1978; Sam *et al*. 2015). While cases of this virus in Malaysia are currently sporadic, it is still considered an important emerging viral zoonosis (Lam *et al*. 2001). Sylvatic lineages have also been demonstrated for all four Dengue virus serotypes in Malaysia involving primates and forest-associated mosquitoes (Rudnick 1966; Cardosa *et al*. 2009; Wolfe *et al*. 2001; Teoh *et al*. 2010; Johari *et al*. 2019).

In Malaysian Borneo, *Aedes albopictus* and *Ae. niveus* mosquitoes have been identified as likely bridge vectors for sylvatic dengue spillover from canopy-dwelling primates. It was concluded that conversion of forests to agriculture will likely enhance the abundance of *Ae. albopictus* vectors which were found to thrive in agricultural areas (Young *et al.* 2017). Dengue is endemic in Malaysia with a total of 51,406 reported dengue cases and 43 fatalities in 2025 (World Health Organization 2026). As such, the sylvatic transmission cycle involving non-human primate hosts, and the effects of land conversion on mosquito vector abundance should not be ignored if comprehensive control and prevention measures for Dengue are to be instituted in the country.

The West Nile virus (*Orthoflavivirus nilense*) is a zoonotic *Culex* mosquito-borne flavivirus that circulates primarily through an enzootic cycle involving wild birds, with humans and other mammals serving as incidental or dead-end hosts (Rossi *et al.* 2010; Ain-Najwa *et al.* 2019). Migratory birds inhabiting the west coast of Peninsular Malaysia, namely Sand plovers (*Anarhynchus mongolus* and *A. leschenaultia*), Common Redshanks (*Tringa tetanus*), Common Sandpipers (*Actitis hypoleucos*), Black-capped kingfishers (*Halcyon pileata*), and residents including Little egrets (*Egretta garzetta*) have been shown to be important reservoirs of the virus (Ain-Najwa *et al.* 2020b). Further evidence of active transmission by *Culex* mosquitoes collected near migratory bird stopover sites along the west coast of Peninsular Malaysia further supports the role of migratory birds in virus maintenance and dispersal (Natasha *et al.* 2023). Antibody titres have also been demonstrated in long-tailed macaques and several bat species (*Cynopterus brachyotis*, *Emballonura monticola* and *Rhinolophus siamensis*) (Ain-Najwa *et al.* 2020a), indicating their role in local transmission cycles, albeit considered less significant than that of birds.

The Japanese encephalitis virus (*Orthoflavivirus japonicum*) is another *Culex* mosquito-borne zoonotic flavivirus maintained in enzootic cycles involving mosquitoes, pigs, and birds. In Malaysia, Japanese encephalitis has been reported for decades and has been described as endemic in several regions, particularly in rural and agricultural landscapes (Kreidl *et al.* 1999; Kumar *et al.* 2018a, 2018b). Serological evidence in domestic livestock, including pigs, bovids, and goats, support the role of pigs as amplifying hosts and wetland birds (including herons and egrets) as the main reservoir hosts that sustain viral circulation and contribute to geographic spread through migratory movement (Oliveira *et al.* 2017; Levesque *et al.* 2024; Kumar *et al.* 2018a). In addition to wild avian hosts, serological evidence indicate exposure among macaques, highlighting the potential involvement of a broader vertebrate host range for Japanese encephalitis transmission in Malaysia (Kumar *et al.* 2018b).

Bacteria

Transmission by arthropod vectors

A number of zoonotic bacteria have been isolated from wild animals and associated arthropod vectors in Malaysia, especially among rodents, non-human primates and birds. The major arthropod-borne zoonotic haemobacteria comprise species of the order Rickettsiales which include the genera *Orientia*, *Rickettsia* and *Anaplasma*. Pathogenic members of Rickettsiales cause a spectrum of acute febrile illnesses in humans that commonly manifest in fever, headache, myalgia, and may progress to vascular injury, neurological disease, respiratory failure, multiorgan dysfunction and death (Valbuena and Walker 2009; Robinson *et al.* 2019; Stewart *et al.* 2021). *Orientia tsutsugamushi*, the causative agent of scrub typhus, is the best-established wildlife-associated zoonotic Rickettsiales in Malaysia, where its transmission cycle between larval trombiculid mites (chiggers) and small-mammal hosts has been extensively studied (Nadchatram 1970; Walker *et al.* 1973; Muul *et al.* 1977; Muul and Chai 1978). A number of forest-dwelling and peridomestic rodents (*Rattus* spp.) and common treeshrews (*Tupaia glis*) are known to harbour the bacterium (Muul *et al.* 1977; Muul and Chai 1978; Ernieenor *et al.* 2021; Alkathiry *et al.* 2022; Mohd-Azami *et al.* 2023).

In addition, several spotted fever group *Rickettsia* with potential zoonotic significance and related to the human-infective species have been detected among wild rodents in the country (Tay *et al.* 2014). The bacterium closely related to *Rickettsia felis*, the causative agent of flea-borne spotted fever, has also been detected in long-tailed macaques, although their role as reservoirs is yet to be established (Tay *et al.* 2015). More recently, *R. felis* DNA was detected in *Laelaps* mites collected from forest rodents (*Maxomys whiteheadi* and *Bandicota indica*) in Selangor, indicating the possible role of these small mammals as sylvatic reservoirs (Mohamad Tahir *et al.* 2025). In addition, *Amblyomma varanense* and *A. helvolum* ticks from Indian pythons (*Python molurus*), and *A. helvolum* from Malayan spitting-cobras (*Naja sumatrana*) in Selangor, have also been shown to harbour spotted fever group Rickettsiae (Kho *et al.* 2015). *Rickettsia* was also detected in ticks collected from wild boars (*Sus scrofa*) in an Orang Asli community, indicating the importance of surveillance for tick borne-pathogen from wildlife at forest–human interfaces (Lim *et al.* 2020).

Wildlife-associated *Bartonella* in Malaysia has been detected mainly in rodents and their associated ectoparasites. Various species of wild rats including those in urban habitats are known to harbour this zoonotic bacterium (Tay *et al.* 2014, 2016; Blasdell *et al.* 2019b; Low *et al.* 2020). *Bartonella* has also been detected in ticks associated with rats, including *Dermacentor auratus* and *Haemaphysalis hystricis* collected from *Rattus tiomanicus* (Asyikha *et al.* 2020), and *Amblyomma cordiferum* infesting *Rattus rattus diardii* (Kazim *et al.* 2025). Bat-associated *Bartonella* has also been reported from bat flies from the families Nycteribiidae and Streblidae, but its zoonotic importance remains uncertain (Peng *et al.* 2024).

Coxiella, a gram-negative obligate intracellular bacterium, has been demonstrated in ticks (*Dermacentor steini* and *H. hystricis*) infecting *S. scrofa* from Selangor (Khoo *et al.* 2016). While the DNA of *Coxiella burnetii* (the agent for Q Fever in humans and animals) was amplified from these ticks, the role of ungulates as reservoirs of Q Fever in Malaysia remains to be elucidated. Tick-borne *Borrelia* spp. including relapsing-fever *Borrelia* (RFB) (*B. miyamotoi*) and Lyme disease *Borrelia* (LDB) (*B. yangtzensis*) genotypes have also been reported in ticks (*Ixodes granulatus*) infesting synanthropic rodents in Peninsular Malaysia (Khoo *et al.* 2018).

Transmission by ingestion (fecal-oral route)

Wild animals are known to harbour a number of zoonotic gastrointestinal bacteria, which are shed in their faeces. While most are normal inhabitants and commensals, pathogenic variants of *Escherichia coli* such as Shiga toxin-producing *E. coli* (STEC), enteropathogenic *E. coli* (EPEC), enteroinvasive *E. coli* (EIEC), enterotoxigenic *E. coli* (ETEC), and enterohaemorrhagic *E. coli* (EHEC) are capable of causing diarrhoea, haemorrhagic colitis, and haemolytic uraemic syndrome in humans (Shah *et al*. 2018). In Malaysia, pathogenic *E. coli* carriage has been demonstrated in birds, bats and rodents sampled from forest, oil palm plantations and human settlements (Bilung *et al.* 2014; Mohamed *et al.* 2022). In addition, Multiple Antibiotic Resistant (MAR) *E. coli* has been detected in bats and rodents for Sarawak (Apun *et al.* 2008).

Salmonella is another gastrointestinal bacterium of zoonotic concern, with birds and reptiles acting as important reservoirs. In Malaysia, *Salmonella* carriage has been reported in both wild and captive snakes (*Malayopython reticulatus*, *Python bivittatus*, *Coelognathus radiatus* and *N. sumatrana*) (Nur Mahiza *et al.* 2007; Abatcha *et al.* 2013), lizards (Noor Asyikin *et al.* 2006; Cheng *et al.* 2014), geckos (Fazhana *et al.* 2007) and chelonians (Noorazrena and Saleha, 2008). These studies revealed the presence of human-infective serovars including *S. typhimurium* with certain strains shown to be resistant to commonly used antibiotics. Reptile-associated salmonellosis is of concern as lizards and chelonians are common pets and transmission can occur if proper sanitisation is not practiced after handling. In addition, metagenomic surveillance revealed the presence of *Salmonella* among rodents (*Niviventer cremoriventer* and *Rattus* spp.) dwelling at forested areas close to human inhabitation in Sarawak (Azmi *et al.* 2025). Zoonotic species of *Campylobacter* with potential of causing acute bacterial gastroenteritis in humans have also been reported among peridomestic wild birds and poultry in the country (Ganapathy *et al.* 2007; Mohamed-Yousif *et al.* 2019), thus increasing the risk of human transmission in the urban environment.

Transmission by direct contact, ingestion, or aerosols

Leptospira is a widespread zoonotic bacterial pathogen associated with Malaysian wildlife. These motile spirochaetes are transmitted through direct contact with urine, tissues or fluids from infected animals, or indirectly through contaminated soil, mud, freshwater, floodwater or vegetation. In Malaysia, wildlife-associated leptospirosis is strongly linked to rodents and small mammals, including bats, squirrels, treeshrews, mongooses, porcupines, and primates (Thayaparan *et al.* 2013, 2014; Siti-Nurdyana *et al.* 2016; Suut *et al.* 2018; Philip and Ahmed 2023). Rodents are important reservoirs as they may carry *Leptospira* in the kidneys and shed them in urine. Over 40% of the rats (*Sundamys muelleri*, *R. rattus*, *R. exulans*) and squirrels (*Callosciurus notatus*) sampled in central Sarawak were positive for anti-*Leptospira* antibodies (Suut *et al.* 2018).

In Peninsular Malaysia, urban-dwelling rodents have also been confirmed as important zoonotic reservoirs. Benacer *et al.* (2013) isolated and molecularly characterised *Leptospira interrogans* and *L. borgpetersenii* from urban rats in Kuala Lumpur. These are pathogenic species associated with human leptospirosis, supporting the role of urban rodents as a major public health risk in Malaysian cities. The influence of urbanisation on rodent-associated *Leptospira* is further corroborated by a study in Sarawak whereby rodents sampled in urban sites had a higher molecular prevalence of the bacteria compared to those inhabiting rural areas (Blasdell *et al.* 2019a). Zoonotic species of *Leptospira* are also known to infect rodents collected from recreational forests and zoological parks in Peninsular Malaysia (Shafie *et al.* 2022), thus posing a risk to visitors and tourist who may come in contact with contaminated water bodies, mud and soil.

In addition to rodents, *Leptospira* exposure has also been demonstrated among a variety of primates (*M. nemestrina*, *M. fascicularis*, *Nasalis larvatus*, *Hylobates muelleri*, *Trachypithecus cristatus*, *P. pygmaeus*), bats (*C. brachyotis*, *P. lucasi*, *Nycteris tragata*, *Hipposideros cervinus*) and mongooses (*Herpestes brachyurus*) from recreational parks and wildlife tourism areas in Sarawak (Thayaparan *et al.* 2013, 2014), indicating that a broader taxon of wild mammals may be involved in the sylvatic transmission cycle and epidemiology of leptospirosis in the country.

Mycobacterium from wild mammals in Malaysia, including species of the *Mycobacterium tuberculosis* complex such as *M. bovis*, have been detected in wild boar (*S. scrofa*) from Selangor (Lekko *et al*. 2021a, 2021b) using both molecular and serological techniques. The detection of *M. bovis* DNA in the local wild boar population is of public health concern because it is a recognised zoonotic pathogen (Suraiya and Farakhin 2018). Since human infection can occur through ingestion, inhalation and direct contact through mucous membranes or broken skin, *Mycobacterium* is of concern for butchers handling wild boar meat, wildlife personnel, farmers at the wildlife–livestock interface, and consumers of inadequately cooked meat.

Protozoa

Transmission by arthropod vectors

Zoonotic malaria is widespread throughout Southeast Asia, and remains the most important arthropod-borne parasitic infection of in Malaysia (Singh *et al.* 2004, Cox-Singh *et al.* 2008; Vythilingam *et al.* 2014; Johnson *et al.* 2024) The disease is caused primarily by the haemoprotozoa *Plasmodium knowlesi* (Coatney *et al.* 1971; Singh *et al.* 2004) although human infections with other zoonotic simian malaria parasites such as *P. cynomolgi*, *P. inui*, *P. coatneyi*, and *P. simiovale* have been recently reported in the country (Ta *et al.* 2014; Grignard *et al.* 2019; Nada-Raja *et al.* 2020; Liew *et al.* 2021; Yap *et al.* 2021). Macaques (*M. fascicularis* and *M. nemestrina*) are the main reservoir hosts (Lee *et al.* 2011; Nada-Raja *et al.* 2022; Johnson *et al.* 2024) and transmission to humans is through the bites of infected forest-associated *Anopheles* mosquitoes (Vythilingam *et al.* 2006, 2008). Multilocus genotyping of *P. knowlesi* infections in humans have shown distinct divergent subpopulations associated with specific macaque hosts and geographical location (Divis *et al.* 2017), with no evidence of sustained human to human transmission (Fornace *et al.* 2023).

Malaysia remains a hotspot for zoonotic malaria with a significant disease burden. In 2024, there were 2164 global cases of *P. knowlesi*, of which Malaysia remains the principal contributor, accounting for 89.0% of these cases and all three deaths (World Health Organization 2025). The sustained sylvatic transmission cycle of zoonotic malaria in primate reservoirs presents a major obstacle for malaria elimination in the country (Chin *et al.* 2020; Mohammad *et al.* 2022). The risk of transmission is associated with environmental and land-use factors, including forest fragmentation, deforestation, and agricultural expansion, which decreases the transmission interface between macaque hosts, mosquito vectors, and humans (Fornace *et al.* 2016, 2019; Johnson *et al.* 2024).

Transmission by ingestion of infective stages – Gastrointestinal protozoa

Many genera of gastrointestinal (GI) protozoa are of zoonotic concern and cause disease in both animals and humans, particularly in rural and Indigenous communities in Malaysia where close contact between animals, humans, and contaminated water sources facilitates faecal-oral transmission. These GI protozoa may cause acute or chronic gastroenteritis, diarrhoea, malabsorption, and mucosal damage, which may be pronounced in immunocompromised individuals and children (Kelly 2013; Di Genova and Tonelli 2016).

Giardia duodenalis is a potentially zoonotic GI flagellate and is relatively common among livestock and companion animals in Malaysia (Farizawati *et al.* 2005; Lim *et al.* 2013; Ngui *et al.* 2014; Sai Gythri and Sharma 2020). *Giardia* infection has also been detected among wildlife in Malaysia suggesting that they may serve as reservoirs for spillover to domestic animals and zoonotic transmission. In Peninsular Malaysia, *Giardia* has been detected in wild macaques (*M. fascicularis*) (Goh and Sharma 2024) and siamangs (*Symphalangus syndactylus*) (Tan and Sharma 2017) housed in local zoos. In Sabah, the flagellate was detected in free-ranging Bornean orangutans (*P. p. morio*) (Tsen *et al.* 2019). *Giardia* is also known to infect synanthropic rodents (*R. rattus diardii*, *R. norvegicus*, *R. tiomanicus*) (Tan *et al*. 2019; Mohd-Qawiem *et al* 2022, 2024; Zainol and Sharma 2022) making them prime reservoir hosts for human transmission. Recent molecular studies in Sabah reported the first detection of zoonotic *Giardia* assemblages A and B in wild hornbills (*Rhinoplax vigil* and *Buceros rhinoceros*) from the Kinabatangan Wildlife Sanctuary, highlighting the potential role of free-ranging birds in maintaining environmental contamination and parasite transmission (Tan *et al.* 2025). In addition, environmental contamination of rivers and recreational waters with *Giardia* cysts supports the possibility of indirect transmission between peridomestic wildlife, domestic animals, and humans through shared water resources (Lim *et al.* 2009; Lee *et al*. 2014). Molecular detection also revealed the presence of zoonotic *Giardia* assemblages in surface water samples from a local zoo (Lim *et al*. 2009) indicating the potential of these captive wild animals to shed human-infective cysts in the peridomestic environment.

Balantidium coli is a ciliate which infects domestic pigs (Tan *et al*. 2014) and dogs (Ngui *et al*. 2014). Among wild mammals in Peninsular Malaysia, Balantidium has been demonstrated in captive Malayan tapirs (*Tapirus indicus*) (Mustapa *et al*. 2014), Sumatran orangutans (*P. abelii*), Bornean orangutans (*P. pygmaeus*), macaques (*M. arctoides*, *M. nemestrina*, *M. fascicularis*), white-handed gibbons (*H. lar*) and siamangs (*S. syndactylus*) (Lim *et al*. 2008, Tan and Sharma 2017). *Balantidium* has also been detected among captive and free-ranging orangutans in Sabah (Tsen *et al*. 2019). To date there are no records of *Balantidium* in birds, reptiles or amphibians from Malaysia.

Entamoeba has been detected in domestic dogs and cats (Ngui *et al*. 2014, 2020) and goats (Tan *et al*. 2017) in Malaysia. Wild animals commonly infected with *Entamoeba* include great apes (*P. abelii*, *P. p. morio*), small apes (*H. lar*, *S. syndactylus*) and macaques (*M. arctoides*) (Tan and Sharma 2017). *Entamoeba* infection has also been demonstrated among synanthropic rodents (*R. argentiventer*, *R. tiomanicus*, *R. exulans*) in Kuala Lumpur (Siti Shafiyyah *et al*. 2012; Lau *et al*. 2014).

Blastocystis, a common intestinal stramenopile reported in humans, is known to infect domestic animals such as dogs, cats, goats, sheep and cattle (Tan *et al*. 2013; Hemalatha *et al*. 2014; Lim *et al*. 2017; Rauff-Adedotun *et al*. 2020) in the country. Among captive primates, *Blastocystis* has been detected in orangutans (*P. abelii*, *P. p. morio*), small apes (*H. lar*, *S. syndactylus*) and macaques (*M. arctoides*, *M. nemestrina*) (Lim *et al*. 2008; Tan and Sharma, 2017). The protozoa have also been isolated from free-ranging Water monitors (*Varanus salvator*) and Mouse deer (*Tragulus* spp.) living in close proximity to human settlements on Tioman Island (Mohd Zain et al., 2017), as well as urban-dwelling rodents (*Rattus* spp.) (Premaalatha *et al*. 2017, 2018; Farah Haziqah *et al*. 2018).

Cryptosporidium is an important zoonotic enteric protozoan because infected hosts shed environmentally resistant oocysts that can contaminate water, soil, food, fomites, and animal-contact environments (Farizawati *et al*. 2005). It is known to infect various domestic animals including companion animals and ruminant livestock (Lee *et al*. 1989; Abdullah

et al. 1999; Ngui *et al*. 2014; Tan *et al*. 2017). *Cryptosporidium* has also been demonstrated in various taxa of animals in zoological facilities (including tigers, orangutans, macaques, langurs and birds), highlighting the risk of exposure and transmission to animal handlers and visitors (Lim *et al*. 2007, 2008; Quah *et al*. 2011; Tan and Sharma 2017).

Transmission by ingestion of infective stages – Tissue protozoa

Tissue-infecting coccidian protozoa including *Toxoplasma* and *Sarcocystis* are important zoonotic pathogens in Malaysia (Brandon-Mong *et al.* 2015; Latif and Muslim 2016). These protozoa have an obligatory two-host life cycle, in which sexual development occurs in the intestine of a definitive carnivorous or omnivorous host, and asexual development produces sarcocysts in the muscles or tissues of an intermediate host. Transmission occurs through ingestion of sporulated oocysts from contaminated soil, water, feed, or food; ingestion of tissue cysts in raw or undercooked meat; and congenital transmission from mother to foetus (Tenter *et al.* 2000; Hill and Dubey 2002).

Although *Toxoplasma* infection is usually asymptomatic or mild (fever, body aches, and swollen lymph nodes) in healthy adults, severe brain and eye damage have been reported in immunocompromised individuals. Transmission of *Toxoplasma* from infected pregnant mothers to their foetus (i.e., congenital toxoplasmosis) may result in significant pathology and birth defects. Domestic carnivores especially cats are the primary reservoirs of *T. gondii*, although the parasite has also been detected in local pigs, goats, cattle, dogs and poultry (Thomas 1979; Chandrawathani *et al.* 2008; Sabri *et al.* 2019; Tan *et al.* 2020; Sabrina *et al.* 2023b). Wild mammals (*N. coucang*, *T. cristatus*, *M. fascicularis*, *M. nemestrina*, *T. glis*, *Maxomys rajah*, *Rattus* spp.) have also been shown to either be actively infected or possess antibodies to the parasites indicating exposure (Zaman and Goh 1970; Lokman *et al.* 1989; Normaznah *et al.* 2015).

Sarcocystis is another important tissue protozoa with a number of focal outbreaks involving both locals and tourists (Latif and Muslim 2016). Humans can act as both intermediate hosts (infection by ingesting oocysts in contaminated water, food) and develop muscular-skeletal related symptoms, or definitive hosts (infection by ingesting mature sarcocysts in meat) and develop gastrointestinal related symptoms. Domestic carnivores (cats and dogs) are known definitive hosts in Malaysia, while cattle, water buffaloes, sheep, goats, pigs and poultry are proven intermediate hosts that develop infective stages (sarcocysts) in their muscles, organs and tissues (Latif *et al.* 2013; Kutty *et al.* 2015; Latif and Muslim 2016; Sabrina *et al.* 2023a). Among local wild animals, *Sarcocystis* has been reported in long-tailed macaque (Kan *et al.* 1979), Sunda slow loris (Zaman and Goh 1968), various species of rodents (Kan 1979; Ambu *et al.* 2011; Fong *et al.* 2014), snakes (*N. kaouthia*, *Ophiophagus hannah*, *M. reticulatus*, *Ovophis convictus*, *Ptyas carinata*, and *Boiga nigriceps*) (Fadil *et al.* 2019; Lau *et al.* 2013), and various captive animals including native species such as sun bear (*Helarctos malayanus*), hornbill (*Berenicornis comatus*), and fish owl (*Ketupa ketupu*) (Latif *et al.* 2010).

Helminths

Transmission by arthropod vectors

Brugia malayi and *B. pahangi* are mosquito-borne filarial nematodes of major veterinary and public-health importance in Malaysia, where the former is a recognised as the causative agent of human lymphatic filariasis, whereas *B. pahangi* is primarily an animal parasite with sporadic zoonotic infection in humans (Laing *et al*. 1960; Mak 1983, 1984; Naing *et al.* 2024). Domestic cats are among the most important animal hosts for both filarial species and act as principal reservoirs (Mak 1984; Muslim *et al*. 2013b). Dogs may also be infected (Vinnie-Siow *et al.* 2019, 2022) but their role in transmission is minimal due to the low prevalence reported. Among wild mammals, *B. pahangi* has been reported in clouded leopards (*Neofelis nebulosa*) (Zahedi *et al.* 1986) and Indochinese leopards (*Panthera pardus*

delacouri) (Strauss and Sivanandam 1966), indicating that wild felids can be naturally infected although their role as major maintenance reservoirs remains undetermined. Wild primates are potential sylvatic reservoirs of *B. malayi* with reports of infected *M. fascicularis*, *T. cristatus*, *T. obscurus* and *P. melalophos* (Buckley and Edeson 1956; Lim and Mak 1978; Mak 1983; Mak *et al.* 1988, 1990). Infection experiments have shown potential carriage of *B. malayi* among civets (*Paradoxurus hermaphroditus*) and Sunda slow loris (*N. coucang*) (Laing *et al*. 1960).

Transmission by ingestion of infective stages

A number of zoonotic helminths are transmitted to humans by ingestion of infective stages, which include the embryonated ova or immature stages (larvae) found in water, food, or contaminated environment. While there are numerous studies on the prevalence of these zoonotic helminths among domestic animals and livestock in Malaysia, data on their infection among wildlife is extremely limited and warrants further investigation. *Toxocara*, *Trichuris* and *Ancylostoma* are relatively common genera of zoonotic gastrointestinal nematodes that infect domestic cats and dogs in Malaysia (Amin-Babjee 1978; Abdullah *et al*. 1990; Ngui *et al*. 2014; Tun *et al*. 2015).

In humans, the migration of the larval stages of *Toxocara* causes pathology of the visceral organs (Visceral Larva Migrans) and eyes (Ocular Larva Migrans) especially in young children and immunocompromised individuals. Among wild mammals, *Toxocara* has been reported in native (*Panthers tigris jacksoni*, *Felis bengalensis*) and exotic felids housed in a local zoologic park (Lim *et al*. 2008), as well as wild civets (*Viverra tangalunga*) (Colón and Patton 2012).

Trichuris causes gastrointestinal related pathology in humans, and is known to infect a diversity if wild mammals including captive and free-ranging primates (*N. larvatus*, *P. p. morio*, *M. fascicularis*, *M. nemestrina*, *T. obscurus*, *T. cristatus*, *H. muelleri*) (Kilbourn *et al*. 2003; Lim *et al*. 2008; Kuze *et al*. 2010; Klaus *et al*. 2018; Teo *et al*. 2019; Tuan Said *et al*. 2022), carnivores (*H. malayanus*, *V. tangalunga*) (Colón and Patton 2012; Abdul -Mawah *et al*. 2023) and wild rodents (*Rattus* spp.) (Leong *et al*. 1979; Premaalatha *et al*. 2018; Tijjani *et al*. 2020).

The larval stage of *Ancylostoma* causes Cutaneous Larva Migrans in humans characterised by creeping eruptions of intensely rash, itching and inflammation. In the wild, this hookworm has been reported from civets (*V. tangalunga*) in Sabah (Colón and Patton 2012). Hookworms (genus not specified) have also been detected in captive primates (*P. pygmaeus*, *H. muelleri*, *M. nemestrina* and *M. arctoides*) (Lim *et al*. 2008).

Ascaris is a large nematode of the digestive tract of humans, with swine acting as principal domestic animal hosts. In Malaysia, both wild and domestic pigs are known to harbour this parasite (Lee *et al*. 1987; Vinnie-Siow *et al*. 2026). Among non-human primates, *Ascaris* has been detected in captive *T. cristatus* and *H. muelleri* (Lim *et al*. 2008), and free-ranging *P. pygmaeus* in Sabah (Kuze *et al*. 2010).

Angiostrongylus malaysiensis is a potentially zoonotic heteroxenous nematode with the larval stages in gastropods, and sexually mature adults and first-stage larvae in the pulmonary artery and lungs of rats, respectively. In Malaysia, various rodent species occupying forest fringe habitats (Lim and Ramachandran 1979) as well as recreational parks in within the city (Low *et al*. 2023) have been shown to be important reservoirs of the parasite.

The trematodes of major zoonotic concern in Malaysia include *Schistosoma* and *Paragonimus*; both genera use snails as intermediate hosts. Human infection with the blood fluke *Schistosoma* is through skin penetration of cercariae which are released from infected snails. The domestic animal hosts of *Schistosoma* in Malaysia include cattle, water buffalo and goats (Krishnasamy *et al.* 1991, 1998; Singh *et al.* 1997; Tan *et al.* 2015; Tookhy *et al.* 2024). Rodent species that act as principal sylvatic hosts for *Schistosoma* include *S. muelleri*, *R. tiomanicus*, *R. argentiventer*, *R. tanezumi*, and *B. indica* (Greer *et al.* 1988; Singh *et al.* 1992, 1997). Thus far, only one report from Sabah has identified free-ranging long-tailed macaque as a host for *Schistosoma* (Kuntz and Myers 1978).

Humans get infected with *Paragonimus* by ingesting metacercariae in infected freshwater crustaceans that are inadequately cooked or pickled. The parasite causes pathology to the lungs, central nervous system and visceral organs. While domestic cats and dogs may be experimentally infected (Kim 1978; Habe *et al.* 1996), the natural definitive hosts recorded from Malaysia include wild felids (*Panthera tigris jacksoni*, *Prionailurus planiceps*, *Catopuma temminckii*, *Panthera pardus*) as well as macaques (*M. fascicularis*) (Lee and Miyazaki 1965; Lim and Betterton 1977; Groves *et al*. 1967).

Cestodes, namely *Hymenolepis*, *Spirometra* and *Taenia* are noteworthy zoonotic pathogens in Malaysia. *Hymenolepis* primarily infects rodents while humans are accidental definitive hosts that acquire infection by inadvertently ingesting arthropods containing cysticercoids, which may be found in contaminated cereals, flour, dried foods or other stored products. The cestode has been detected in a number of synanthropic rodents including *R. tanezumi*, *R. tiomanicus*, *R. norvegicus*, *R. argentiventer* and *R. exulans* (Leong *et al*. 1979; Krishnasamy *et al*. 1980; Paramasvaran *et al*. 2009; Mohd Zain *et al*. 2012; Shafiyyah *et al*. 2012; Tijjani *et al*. 2020), highlighting the risk of rodent contamination of food-storage areas, kitchens, animal-feed stores, markets and eateries.

Spirometra has a complex aquatic life cycle involving copepods, vertebrate intermediate or paratenic hosts, and carnivorous definitive hosts. The adult tapeworms inhabit the small intestine of felids, canids and other carnivorous mammals, whereas their plerocercoid larvae (spargana), reside in the tissues of amphibians, reptiles, mammals and occasionally birds. Humans may acquire the infection by drinking untreated water containing infected copepods and eating raw or inadequately cooked tissues containing the plerocercoid larvae (Kuchta *et al*. 2024). The larvae may subsequently migrate into subcutaneous tissues, muscles, the eye, central nervous system or internal organs. In Malaysia, coproscopy revealed adult *Spirometra* infection among dogs and cats in rural areas (Ngui *et al*. 2014) as well as captive leopard cats (Lim *et al*. 2008), while the spargana stage as been detected in frogs (*Fejervarya cancrivora*) from Selangor (Kavana *et al*. 2015).

Humans are the normal definitive hosts of the adult *Taenia* tapeworms, whereas domestic pigs or cattle act as the principal intermediate hosts depending on the *Taenia* species. Humans develop intestinal taeniasis after consuming viable cysticerci in inadequately cooked pork, and human cysticercosis occurs when *Taenia* ova are ingested. The larvae migrate to the skeletal muscles, subcutaneous tissues, the eye or central nervous system, where neurocysticercosis may develop (Teoh 1976; Chua *et al*. 2017). Larval stages of *Taenia* have been recovered from various species of rats including *R. rattus*, *R. tanezumi* and *R. norvegicus* (Leong *et al*. 1979; Syed-Arnez and Mohd Zain 2006; Mohd Zain *et al*. 2012; Tijjani *et al*. 2020; Yamamoto *et al*. 2024). The prevalence of zoonotic cestodes among wild animals in Malaysia remains relatively under studied. Future surveillance should prioritise molecular identification because coproscopy alone may not be reliable to distinguish between species of zoonotic concern.

ANTHROPOGENIC LANDSCAPE ALTERATION AND ITS EFFECTS ON ZOONOTIC DISEASE TRANSMISSION

Human-mediated landscape alterations, including deforestation, forest fragmentation, agricultural expansion, mining, road construction, peatland drainage, and urban encroachment, can alter the dynamics of zoonotic disease transmission by changing the contact interface between wild animal reservoirs, feral and domestic animals, livestock, vectors, intermediate hosts, and humans (Patz *et al.* 2004; Shah *et al.* 2019; Gibb *et al.* 2020; Plowright *et al.* 2021, 2024; Johnson *et al.* 2024). Land-use change is a significant driver of zoonotic disease emergence because it disrupts the ecological balance, displaces many wildlife species, increases human access to forested areas, and establishes new wildlife–human interfaces (Rulli *et al.* 2025). Degraded and anthropogenically modified landscapes have also been shown to increase the population of peri-domestic wildlife and intensify zoonotic pathogen reservoirs and spillover (Gibb *et al.* 2020). These detrimental effects of land conversions are particularly apparent in Southeast Asia, a region with high wildlife biodiversity, dense human populations, expanding crop and livestock frontiers, and dependence on forest-edge livelihoods (Shah *et al.* 2019; Tobin *et al.* 2024).

The primary influence of habitat degradation on zoonotic disease transmission is by the creation and expansion of ecotones (ecological transition zones) between adjacent natural and disturbed habitats (e.g. forest–agriculture/plantations, forest–livestock farms, and forest–human settlement). These ecotones increase the contact between vectors, wildlife, domestic animals, and humans that would otherwise have minimal interaction (Despommier *et al.* 2006; Plowright *et al.* 2021). Transition habitats often contain high resource heterogeneity, altered microclimates, disturbed vegetation, poor drainage, livestock waste and feed, and human refuse; all of which can influence host and vector population dynamics. Ecotones are also frequently inhabited by synanthropic animal taxa with wide ecological plasticity, including rodents, bats, non-human primates, wild pigs, small carnivores, birds, reptiles, as well as feral dogs and cats. These taxa efficiently exploit food resources and shelter associated with human-modified landscapes, which often result in high population expansion rates. This is of major public health concern since many species of synanthropic wildlife serve as important pathogen reservoirs, amplifiers, and bridge hosts in zoonotic disease transmission systems (Gibb *et al.* 2020; Plowright *et al.* 2021, 2024).

Habitat degradation does not necessarily create new pathogens; rather, it changes ecological and social conditions that increase the probability of pathogen spillover (Plowright *et al.* 2021, 2024). Forest clearance and fragmentation can compress wildlife into smaller habitat patches, alter food availability, and push reservoir species into closer contact with farms, orchards, plantations, settlements, and peri-urban environments. These changes may increase exposure to infectious saliva, urine, faeces, blood, arthropod vectors, or contaminated water and soil. Agricultural land use has also been associated with elevated infectious disease risk in Southeast Asia, with one analysis reporting that people living or working in agricultural land-use settings in the region had higher odds of infection than those in non-agricultural settings (Shah *et al.* 2019).

The effects of human-modified landscapes and ecotonal interfaces on zoonotic disease transmission is exemplified in the local 1998/99 Nipah virus (NiV) outbreak which linked habitat disruption, agricultural intensification, wildlife reservoirs, and livestock amplification to the infection in humans (Looi and Chua 2007; Kulkarni *et al.* 2013). Fruit bats (*Pteropus hypomelanus* and *P. vampyrus*) were identified as the natural reservoir host of the virus, while pigs served as amplifiers. Evidence suggests that spillover occurred when fruit bats were drawn into orchard surrounding pig-farms, where bat-contaminated fruit or excretions likely exposed pigs to the virus. Haze-related flowering and fruiting failure of forest trees coupled with increasing deforestation probably drove the migration of the forest

fruit bats to cultivated orchards (Looi and Chua 2007). This example provides evidence for the complex interaction between diseases epidemiological risk factors including habitat alteration, climate change, wildlife reservoirs and domestic animal amplifiers which created a high-risk bat–pig–human transmission pathway (Looi and Chua 2007; Pulliam *et al.* 2012).

The widespread and potentially fatal zoonotic malaria in Southeast Asia caused by *Plasmodium knowlesi*, *P. cynomolgi* and *P. inui* provides another compelling example of deforestation and ecotone-mediated zoonotic disease transmission (Fornace *et al.* 2016; Johnson *et al.* 2024; Vythilingam and Jeyaprakasam 2024). These apicomplexan haemoparasites are naturally maintained in non-human primates (mainly macaques) and are transmitted to humans by the bite of forest-associated *Anopheles* mosquitoes (Warthon *et al.* 1962; Coatney *et al.* 1971; Vythilingam *et al.* 2008, 2014, 2021). In Southeast Asia, zoonotic malaria remains a major obstacle to malaria elimination certification as currently defined by the World Health Organization (WHO) because it is maintained in non-human primate reservoirs and cannot be removed through human case management alone (Fornace *et al.* 2023). This is of particular concern locally as Malaysia records the highest number of human zoonotic malaria cases and is a global hotspot of *P. knowlesi*, accounting for 89.0% of all reported infections and all three zoonotic malaria deaths in 2024 (World Health Organization 2025).

It has been demonstrated that agricultural expansion and forest fragmentation influence *P. knowlesi* exposure, supporting links between land-use change and zoonotic malaria transmission (Fornace *et al.* 2019). Vector studies in Sabah also show that human exposure to zoonotic malaria vectors occurs across village, farm, and forest habitats, while vector composition changes across forested to deforested ecotones in emerging areas of zoonotic malaria transmission (Wong *et al.* 2015; Hawkes *et al.* 2019; Brown *et al.* 2020). This is important because fragmented landscapes may create suitable vector habitats and increase outdoor biting exposure during farming, plantation work, forest visits, hunting, and evening peri-domestic activities.

Recent regional modelling indicates that *P. knowlesi* risk remains widespread across Southeast Asia and is shaped by environmental variables, forest cover, and land-use dynamics, including plantation development (Johnson *et al.* 2024; Tobin *et al.* 2024). Collectively, these studies have shown that anthropogenic habitat degradation functions primarily as a risk amplifier rather than as a single independent cause of zoonotic emergence. Ecotones are central to this process because they represent the spatial interfaces where wildlife reservoirs, domestic animals, vectors, contaminated environments, and humans most frequently intersect. These examples support a One Health interpretation in which land-use policy, biodiversity conservation, agricultural planning, vector ecology, wildlife surveillance, livestock biosecurity, water management, and public-health preparedness are treated as interconnected components of zoonotic disease prevention.

ZOONOTIC DISEASE SPILLOVER RISK: A VITAL COMPONENT FOR ENVIRONMENTAL IMPACT ASSESSMENTS (EIAs)

Environmental Impact Assessment (EIA) in Malaysia should explicitly include assessment of zoonotic disease spillover risk because anthropogenic landscape alterations and wildlife displacement can alter the wildlife–human disease transmission interface which has been shown to influence the spread of zoonotic diseases. Under Malaysia's EIA system, activities listed as "prescribed activities" under the *Environmental Quality (Prescribed Activities) (Environmental Impact Assessment) Order 2015* are subject to EIA requirements before implementation or approval (Department of Environment Malaysia 2015). Although the Order does not expressly require pathogen-specific zoonotic spillover assessment, several

prescribed activities listed in the First and Second Schedules are directly relevant to spillover risk because they involve forest conversion, wildlife-habitat disturbance, livestock intensification, wetland drainage, tourism development in protected areas, road construction near environmentally sensitive areas, waste treatment, housing, and township development. These activities can alter ecological interfaces among wildlife reservoirs, domestic animals, vectors, workers, and nearby communities; therefore, justifying zoonotic spillover risk evaluation as part of the environmental and health-risk assessment.

Health Impact Assessment (HIA) is also recognised within Malaysia's National Environmental Health Action Plan, 2021. The Malaysian HIA-in-EIA guidance describes HIA as a systematic process for identifying the likely adverse health consequences of proposed projects and provides requirements for conducting and reporting HIA within EIA (Ministry of Health Malaysia 2021). However, conventional EIA and HIA practice often emphasises pollution, water quality, air quality, occupational health, waste management, and vector breeding, while wildlife-associated pathogen spillover is neglected and not considered a formal risk pathway. In a biodiversity-rich country such as Malaysia, this is a critical gap because development projects can change wildlife movement, feeding behaviour, roosting patterns, vector ecology, livestock exposure, and human–wildlife contact.

The Nipah virus outbreak illustrates this clearly: deforestation, ecological stress, fruit cultivation near pig farms, and agricultural intensification created conditions for repeated bat-to-pig transmission of the virus (Chua 2002; Pulliam *et al.* 2012; Rahman *et al.* 2010, 2013). Similarly, sylvatic dengue studies in Malaysia show that forest conversion and urbanisation can alter *Aedes* mosquito communities, increasing bridge-vector exposure between wildlife, humans, and modified environments (Young *et al.* 2017; Johari *et al.* 2019). Wildlife displacement is also relevant because long-tailed macaques in Peninsular Malaysia have been shown to shed Macacine Herpesvirus 1, creating occupational risks during capture, translocation, rescue, or conflict-management activities (Lee *et al.* 2015). In Malaysian Borneo, Fornace *et al.* (2016) found that spatial patterns of human *P. knowlesi* malaria in Sabah were associated with landscape factors, including forest cover and fragmentation, supporting the hypothesis that deforestation and associated environmental change contribute to zoonotic malaria emergence.

Anthropogenic environmental changes including deforestation, reduced habitat complexity through monoculture of crops, creation of large ecotone areas, and ultimately biodiversity loss create ecological linkage mechanisms involving wildlife hosts and vectors that have negative impacts on human health (Young *et al.* 2017; Davison *et al.* 2019, Cooper *et al.* 2020). Recently, Johnson *et al.* (2024) further strengthened the reservoir-host component of this argument by showing that landscape characteristics drive zoonotic malaria prevalence in non-human primates, linking environmental change directly to infection patterns in macaque reservoirs. These examples show that EIA and HIA should move beyond general vector and waste considerations to explicitly assess how development may alter wildlife ecology, pathogen reservoirs, vector abundance, domestic animal contact, and human exposure pathways.

EIA should therefore incorporate zoonotic spillover risk as a formal component of project screening, scoping, baseline studies, impact prediction, mitigation, monitoring, and post-approval compliance. At the screening stage, projects involving forest clearance, plantation expansion, livestock development, dams, roads, quarrying, mining, tourism infrastructure, waste facilities, or development near protected areas should be flagged for zoonotic spillover assessment. At the scoping stage, the assessment should identify likely wildlife reservoirs, livestock or companion animal bridge hosts, vectors, nearby communities, roosting sites, migration corridors, and conflict-prone wildlife species. Baseline studies

should include wildlife presence, vector abundance and potential transmission routes/risk pathways, domestic animal density, land-cover mapping, waste and water management, and available human or animal disease records. Where risk is plausible, targeted pathogen surveillance, and consultation with veterinary, wildlife, environmental health, and public-health authorities should be incorporated.

The implications of human-mediated landscape alteration on One Health are substantial. One Health recognises that human health, animal health, and ecosystem health are interdependent. In the Malaysian EIA context, this means that zoonotic disease risk cannot be adequately assessed by environmental consultants, public-health authorities, veterinarians, or wildlife managers working separately. Applying zoonotic disease risk spillover in EIA's would require inter-agency involvement including the Department of Environment, Ministry of Health, Department of Veterinary Services, Department of Wildlife and National Parks, state wildlife agencies, local authorities, and project proponents. Such integration would allow development decisions to consider not only habitat loss and pollution, but also pathogen emergence pathways created by ecological disruption, and consequently safeguard the health of humans, animals and the environment through a concerted One Health framework.

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