House crows (Corvus splendens): the carrier of pathogenic viruses or the misunderstood bird?

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ABSTRACT

The house crow (Corvus splendens) is globally recognised as a pest. It is an invasive species that can populate Malaysia’s urban landscape and urban coastal areas. C. splendens was imported from Sri Lanka to Klang, Malaysia, in the 1890s to control caterpillars on coffee plantations. After a few decades, crows are able to adapt and co-exist with humans as a result of significant growth in the human population and urbanization. These urban pests are important due to the large volume of faecal droppings on buildings and near human dwellings. In other parts of the world, house crows can transmit pathogens and diseases such as chlamydiosis, salmonellosis, colibacillosis, and avian tuberculosis. They also carry human pathogens such as Salmonella spp., Shigella serotypes, Vibrioaceae spp., Newcastle disease virus (NDV), avian influenza virus (AIV) and West Nile virus (WNV) that can be transmitted to humans through their faeces. The first AIV transmission from birds to humans that caused a pandemic was alarming because of the risk of AIV and other avian virus transmission from birds. This prompted investigations into crow populations in urban centres. This review details the potential of C. splendens to spread AIV, NDV and WNV in Malaysia’s highly urbanized areas.

Introduction

In Malaysia, there are two distinct species of crows which are house crow (C. splendens) and jungle crow (Corvus macrorhynchos). C. splendens preferred to live in urban areas (Kurosawa et al. 2003) while C. macrorhynchos preferred to live in forest or rural areas for roosting and breeding (Shanbhag et al. 2012). C. splendens is also known with several names such as the Indian, grey-necked, Ceylon and Colombo crow (Krzemińska et al. 2016). Globally, they are recognized as pests and are one of the most invasive species that can establish a sizable population in the urban landscape and coastal areas in Malaysia (Wilson et al. 2015). This is due to the affinity of C. splendens toward open rubbish tips, food scraps and urban food sources (Csurhes 2016). Despite being unhygienic and noisy, C. splendens is perhaps best known for its aggressiveness. House crows have been reported to steal people’s food and kill the chicks of native birds since this species is not afraid of people or other birds (Feare and Mungroo 1990; Kamel 2014; Csurhes 2016). C. splendens have also been reported to harbour numerous pathogens, including avian influenza virus (AIV) (Fraser et al. 2015), West Nile virus (WNV) (Kamel 2014) and Newcastle disease virus (NDV) (Cooper 1996).

Influenza A virus (IAV) is a global concern for both animal and public health. Except for the new H17N10 and H18N11, isolated from bats (Wu et al. 2014), all virus subtypes from H1–H16 and N1–N9 can be found in aquatic birds (Kombiah et al. 2020). AIVs can be transmitted to humans by exposure to contaminated environments, directly from infected birds or an intermediate host (Fadel and Affi 2017). Highly pathogenic avian influenza (HPAI) H5N1 virus has been reported to circulate in India among different species of birds, including the C. splendens, resulting in die-off due to H5N1 and H9N2 in 2015 (Kombiah et al. 2020). In early 2004, the first human case of H5N1 was reported in Thailand, this strain may have mortality rates up 60% mortality rate (CNN 2004), which is concerning because the 1918 pandemic that killed 3% of the human population had only a 20% mortality rate (Vora 2012). In a 2017 study, it was found that 39 out of 44 house crow samples tested positive for AIV, which corresponds to 88.6% of the population (Fadel and Affi 2017).

In the United States of America, the Corvus spp. play a crucial role in transmitting WNV because they are highly susceptible to the virus and act as amplifying hosts (Hinton et al. 2015). WNV spread among American crows (C. brachyrhynchos) likely by a mosquito vector (Hinton et al. 2015) or via bird-to-bird transmission (fecal-oral) (Dawson et al. 2007). In 2004–2013, out of 1513 WNV-positive bird carcasses were collected in Orange County, South California (Liao et al. 2014), 82.7% of the WNV-positive birds were C. brachyrhynchos. Several reports in the past stated that the C. splendens plays a vital role in transmitting the virulent strains of NDV to domestic poultry (Rehan et al. 2019). The transmission of NDV from C. splendens to the...
poultry industry poses a serious threat to several countries, including Ukraine, Russia and Kazakhstan (Korotetskii et al. 2010). NDV is also a real concern to Pakistan (Rehan et al. 2019), Egypt (Dewidar et al. 2021) and Bangladesh (Khatun et al. 2018), as it is a major cause of losses among poultry producers. In the region of Punjab, Pakistan, 16% (4 out of 25) of Corvus spp. tested positive for NDV (Munir et al. 2015).

Malaysia is one of the highest poultry consumers with an estimate of 1.44 million tons of poultry meat production in 2014 (Wahab and Rittgers 2014). Poultry consumption among Malaysians was approximately 49.3 kg per capita in 2020, 48.7 kg per capita in 2021 (Hirschmann 2021a) and expected to increase up to 51.28 kg per capita by 2025 (Hirschmann 2021b). The increasing poultry demand extends the potential of disease transmission from an infected Corvus spp. to poultry, posing major economic consequences, especially in the local poultry industry (Rehan et al. 2019). The diseases have the potential to be spread to humans via poultry or direct contact with the Corvus splendens (Islam and Ahmed 2019). The majority of AIV, NDV and WNV-infected humans were reported to visit live poultry markets or had a history of direct poultry handling (Uyeki and Peiris 2019). Food preparation from infected poultry and raw product consumption (such as drinking blood or eating uncooked embryo-nated eggs) have all been linked to an increased risk of disease transmission from poultry (Harder et al. 2016). Alternatively, the spread of harmful pathogens from Corvus splendens to humans can happen through direct and indirect contact with nasal secretions, bodily fluids and faeces shed by the infected Corvus splendens (Summa et al. 2018).

In this review, we investigate the potential of Corvus splendens to transmit pathogens, especially those that cause AIV, NDV and WNV, among Malaysia’s local poultry and in highly urbanized areas. We also summarize the current state of our understanding of how Corvus splendens can affect the transmission of diseases in poultry and humans. Knowledge about Corvus splendens as a carrier of pathogenic viruses can potentially help prepare for and mitigate potential disease outbreaks into poultry, and subsequent transmission to humans.

Corvus splendens in Malaysia

C. splendens is an invasive species found worldwide except for South America and Antarctica (Krzemińska et al. 2016). This species has ecological plasticity (Montgomery 2019), which explains the presence of Corvus splendens in small breeding populations in Netherlands and South Africa (Krzemińska et al. 2016). According to Ryall (2016), Corvus splendens migration to new countries is attributable to several factors including increased global trade and faster ship travel between countries. Inter-country migration can happen when Corvus splendens acts as a ‘hitchhiker’, travelling on ships to nearby islands and mainland sites. Due to this, there were reported cases of singles or pairs of Corvus splendens in certain places such as Mungab Island of South Korea and Nokomis Beach of Florida, United States of America. Corvus splendens can also migrate via human facilitated introduction of this species into its non-native range (for example the crow introduction to Zanzibar from India in 1890s) to combat the caterpillar plagues in a coffee plantation and handle anthropogenic wastes (Krzemińska et al. 2016).

In Malaysia, C. splendens was first introduced when the birds hitchhiked on incoming Indonesian ships in the 1800s (Wilson et al. 2015). Importation of Corvus splendens during the British occupation from Sri Lanka to Port Klang and Penang to resolve the caterpillar plague on the coffee plantation in the twentieth century further aided the spread of Corvus splendens across Peninsular Malaysia. Corvus splendens are associated with human habitations and are often seen in urban areas while Corvus macrorhynchos are usually found in human habitations and landscapes at higher altitudes (Mahesh and Suseela 2021). In Figure 1, the differences in appearance between Corvus splendens and Corvus macrorhynchos are highlighted. Corvus splendens has broad, dull greyish feathers covering the nape, upper mantle, rear ear-coverts, neck and breast, while Corvus macrorhynchos is all black with purplish to dark bluish gloss feathers (Robson 2019). Both species posed a threat to native birds by pecking at them and stealing their eggs and food, however Corvus macrorhynchos tend to be more aggressive, especially when food sources are scarce (Shanbhag et al. 2012). Even so, C. splendens is still one of the world’s worst invasive species as C. splendens has a higher population (Shanbhag et al. 2012), excellent adaptability to various environments (Fraser et al. 2015), and negative impacts on native birds, vertebrates and invertebrates (Yap and Sodhi 2004; Kamel 2014). C. splendens also posed a threat to humans as there were cases of bird strikes on airplanes, snatching food and swooping at people walking in parks and streets (Suliman et al. 2011; Shamba and Jonah 2017). C. splendens can become a disease carrier for humans and domestic animals (Suliman et al. 2011) as they can also be infected by the same pathogens such as Campylobacter spp., Escherichia coli and Salmonella spp. (Ryall and Meier 2008). The rapid increase in C. splendens population has also caused several problems in urban areas, such as damage to buildings and tourist attraction sites due to faecal droppings, annoying noises, acting as a crop pest, competing with native birds, and replacing native biodiversity (Alias and Hashim 2016).

Corvus splendens have never been observed to live independently of humans. It can be found abundantly in sites with poor food waste and garbage management (Alias and Hashim 2016). This is because C. splendens is an opportunistic feeder known to scavenge on carcasses, stealing human food, invade a wide range of food crops, and kill livestock which includes poultry, young sheep and goats (Fraser et al. 2015). Therefore, C. splendens acts as an indicator of poor cleanliness and health. It has also become a threat to the indigenous bird species, as C. splendens can result in species displacement by attacking, killing and destroying the nests and eggs of birds (Fraser et al. 2015). It is also the culprit for reducing the number of small reptiles and amphibians (Kamel 2014). Furthermore, the close proximity between C. splendens and other birds and humans may contribute to spreading harmful pathogens through direct and indirect contact with the nasal secretions, bodily fluids and faecal droppings (Summa et al. 2018).

Corvus splendens as a disease carrier

Pathogen spillover between backyard chickens and wild birds has become more commonly reported in poultry agriculture
Emerging and re-emerging avian infectious diseases have become a threat to birds all around the globe and may contribute to the extinction of species when coupled with invasive species displacement (Smith et al. 2006). Repeated disease transmission of multi-host pathogens into recipient species, such as the spillover of pathogens from wild birds to domestic chickens, can cause pathogen establishment and spillback from backyard poultries (Cross et al. 2019), for example, the H5N1 goose/Guangdong strain (Haider et al. 2017). NDV is also one of the poultry-wild bird transmission concerns as all bird species are susceptible to the virus replication, shedding and transmission (Snoeck et al. 2013). Free-ranging backyard flocks are potential sources of pathogens spillover into resident and endemic countries for many kinds of infectious diseases, including NDV (Gottdenker et al. 2005; Hernandez-Divers et al. 2008). Previously dead crows were found near poultry farms only after the outbreak, such as the isolation of H5N1 from two *C. macrorhynchos* after poultry outbreaks in the country (Nagarajan et al. 2010). The same virus strain was also isolated from *C. corone* and *C. macrorhynchos* near outbreak sites in Bangladesh (Khan et al. 2014). Studies on the infection dynamics are still limited. However, *Corvus* spp. are terrestrial birds that find good accessibility to food from backyard poultry waste products, making them a good candidate in disease transmission as their natural residence is located near human environments and close to poultry habitats (Fadel and Affi 2017). Chickens can be infected by WNV, but they do not develop clinical symptoms, do not re-infect mosquitoes and are considered dead-end hosts for WNV (Langevin et al. 2001), thus they are often used as sentinels to monitor for WNV transmission (Holcomb et al. 2022). Humans are also considered dead-end hosts for WNV but may manifest symptoms such as encephalitis and meningitis which can be fatal in humans (Papa et al. 2010).

Humans are susceptible to avian infectious diseases that have been circulating in a variety of species, including in *C. splendens* (Summa et al. 2018). Chlamydiosis, salmonellosis, colibacillosis, arizonosis, avian tuberculosis, histoplasmosis and allergic alveolitis are among the avian diseases infecting humans (Jacob et al. 2011). In addition, *C. splendens* also carry human pathogens such as *Salmonella* spp., *Shigella* serotypes, *Proteus* spp., *Vibrio* spp., *Pseudomonas* spp., *Escherichia coli*, *Campylobacter* spp., NDV, AIV and WNV (Cooper 1996; Kamel 2014; Fraser et al. 2015). These diseases can be transmitted to humans in many ways, as the birds shed these pathogens in their mucous, saliva and faeces (Uyeki and Peiris 2019), as demonstrated by the detection of pathogens in cloacal swab samples (Alias and Hashim 2016) and bird droppings (Prathipa et al. 2015).

**Influenza A virus**

Influenza is a negative-sense RNA, classified into influenza types A, B, C and D (Ahmed et al. 2018). Influenza A virus (IAV) is a virus that most commonly affects birds and humans (Du et al. 2019). Older adults and children are among the high-risk groups who are susceptible to IAV. Older adults (aged 75 and over) significantly have lower body temperatures (compared to younger adult) when infected with influenza-associated pneumonia, which may cause misdiagnosis and delay in treatment because it does not meet the fever threshold for influenza, making older adults susceptible to IAV with asymptomatic infections, probably because of their weakened innate and adaptive immune responses (Wong et al. 2020). Meanwhile, children (those under the age of six) are more vulnerable to IAV, possibly due to a lack of immune history and a narrow immune response that targets the IAV haemagglutinin of the strain that caused the infection only, as opposed to adults, who have a much broader response, including protection against the majority of group 1 subtype haemagglutinin (Meade et al. 2020). Each year, influenza infection is estimated to cause around 3–5 million cases of severe illness and 250,000–500,000 deaths in developing countries (Parash et al. 2019).
**Influenza A virus in history**

The pandemic potential of Influenza A virus outbreak has been recognized since the Spanish flu outbreak, also known as The Great Pandemic of 1918–1919 (Beveridge 1991). Spanish flu, which started in late August in 1918 (Reid et al. 2001), eventually helped to end World War I since thousands of soldiers were infected. It caused at least 50 million deaths worldwide (Taubenberger et al. 2019). The 1918 H1N1 virus underwent genetic reassortment and caused several more outbreaks, which are 1957 H2N2, 1968 H3N2 and 2009 H1N1pdm. The 2009 H1N1pdm is genetically similar to the 1918 Spanish flu, with additional gene swapping between avian, swine and human origin, where pigs are considered as ‘mixing vessels’ for the generation of the hybrid (Taubenberger et al. 2019). Thus, it gained its name, the swine flu. The ability of IAVs to mutate and infect a broad host range is concerning, as it has the potential to mutate into a highly pathogenic virus in the future. In Malaysia, influenza cases are usually seen without seasonal trends, with 22.3% seroprevalence of seasonal H1N1 and 14.7% for H3N2. The 2009 swine flu outbreak in Malaysia resulted in 12,307 reported cases, with 77 reported deaths (Jamal and Sam 2015).

**Avian influenza virus**

Avian influenza A viruses (IAVs) are mostly transmitted to humans through the reservoir, which is mainly waterfowl, either directly or indirectly through intermediate hosts such as swine and poultry (Ahmed et al. 2019). IAVs (H1N1, H2N2 and H3N2) with stable human-to-human transmissions have previously caused pandemics and are currently responsible for epidemics. The IAV in wild aquatic birds evolved slower than the IAV in poultry and humans (Wright et al. 2013). IAVs can be classified into two types which are the low pathogenic IAV (LPAIV) (H9N2 and H10N8) and highly pathogenic IAV (H5N1) (H5N1 and H7N9). The subtypes of IAV from birds that have crossed the species barrier and infected humans are H5N1, H5N6, H6N1, H7N2, H7N3, H7N4, H7N7, H7N9, H9N2, H10N7 and H10N8, all of which can lead to sporadic infections or fatalities in humans (Ahmed et al. 2018). Figure 2 shows how IAVs are transmitted from natural reservoirs to humans either directly or indirectly via the intermediate hosts such as swine and poultry. Previously, there were several reports of H5N1 isolation from Corbus sp. For example, in 2011, H5N1 was isolated from C. splendens in Bangladesh (Khan et al. 2014) and it was also isolated from C. macrorhynchos in Japan around 2004 (Tanimura et al. 2006). Even though existing LPAIVs and HPAIVs do not cause stable human-to-human transmission, they nonetheless constitute a threat to future pandemics (Wright et al. 2013). Thus, surveillance studies of IAVs are strongly encouraged since the data is lacking, especially in developing countries.

**LPAIV and HPAIV outbreaks in domestic poultry**

LPAIV was detected in Malaysia in 1989, and strains such as H4N3, H4N6 and H3N6 were detected from passerines and domestic birds (Ibrahim et al. 1990). H4N3 isolates were found from a dead magpie robin (Copsychus saularis) at Selangor transit aviary and from a sick, yellow-vented bulbul (Pycnonotus goiavier) that could not fly. H2N9 and H6N5 were isolated in 1992 (Verhagen 2016), H7N1 was detected in 1994; H10N5 in 1998; H3N2 in 2002 (Alexander 2007); H3N8 in 2004 (Ng et al. 2006); H9N2 in 1998 (He et al. 2013); and H3N2 in 2010 (Mohidem et al. 2017). There are multiple reasons for the spread of LPAIV, including chicken smuggling, migration of the infected wild birds, cross-country poultry trade, producers and trader’s business activities, and commercial movements of birds and tourism activities in which infected humans may help spread the diseases (Wan and Tariq 2018).

As for HPAIV in Malaysia, there were four waves of the H5N1 outbreak from 2004 to 2017, that did not cause any human deaths (Wan and Tariq 2018). The H5N1 outbreak was first detected in Kelantan in 2004 (Mohidem et al. 2017). The HPAIV outbreak was restricted to around 12 localities in Kelantan near the Thailand border. H5N1 that caused the outbreak in Kelantan belonged to the 1.2.3 and 2.3.4 clades of the Vietnam/Thailand/Malaysia (VTM) strain. In poultry farms around the vicinity, the viruses were detected in ducks and chickens (Sharifah et al. 2005). The viruses were also detected in Kuala Lumpur and Perak in the same year (Rafidah and Asiah 2004). It was also noted that the second outbreak detected in Kuala Lumpur, Perak and Penang in 2006 had genetic similarity with the Fujian-like sublineage (clade 2.3.4) outbreak in 2004. The HPAIV H5N1 variant also shared similarities with both Indonesia and China strains, but the HA gene of H5N1 in 2006 does not group with the VTM sub lineage as in 2004. The next outbreak was in 2007 and was detected in Selangor, Kuala Lumpur and Kelantan in 2007 (Wan and Tariq 2018). The outbreak was due to the import of domestic fowl from neighbouring countries and tourism activities (WHO 2007). Kelamantan also had the same H5N1 outbreak in the same year. However, there were no reported cases of the H5N1 outbreak in Sabah and Sarawak. In 2017, another outbreak occurred at 43 locations and six districts in Kelantan. At the moment, no human cases of H5N1 infections have been reported in Malaysia, although it has gradually affected the neighbouring countries since the first death was reported in Thailand (Tee et al. 2009).

**West Nile virus**

West Nile virus (WNV) is also one of the pathogens that Corvus spp. can harbour (Kamel 2014). It is a positive-sense single-stranded RNA virus that is a member of the flavivirus genus and belongs to the Japanese encephalitis antigenic complex of the family Flaviviridae. WNV is an arbovirus and is maintained in a cycle involving transmission between birds and mosquitoes (Culex spp.) (Pierson and Diamond 2013). Figure 3 shows the transmission of this virus between the vector, amplifying host and mammals, as well as via other possible routes of transmission. Humans and other mammals are considered incidental and dead-end hosts. WNV primarily consists of two lineages. Lineage 1 is associated with human clinical encephalitis, while lineage 2 is not associated with human clinical encephalitis (Bakonyi et al. 2006). Since its first discovery in Uganda, WNV has been a prevalent mosquito-borne disease associated with 14.7% for H3N2. The 2009 swine flu outbreak in Malaysia resulted in 12,307 reported cases, with 77 reported deaths (Jamal and Sam 2015).
with sporadic outbreaks of moderate sickness in humans in Africa, the Middle East and Europe until the mid-1990s (Hayes et al. 2005). WNV has been a common mosquito-borne disease in the continental United States of America since first introduced in 1999 on the East Coast. In the United States of America, WNV resulted in 29,000 human cases and more than 1100 deaths from 1999 to 2008 (Sugumaran et al. 2009). This indicates that WNV infections have high morbidity and mortality rates in humans and equines (Thomas-Bachli et al. 2020). Rarely, WNV also can be transmitted via organ donation, blood transfusion and breast-feeding (Rossi et al. 2010).

Some Passerine species, including Corvids like C. brachyrynchos and blue jays (Cyanocitta cristata), are susceptible to WNV infection and have the potential to produce high levels of viremia and mortality. According to Komar et al. (2003), the most fatal WNV infections in birds occurred in Corvus brachyrynchos, which is related to the nature of Corvids carrion-feeding behaviour, which may expose the bird to the virus by eating infected bird carcases. The same rule might apply to C. cristata as they also feed on carcases. Until 2014, there was no data on WNV cases in wild birds in Malaysia, but several studies showed low prevalence (1.21%) (9/742) among Malaysia’s Orang Asli (Marlina et al. 2014) and 4.41% (3/68) in companion bird populations in Selangor (Rais et al. 2011). The study is important since Malaysia’s Orang Asli lives in rural areas, the frontier of the jungle and in the centre of the jungle where Culex pipiens mosquitoes can be abundantly found (Marlina et al. 2014). However, in 2020, the first reported study on the prevalence of WNV found a WNV seropositive rate of 18.71% and a molecular prevalence of 15.2% in migratory and resident wild birds found on the west coast of Malaysia. Phylogenetic analyses of the isolates revealed 99% similarity to the strains from South Africa and were clustered under lineage 2 (Yuseri et al. 2019). This finding indicates that WNV is circulating among the local wild birds and can be attributed to several key factors; the presence of migratory birds which may harbour the virus, the presence of breeding sites for mosquitoes especially a wide variety of Culex mosquito abundance in Malaysia that mainly serve as vectors, and the ability of the virus to infect a wide range of susceptible hosts. Active surveillance of WNV in birds is crucial in order to understand WNV transmission cycles. Thus, this may help in preventing the chain of transmission towards humans especially those with low antibody levels that are likely to develop severe symptoms.

**Newcastle disease virus**

Newcastle disease virus (NDV) is panzootic in racing pigeons, and it is still a significant concern in commercial poultry breeding because it can cause death even among vaccinated poultry.
NDV are enveloped viruses with negative single-stranded RNA belonging to the genus Orthoavulavirus in the family Paramyxoviridae (Miller and Koch 2013). NDV can be transmitted by inhaling or ingesting the virus shed in faeces and respiratory secretions by diseased or carrier birds. The paramyxovirus strains can be categorized by the avian species it infects. Avian paramyxovirus-1 is highly susceptible to chickens; avian paramyxovirus-2 and avian paramyxovirus-3 cause disease in poultry, while avian paramyxovirus-6 and avian paramyxovirus-7 cause disease in turkeys (Alexander 2000). NDV is divided into three pathotypes: namely velogenic, mesogenic and lentogenic. NDV is believed to be spread by migratory birds of the Nearctic (mild respiratory waterfowl type) or the jungle bird of the tropics (severe viscerotropic type) (Hanson 1976).

In Malaysia, NDV with genotypes VI and VII are commonly found in imported birds. For genotype VI, Vla viruses are the most common ones. Although the genotype Vla has not led to outbreaks in Malaysia, it should not be ignored, as it has been reported to cause two outbreaks in South Africa. Conversely, genotype VII is usually associated with an NDV outbreak, especially in the Middle East and Asia. In Malaysia, genotype VII caused numerous outbreaks based on the data from 2000 until 2012. Genotype VIIi has been isolated from poultry, which is the same virus that caused the NDV outbreak in Pakistan and Indonesia (Leow et al. 2019; Dewidar et al. 2021). According to Geetha et al. (2011), NDV was found in C. splendens droppings, thus suggesting the role of C. splendens in the epidemiology of NDV. We hypothesized that C. splendens might be infected with NDV from migrating birds and thus served as an intermediate host for NDV transmission in poultry.

Since NDV is a highly fatal disease, it is considered a global threat to the poultry industry, as it is still infective despite intensive vaccination. A major outbreak in the USA resulted in 4 million bird (backyard poultry flocks and most birds) deaths and losses of USD 162 million during the Exotic Newcastle disease outbreak (Rehan et al. 2019). In Pakistan, the poultry industry is one of the country’s most significant sources of income, which contributes USD 2 billion of profit per year. The outbreak in 2012 caused the death of approximately 45 million poultry in the Jallo Wildlife Park, Punjab, Pakistan. NDV kills millions of village backyard poultry in Bangladesh yearly and impacts the household income of those in poor rural areas (Khatun et al. 2018). Every year, NDV causes losses of approximately USD 289 million in Bangladesh. These outbreak incidents prove that active NDV surveillance programmes should be carried out to prevent future outbreaks, leading to enormous losses for poultry producers.
Corvus splendens control programme in Malaysia

*C. splendens* is classified as a bird pest in Malaysia due to its role as a public nuisance and health threat. Among the suggested ways to reduce the bird pest problem is the periodic shooting of the *C. splendens* that the City Councils conduct in hot-spot areas like Klang, Kepong, Cyberjaya, Cheras, Kajang, and other states as an initiative to cut down the population of *C. splendens*. Other control methods practiced by Southeast Asian countries to address the overpopulation of bird pests like *C. splendens* include direct control, sterilization of birds, scaring and bio-acoustics technique and habitat modification (Yap and Sodhi 2004).

Direct control of birds includes baits and explosives; however, it is ineffective as the birds are quickly replaced by the number of juveniles either by reproduction or migration. The sterilization technique involved using chemosterilants, which can be laborious due to the efficiency of the chemicals towards different species of birds. Scarecrows are able to frighten away some bird species, but not *C. splendens*, as the species is very comfortable living among humans. As for habitat modification for *C. splendens*, there are several initiatives to prevent habitation of *C. splendens*, such as changes in the rubbish bin design and planting less suitable trees for house crows nesting, which will reduce the house crow population, but this may take a long time before becoming effective.

Additionally, a lack of precaution taken by the authorities during shooting exercises imposed high risks during and after these events. For decades, ongoing management has failed to eradicate the species, while they have successfully established a sizable population in several cities in Malaysia. Therefore, we call for the proper management of these birds to be implemented, with a better understanding of the species for efficient control of their population to avoid human health concerns and detrimental effects on the environment, economy, and livestock. Two types of control measures have been shown to successfully eradicate *C. splendens*: physical control and chemical control (Shivambu et al. 2020). Successful physical control of *C. splendens* can be seen in Yemen in which they collect and kill the young birds followed by shooting of adults. In Australia, *C. splendens* were shot at the point of entry, thus stopping the establishment of *C. splendens* in the country (Ryall 2002). Mauritius’s chemical control includes poisoning the house crows with starlicide (Puttoo and Archer 2004) and α-chloralose poison (Feare and Munroo 1990).

In Malaysia, shooting adult *C. splendens* is a common practice aimed at reducing their number. Chemical control can also be employed, however, this requires proper handling practice, such as by mixing chemicals with food waste in the crow’s territory, to avoid the non-target bird species (Dolbeer and Linz 2016). Other than that, public support plays a vital role in ensuring the success of the eradication programme. This can be done by creating awareness of how *C. splendens* can spread harmful pathogens towards humans and the importance of proper garbage management in reducing the number of *C. splendens*.

Conclusion

*C. splendens* is well-known to cause bacterial infection in humans (Fraser et al. 2015). However, the possibility of *C. splendens* transmitting viruses is still a neglected topic in Malaysia since there have never been abundant bird deaths reported due to viral infection in Malaysia. An NDV surveillance study is also crucial since Malaysia is one of the highest poultry consumers in the world, and the poultry industry is an essential source of supply protein to Malaysians. It has also been proven that NDV can cause significant loss in a country’s economy due to the sacrifice of poultry to stop the spread of the disease. In the past, the influenza virus was once ignored due to the difficulty in diagnosing the symptoms in humans. Presently, the seroprevalence and surveillance data of AIVs are still lacking due to socio-economic costs and diagnostics facilities. WNV is also neglected due to the absence of reported cases in Malaysia. However, Malaysia is a suitable habitat for the WNV vector, *Culex pipiens*, and the climate is preferable for migrating birds during the Northern and Southern winter periods. Hence, the possibility of WNV infection in the future should be studied, and surveillance must be taken as a preventative measure. Furthermore, the transmission of viruses such as AIV, NDV and WNV has been reported from the *C. splendens* to the local flocks in other countries through surveillance studies. Thus, an active surveillance study may help prevent the spread of these RNA viruses carried by the ubiquitous *C. splendens* presence in the city.

Ethical approval

This article does not contain any studies involving animals performed by any of the authors.

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