The risk from SARS-CoV-2 to bat species in England and mitigation options for conservation field workers

Abstract

1. The newly evolved coronavirus, SARS-CoV-2, which has precipitated a global Covid-19 pandemic among the human population, has been shown to be associated with disease in free-living wild animals.
2. Bats (Chiroptera) have been shown to be susceptible to experimental infection and therefore may be at risk from disease when in contact with infected people. Numerous conservation fieldwork activities are undertaken across the United Kingdom bringing potentially infected people into close proximity with bats.
3. In this study we analysed the risks of disease from SARS-CoV-2 to free-living bat species in England through fieldworkers undertaking conservation activities and ecological survey work, using a qualitative, transparent method devised for assessing threats of disease to free-living wild animals.
4. The probability of exposure of bats to SARS-CoV-2 through fieldwork activities was estimated to range from high to low, depending on the proximity between bats and people during the activity. The likelihood of infection after exposure was estimated to be high and the probability of dissemination of the virus through bat populations medium. The likelihood of clinical disease occurring in infected bats was low and therefore the ecological, economic and environmental consequences predicted to be low. The overall risk estimation was low and therefore mitigation measures are advisable. There is uncertainty in the pathogenicity of SARS-CoV-2 in bats and therefore in the risk estimation.
5. Disease risk management measures are suggested, including the use of personal protective equipment, good hand hygiene and following the existing government advice.

6. The disease risk analysis should be updated as information on the epidemiology of SARS-CoV-2 and related viruses in bats improves. The re-analysis may be informed by health surveillance of free-living bats.

Key Words

Bats; Chiroptera; Conservation Interventions; Covid-19; Fieldworkers; SARS-CoV-2

Word Count

9945

Introduction

SARS-CoV-2 is the name given to the newly evolved coronavirus which at the time of writing is responsible for the Covid-19 global pandemic in humans (Gorbalenya et al. 2020). SARS-CoV-2 belongs to the Betacoronavirus genus within the Coronaviridae family (Masters 2006, de Groot et al. 2012). Coronaviruses are enveloped ribonucleic acid (RNA) viruses, have the largest genomes among all RNA viruses and are capable of infecting avian and mammalian species, including humans, and causing a variety of diseases (Masters 2006, de Groot et al. 2012). For example, SARS-CoV-2 is a close relative of the coronaviruses MERS-CoV and SARS-CoV responsible for causing outbreaks of Middle East Respiratory Syndrome (MERS) and Severe Acute Respiratory Syndrome (SARS) respectively in humans in recent years. Both viruses are considered to have originated from animal reservoirs (Gorbalenya et al. 2020, Lu et al. 2020, Wassenaar & Zou, 2020). Reports suggest that SARS-CoV-2 originated from a free-living wild animal reservoir as is thought to be true for the agents of 60-70% of emerging diseases (Jones et al. 2008, Wang & Crameri 2014). Although some coronaviruses are host specific, others appear capable of infecting multiple host species (Drexler et al. 2014). SARS-CoV-2 is likely to infect and replicate in numerous non-human mammalian host species in addition to humans. Specifically, there is growing evidence that SARS-CoV-2 may be transmitted as a zooanthroponosis from humans to animals.

There are 18 species of bats (order: Chiroptera) in England, of which 17 are known to be breeding (Bat Conservation Trust 2020a), and all of which are protected by the Wildlife and Countryside Act of 1981 and the Conservation of Habitats and Species Regulations 2017. Bat species in England belong to seven genera: *Myotis, Barbastella*, *Plecotus*, *Pipistrellus, Rhinolophus*, *Nyctalus* and *Eptesicus*. Two English bat species are classified as 'near threatened' on the IUCN red list of threatened species: barbastelle (*Barbastella barbastellus*) and Bechstein's bat (*Myotis bechsteinii*) (IUCN Red List of Threatened Species 2020). The greater and lesser horseshoe bats (*R. ferrumequinum* and *R. hipposideros*, respectively) are both in global decline (IUCN Red List of Threatened Species 2020). Bats are monitored using numerous methods across England for conservation, research and as part of the built development process, including through field and roost surveys, harp trapping and mist netting, and radio tracking. Fieldworkers, therefore, may come into direct contact with bats through these activities and could transmit infectious agents, including SARS-CoV-2, to them.

In an effort to improve our understanding of the threat of SARS-CoV-2 to free-living bat populations, a recent report investigated the probability of exposure, infection and dissemination of SARS-CoV-2 to North American bat populations as a result of contact with people undertaking rehabilitation and field activities and concluded that there was a 'non-negligible risk of transmission of SARS-CoV-2 from humans to bats' although a consequence assessment was not undertaken, nor was the risk of disease in bats assessed (Runge et al. 2020).

The purpose of this paper is to analyse the risks of SARS-CoV-2-disease in free-living bat species in England as a result of contact with people involved in field conservation initiatives and ecological survey work and to provide appropriate disease risk management options.

Methods

A qualitative disease risk analysis (DRA) was undertaken to assess the risk of disease from the hazard SARS-CoV-2 to free-living bats (Chiroptera) from fieldworkers carrying out bat conservation interventions and development activities in England. The probability of disease occurring and the magnitude of the possible consequences to bat populations were assessed and mitigation methods proposed based on this risk. The Sainsbury and Vaughan-Higgins' (2012) DRA method, developed using the foundation provided by the World Organization for Animal Health (OIE) (Murray et al. 2004) and modified by Bobadilla Suarez et al. (2015) and Rideout et al. (2016), with further consideration of previous qualitative DRA methods (Davidson & Nettles 1992, Leighton 2002) was used in this report. Disease risk assessment was carried out according to the method described by the OIE (Murray et al.

2004). In addition, an exposure assessment was included, using the principles described by Murray et al. (2004), to assess the exposure of humans to SARS-CoV-2. The biological pathways that might permit bats to be exposed and infected with SARS-CoV-2 were assessed, as well as the probability of this occurring. The process whereby SARS-CoV-2 could disseminate through bat populations and the probability of dissemination was described. The likelihood and severity of biological, economic, and environmental consequences associated with the establishment and spread of SARS-CoV-2 was assessed. Using the method described in Murray et al. (2004), results of the exposure and consequence assessments were combined to qualitatively assess the risk of disease associated with SARS-CoV-2 to bat species in England (negligible, very low, low, medium or high).

Results

Hazard identification

Justification for SARS-CoV-2 as a hazard to bat species (Chiroptera)

Here, SARS-CoV-2, as a hazard for free-living bat species, is justified on the basis of the likelihood of infection and disease in the order Chiroptera, the severity of the disease and whether transmission can occur between bats.

Infection and disease associated with SARS-CoV-like coronaviruses in non-human mammals

Studies have demonstrated considerable species differences in the ability of SARS-CoV-like coronaviruses to replicate effectively within cells and cause disease in the host. Evidence of infection with SARS-CoV has been detected in raccoon dogs (*Nyctereutes procyonoides*) and several bat species (*Rhinolophus* spp.) without reported clinical disease (Guan et, al. 2003, Li et al. 2005, Cheng et al. 2007, Wassenaar & Zou 2020). SARS-CoV-like viruses have, however, also been isolated from Himalayan palm civets (*Paradoxurus hermaphroditus*) shown experimentally to be susceptible to clinically detectable disease from two separate virus isolates (Guan et al. 2003, Wu et al. 2005, Shi & Hu 2008).

Infection and disease associated with SARS-CoV-2 in non-human mammals

Preliminary reports have described the ability of SARS-CoV-2 to infect 11 non-human mammalian hosts: domestic cats (*Felis catus*), domestic dogs (*Canis familiaris*), transgenic house mice (*Mus musculus*), domestic ferrets (*Mustela putorius furo*), American mink (*Neovison vison),* Egyptian fruit bats (*Rousettus aegyptiacus*), Syrian hamsters (*Mesocricetus auratus*), Malayan tigers (*Panthera tigris jacksoni*), Amur tigers (*Panthera tigris altaica*), African lions (*Panthera leo*) and rhesus macaques (*Macaca mulatta*) (Balkema-Buschmann et al. 2020, Bao et al. 2020, Chan et al. 2020, Deng et al. 2020, Goumenou et al. 2020, ProMed International Society for Infectious Diseases 2020a, ProMed International Society for Infectious Diseases 2020b, ProMed International Society for Infectious Diseases 2020c, Shi et al. 2020; World Organisation for Animal Health (OIE) 2020, Zhang et al. 2020). In eight of these mammalian species (domestic ferrets, Malayan tigers, Amur tigers, African lions, domestic cats, Syrian hamsters, American mink and transgenic house mice) infection has been associated with disease (Balkema-Buschmann et al. 2020, Bao et al. 2020, Calle, 2020, Chan et al. 2020, ProMed International Society for Infectious Diseases 2020b, Shi et al. 2020, World Organisation for Animal Health (OIE) 2020). Domestic pigs (*Sus scrofa domesticus*), domestic chickens (*Gallus gallus domesticus*) and domestic ducks (*Anas platyrhynchos*) are not thought to be susceptible to infection with SARS-CoV-2 (Balkema-Buschmann et al. 2020, Shi et al. 2020).

The virus has been shown to replicate effectively in the upper respiratory tract of domestic ferrets (Mustelidae; Carnivora) and cause clinical disease (Shi et al. 2020). Two ferrets in Shi et al.'s (2020) study developed fever and loss of appetite 10 to 12 days after experimental inoculation with the virus. Post mortem examination of these animals showed evidence of lymphoplasmacytic perivasculitis and vasculitis, increased numbers of type II pneumocytes, macrophages, and neutrophils in the alveolar septa and alveolar lumen, and mild peribronchitis in the lungs, suggesting that ferrets are susceptible to the clinical disease associated with SARS-CoV-2. Balkema-Buschmann et al. (2020) also demonstrated through experimental study that SARS-CoV-2 could replicate efficiently in ferrets and high viral RNA yields were detected in nasal washes from ferrets two to eight days post infection. In addition, 100% (n=3) of non-inoculated ferrets which were kept in contact with experimentally infected ferrets also became infected and viral RNA was detected in nasal washes from 12 days post-contact. SARS-CoV-2 reactive antibodies were detected from day 8 in the inoculated ferrets and in one in-contact ferret on day 21 (Balkema-Buschmann et al. 2020).

An outbreak of respiratory disease at two American mink farms in the Netherlands was thought to be associated with SARS-CoV-2 after clinically sick mink (numbers not reported) at both farms tested positive for the virus (ProMed International Society for Infectious Diseases 2020b). This finding suggests that other members of the Mustelidae family may be susceptible to the disease and dissemination through populations in close proximity may occur.

There is evidence to suggest that other members of the Carnivora order are susceptible to disease from SARS-CoV-2. Four domestic dogs have tested positive for the virus, all of which had been in contact with an infected owner. None of the dogs showed signs of clinical disease associated with SARS-CoV-2, and although one dog died during the infection period, it was 17 years old and had multiple underlying diseases which were attributed as the cause of death (Goumenou et al. 2020). Despite this evidence, over 3500 dogs, cats and horses (*Equus caballus*) showing respiratory disease (species numbers not reported) screened for SARS-CoV-2 by IDEXX laboratories in South Korea in February and March 2020 tested negative (IDEXX.com 2020). Given that there were 7,755 human patients with confirmed Covid-19 in Korea as of the 13th March 2020, this finding suggests that, whilst it remains possible for domestic dogs in contact with humans to become infected, occurrences are likely to be rare (COVID-19 National Emergency Response Centre 2020).

Felids, similarly to mustelids, appear to be susceptible to disease as a result of SARS-CoV-2 infection. Shi et al. (2020) showed that the virus replicates effectively in domestic cats and can transmit between them via respiratory droplets. Moreover, two juvenile cats in the same study which were experimentally inoculated with SARS-CoV-2 were found to have severe lesions in the nasal and tracheal mucosal epithelia and lungs, highlighting their susceptibility to disease (Shi et al. 2020). In a preliminary study in Wuhan, China, 102 serum samples were collected from domestic cats during the outbreak of Covid-19 in humans, and 14.7% were positive for the receptor binding domain (RBD) of SARS-CoV-2 by indirect enzyme linked immunosorbent assay (ELISA), suggesting that SARS-CoV-2 infected the cat population in Wuhan during the outbreak (Zhang et al. 2020). There are also several case reports of owned domestic cats testing positive for SARS-CoV-2, for example a case in Belgium, a case in Hong Kong, and two cases in the USA (Hong Kong's Information Services Department 2020, ProMed International Society for Infectious Diseases 2020c, USDA Animal and Plant Health Inspection Service 2020).

Wild carnivore species held in captivity in the USA have been found to be susceptible to disease as a result of SARS-CoV-2 infection. Two Malayan tigers, three African lions and two Amur tigers held in the same zoological institution began showing mild signs of respiratory disease after contact with a SARS-CoV-2 infected keeper. Subsequently, duplicate nasal and oropharyngeal swabs from one Malayan tiger and one African lion tested positive on quantitative polymerase chain reaction (qPCR) for SARS-CoV-2, while results from a further three African lions and four tigers (Malayan and Amur) tested positive three weeks later (Calle 2020, ProMed International Society for Infectious Diseases 2020a, World Organisation for Animal Health (OIE) 2020).

There is conflicting evidence on the ability of SARS-CoV-2 to infect and cause disease in rodent species. Angiotensin two converting enzyme (ACE2) is a type I transmembrane metallocarboxypeptidase expressed in vascular endothelial cells and renal epithelial cells (Jiang et al. 2014). Zhou et al. (2020) demonstrated that SARS-CoV-2 could utilise ACE2 to gain entry into human cells, as had previously been discovered for SARS-CoV (Li et al. 2003, Kuba et al. 2005). In order to study the importance of

ACE2 for SARS-CoV-2, human ACE2 (hACE2) transgenic mice were used as a disease model and compared to wild type mice. When intranasally inoculated with SARS-CoV-2, hACE2 transgenic mice showed clinical signs of body weight loss along with multiple histopathological changes including interstitial pneumonia. Viral RNA was detected in the lungs of transgenic mice by quantitative PCR at one, three, five and seven days after inoculation and infectious SARS-CoV-2 could be isolated from the lungs. Neither wild-type mice or controls exhibited clinical signs throughout the study, nor was viral DNA detected at any time. (Bao et al. 2020). These findings emphasize the importance of hACE2 gene for infection by SARS-CoV-2.

A preliminary study by Chan et al. (2020) further considered the importance of the hACE2 gene for predicting disease from SARS-CoV-2. Genetic components of several mammalian species were investigated with the aim to identify an appropriate animal disease model for SARS-CoV-2 based on similarity of the ACE2 gene to hACE2. Rhesus macaque ACE2 was found to be 100% identical to hACE2 at the interface region, and the ACE2 gene of Syrian hamsters and common marmosets (*Callithrix jacchus*) differed by only 3-4 mutations. Rhesus macaques can be successfully infected with SARS-CoV-2 and show disease signs (Deng et al. 2020), further supporting the importance of hACE2 gene similarity on infection risk. Based on their results, Chan et al. (2020) identified Syrian hamsters as a possible disease model and experimentally intranasally inoculated them with SARS-CoV-2. These hamsters could be consistently infected and displayed a range of clinical signs including rapid breathing and weight loss. Histopathological changes were reported, from diffuse alveolar damage and apoptosis in the initial exudative phase, to airway and intestinal involvement, spleen and lymphoid atrophy and tissue repair in the later proliferative phase. Moreover, experimentally infected hamsters consistently infected naïve hamsters housed within the same cage, resulting in similar clinical signs (Chan et al. 2020). This study provides further evidence that non-human mammalian species from different orders can be infected with SARS-CoV-2 and are susceptible to disease. It also accentuates the likelihood that species susceptibility to SARS-CoV-2 is intrinsically linked to the similarity of their ACE2 gene to that of hACE2. Luan et al. (2020) analysed ACE2 proteins from several genera, and found that ACE2 proteins from 16 primate species and two species from the Cricetidae family had at least 90% similarity to the hACE2 SARS-CoV-2 binding domain, supporting previous evidence that species in the order Primates and family Cricetidae are likely to be susceptible to infection. Luan et al. (2020) presented the first evidence that SARS-CoV-2 may be able to infect species from the families Bovidae and Cetacea; five bovid species and three species of Cetacea had ACE2 proteins with at least 90% similarity to hACE2 (Luan et al. 2020).

Infection and disease associated with coronaviruses in bats

Over 200 novel coronaviruses have been identified in free-living bats from Asia, Africa, North America, South America and Europe from all 10 bat families studied, making them the most widely distributed viruses within the Chiroptera order (Lau et al. 2005, Poon et al. 2005, Woo et al. 2006a, Dominguez et al. 2007, Gloza-Rausch et al. 2008, Donaldson et al. 2010, August et al. 2012, Anthony et al. 2013, Hashemi-Shahraki et al. 2013, Lelli et al. 2013, Memish et al. 2013, Chen et al. 2014, Bentim Góes et al. 2016). Viruses closely related to those responsible for the human MERS-CoV and SARS-CoV pandemics, as well as porcine epidemic diarrhoea virus (PEDV) and Swine Acute Diarrhoea Syndrome virus (SADS-CoV) in pigs, have been identified from bats (Guan et al. 2003, Tang et al. 2006, Ge et al. 2013, Hashemi-Shahraki et al. 2013, Memish et al. 2013, Hu et al. 2017, Lau et al. 2018, Zhou et al. 2018) suggesting that bats are important natural reservoirs for emerging coronaviruses (Li et al. 2005, Munster et al. 2016). Alphacoronavirus (one of the four coronavirus genera) strains have been detected in the faeces of two species of British bats: Natterer's bat (*Myotis nattereri*) and Daubenton's bat (*Myotis daubentonii*), out of seven surveyed species (August et al. 2012).

Although persistently infected with numerous viruses, bats rarely show clinical signs of disease (Sulkin & Allen 1974). Despite various surveillance and experimental studies undertaken across the world to identify coronaviruses in bat samples, clinical and pathological (gross and microscopic) signs of disease have not been noted in association with these coronaviruses (Lau et al. 2005, Poon et al. 2005, Lau et al. 2010, Watanabe et al. 2010, Lelli et al. 2013, Munster et al. 2016). Interestingly, MERS-CoV has been found to co-exist with cells from insectivorous big brown bats (*Eptesicus fuscus*) in vitro, although the mechanisms behind this are not fully understood (Banerjee et al. 2020). As mentioned, hACE2 has been shown to be an important cell entry receptor for SARS-CoV like viruses. A coronavirus, closely related to SARS-CoV, has been identified in bats and experimentally shown to use ACE2 as an entry receptor in humans, civets and Chinese horseshoe bat (*Rhinolophus sinicus*) cells (Ge et al. 2013). However, although infection is possible, disease does not appear to occur in infected Chinese horseshoe bats, which suggests a more complex mechanism behind the infectivity of the virus in these animals. It has been suggested that bats are able to mount specific immune responses to combat coronaviruses. Banerjee et al. (2020) showed experimentally that basal levels of type I interferon in the persistently infected bat cells were higher when compared to uninfected cells and viral replication increased when this interferon response was disrupted. No signs of disease associated with coronaviruses have been reported in bats in England or the UK.

Infection and disease associated with SARS-CoV-2 in bats

SARS-CoV-2 is, similarly to other coronaviruses, thought to have originated from bats. The virus has a 96.2% overall genome sequence identity to a bat coronavirus previously detected in free-living, wild intermediate horseshoe bats (*Rhinolophus affinis*) from the Yunnan province of China, compared to 79.5% identity to SARS-CoV (Zhou et al. 2020). The consumption of bat products for traditional Chinese medicine, and the prevalence of these species among wet markets in China highlights the potential for disease cross-over (Woo et al. 2006b). Indeed, the SARS-CoV-2 outbreak has been linked to a wet market in Wuhan, Hubei Province, China (Bogoch et al. 2020, Lu & Stratton 2020, Rothan & Byrareddy 2020).

There is evidence that SARS-CoV-2 can infect bats but its ability to cause disease is uncertain. There is an apparent resistance within the order Chiroptera to disease as a result of infection of coronaviruses in general, and limited evidence to suggest that the same may be true for SARS-CoV-2. Balkema-Buschmann and colleagues (2020) experimentally inoculated nine Egyptian fruit bats intranasally with SARS-CoV-2, which resulted in a 'transient respiratory tract infection' (Balkema-Buschmann et al. 2020). Virus replication was detectable in the nasal epithelium, trachea, lung, and lung associated lymphatic tissue, although no clinical signs were noted in these animals. Viral DNA was detected in the nasal epithelium of one of three in-contact bats after 21 days suggesting that natural transmission is possible within Egyptian fruit bats. It is uncertain if European bat species will react in the same manner as fruit bats to exposure and infection with SARS-CoV-2, and whether disease will occur in these species. It is also important to caution that the experimental study by Balkema-Buschmann and colleagues (2020) was undertaken in laboratory rather than field settings and may not reflect natural exposure in free-living bats, and subsequently steadfast conclusions cannot be drawn.

Conflicting evidence on the susceptibility of bats to SARS-CoV-2 was presented in a preliminary study which analysed the genetic similarity of bat ACE2 gene to that of hACE2. Of the 37 bat species analysed, eight had a low similarity, and 29 had a very low similarity (Damas et al. 2020). Considering that hACE2 is an important cell entry receptor for SARS-CoV-2, Damas et al's (2020) research is counter to the evidence from Egyptian fruit bats above. It is possible that other entry receptors present in bats can be utilised by the SARS-CoV-2 alongside ACE2.

Disease Risk Assessment

Human exposure assessment

Within the UK, cases of SARS-CoV-2 infection in humans number over 298,140 confirmed as of 17th June 2020 (World Health Organization 2020b). Humans are exposed to SARS-CoV-2 directly through aerosol droplets, spread by coughing or sneezing from an infected individual, or indirectly through touching of contaminated surfaces (Kampf et al. 2020, Rothan & Byrareddy 2020), as is the case with other coronaviruses (de Groot et al. 2012). Coronaviruses have been shown to persist on inanimate surfaces for up to nine days and, at low temperatures, persistence can be as long as 28 days (Ijaz et al. 1985, Kampf et al. 2020), although experimental evidence suggests that the survival of SARS-CoV-2 is likely to be 72 hours on stainless steel and plastic (van Doremalen et al., 2020). SARS-CoV-2 has also been detected in the faeces of humans (Calle 2020, Holshue et al. 2020, World Organisation for Animal Health (OIE) 2020), and therefore, faecal-oral transmission may be possible, as for other closely related coronaviruses (Yeo et al. 2020). However there remains doubt about the infectivity of virus in human faeces because rectal swabs taken from experimentally inoculated ferrets tested positive for viral RNA, though at lower levels than nasal washes and infectious virus was not detected in any rectal swabs. Counter to the findings in ferrets, rectal swabs from experimentally inoculated beagles also tested positive for viral RNA (Shi et al. 2020). Given the high prevalence of infection in people at the time of writing, that SARS-CoV-2 can be transmitted directly, and that the virus is persistent in the environment, there is a high likelihood of human exposure to SARS-CoV-2 at the time of writing.

Human infection is thought to occur through contact of viral particles with exposed mucous membranes including the eyes, nose and oral cavity (Lu et al. 2020, Zheng 2020). There is thus a high likelihood of infection of humans with SARS-CoV-2.

The reproductive number (R0) for SARS-CoV-2 is considered high with suggestions that in a naïve human population an average of two to four new infections may be generated from a single infectious human (Liu et al. 2020). The average incubation period is estimated to be between two and 14 days, with a median of four days, and it is not known to what extent shedding of the virus may occur within this period prior to the onset of clinical signs (Guan et al. 2020, Mizumoto et al. 2020, Yee et al. 2020). The availability of tests for SARS-CoV-2 for non-essential human workers in the UK remains low at the time of writing and therefore the infection status of individuals where clinical signs are either absent or mild is unlikely to be known. Based on the current epidemiological understanding of SARS-CoV-2 in humans there is a high likelihood of dissemination through the human population.

Bat exposure assessment

Numerous conservation, research and built development activities are undertaken in England which involve direct contact of personnel with bats and could provide an exposure route for bat species to SARS-CoV-2 through respiratory, oral or oro-faecal routes. Bats are caught in mist nets or harp traps, then handled to identify key parameters such as species, sex and body weight. Radio-tracking devices may also be attached to the animals. In other work, roosting areas for bats, which are often small, enclosed spaces, may be entered by fieldworkers as part of investigations. Endoscopes may be used to detect bat presence in tree cavities, buildings or caves. Bat detectors may be used in outdoor areas outside bat roosts, or other field locations.

Reports of transmission of SARS-CoV-2 from asymptomatic carriers, before the onset of clinical signs, have been published (Bai et al. 2020, Rothe et al. 2020, Zou et al. 2020). Therefore, asymptomatic infected fieldworkers are a potential source of exposure to bats. Exposure of the bats to SARS-CoV-2 could occur through direct contact with viral particles in respiratory droplets of infected fieldworkers as a result of coughing and sneezing in the vicinity of bats. Although there is doubt about the infectivity of SARS-CoV-2 in human faeces, as noted above, faecal-oral transmission remains a further possible route through which bats may become exposed, for example through contact with unwashed hands of infected fieldworkers. Indirect transmission may occur through contact of the fieldworker with equipment (for example, nets, traps or measuring tools), contaminating these fomites with viral particles either through aerosol droplets or faecal particles. Coronaviruses can persist on inanimate surfaces for up to 28 days under the right conditions (Kampf et al. 2020), and there is experimental evidence to show that SARS-CoV-2 can persist for 72 hours on plastic and stainless steel, and for shorter time periods on copper (24 hours) and cardboard (four hours), after which viral titres are greatly reduced (van Doremalen et al. 2020).

Given the numerous activities by fieldworkers which involve close contact with, and handling of, free-living bats in England, that exposure can occur through aerosol droplet, coughing or sneezing, or indirectly through contaminated inanimate objects, there is a high likelihood of exposure of bats to SARS-CoV-2 when handled by infected fieldworkers, or when in contact with contaminated surfaces. There is a medium likelihood of exposure of roosting bats to SARS-CoV-2 when infected fieldworkers enter roosts because of the close proximity between fieldworkers and bats and opportunity for aerosol transmission. There is a very low probability of exposure of bats to SARS-CoV-2 through use of bat detectors because the distance between fieldworker and bat is more than two metres (GOV.UK 2020).

There is evidence of infection with coronaviruses, including of the Betacoronavirus genera, in the genera of bat present in England: *Myotis* spp. (Woo et al. 2006a, August et al. 2012, Anthony et al. 2013, Rizzo et al. 2017), *Barbastella* spp. (Tang et al. 2006), *Plecotus* spp. (Rizzo et al. 2017), *Nyctalus* spp. (Tang et al. 2006, Lelli et al. 2013), *Pipistrellus* spp. (Woo et al. 2006a, Lelli et al. 2013), *Eptesicus* spp. (Dominguez et al. 2007, Donaldson et al. 2010, Anthony et al. 2013) and *Rhinolophus* spp. (Lau et al. 2005, Li et al. 2005, Tang et al. 2006, Woo et al. 2006a, Hu et al. 2017, Rizzo et al. 2017, Zhou et al. 2018). In the only study undertaken to date surveying the coronaviruses present in free-living bats in the UK, August et al. (2012) found two strains of alphacoronavirus in the faeces of *M. nattereri* and *M. daubentonii*. A SARS-CoV-2-like virus has been detected in free-living intermediate horseshoe bats (*Rhinolophus affinis*) in China (Zhou et al. 2020) and, on this basis, bats of the genus *Rhinolophus* spp. in England may be susceptible to SARS-CoV-2. There is experimental evidence to suggest that if bats from the genus *Rousettus* are exposed to SARS-CoV-2, they will become infected (Balkema-Buschmann et al. 2020) but no bats from this genus reside in England. Given the over 200 species of coronaviruses which infect bats, that all bat genera present in England have been found to be infected with coronaviruses and a SARS-CoV-2-like virus has been detected in one genus (*Rhinolophus* spp.), there is a medium likelihood that species of bat in England will become infected with SARS-CoV-2.

Given that animal to animal transmission has been shown for *Rousettus aegyptiacus* bats, as well for cats, hamsters and ferrets (Chan et al. 2020; Shi et al. 2020), and that bats often roost in large numbers, which may aid in facilitating disease dissemination within populations (Knight & Jones 2009, Lau et al. 2010), there is a medium probability of dissemination of SARS-CoV-2 amongst bat populations in England.

Consequence assessment

There is a medium likelihood that a bat exposed to an infected human will become infected with SARS-CoV-2.

There is experimental evidence to show that Egyptian fruit bats can become infected after exposure to SARS-CoV-2 (Balkema-Buschmann et al. 2020). In Balkema-Buschmann et al's (2020) study, no clinical signs were noted in infected bats, no further research has been undertaken to date and the pathogenesis of SARS-CoV-2 in other bat species remains unclear. Infection of fruit bats with SARS-CoV-2 has also only been demonstrated under experimental conditions, and it is therefore unclear whether free-living bats will respond to exposure in the same manner. The literature suggests that when bats are exposed to other coronaviruses, including closely related betacoronaviruses, persistent infection occurs in the absence of clinical disease (Lau et al. 2005, Poon et al. 2005, Lau et al. 2010, Watanabe et al. 2010, Lelli et al. 2013, Munster et al. 2016). Given the experimental evidence of infection in Egyptian fruit bats infected with SARS-CoV-2 in the absence of clinical disease, and the limited research available in other species of bat, there is a low likelihood of disease associated with SARS-CoV-2 infection in free-living bat species in England. Therefore, there is a very low likelihood of biological consequences through a disease outbreak in bat populations in England at field sites, and a very low likelihood of severe disease and mortality occurring in these animals. There is a low likelihood of economic consequences, through a need for increased monitoring of bat populations, to assess the effects of an outbreak of SARS-CoV-2 associated disease. There is a low likelihood of environmental consequences as a result of SARS-CoV-2 associated disease in bat populations in England through decline of population numbers.

<u>Risk estimation</u>

Based on the current understanding of SARS-CoV-2 there is a high likelihood of exposure, infection and dissemination of SARS-CoV-2 in the human population. There is a high to very low likelihood that bats will be exposed to SARS-CoV-2 as a result of human fieldwork activities at conservation sites, depending on the activity involved. There is a medium likelihood of infection of bats if exposed, and a medium likelihood of dissemination through the population. There is a low likelihood of clinical disease and a disease outbreak in free-living bat populations and a low probability of economic, environmental or biological consequences as a result of a decline in bat populations and monitoring methods. The overall risk of SARS-CoV-2-associated disease to bat populations in England is estimated to be LOW.

<u>Risk management</u>

Risk evaluation

The overall risk estimation is considered low and it is therefore recommended that risk management methods are employed to mitigate this risk.

Option evaluation

To reduce the risk of exposure of bat populations to SARS-CoV-2, careful consideration should be given as to the necessity of each monitoring/survey visit to a bat site. English government guidance should be followed with respect to minimising travel and avoiding public transport. Contact of fieldworkers with minimal other people should also be practiced, depending on the current governmental guidance. Fieldworkers showing clinical signs of Covid-19 disease or who have been in contact with a person displaying symptoms within 14 days should not undertake fieldwork activities. All such persons should seek SARS-CoV-2 testing and, if possible, obtain a clear test result before returning to fieldwork activities. If testing is not possible, the individual should self-isolate for a minimum of 14 days before commencing fieldwork.

Despite following these rules, symptom-based screening of humans is likely to be ineffective at preventing transmission due to the risk from infected but asymptomatic hosts transmitting the virus, and further measures should be implemented to stop viral spread (Hoehl et al. 2020). Currently the use of personal protective equipment (PPE) and good hygiene are considered to be the most effective measures against transmission of the virus (Yee et al. 2020). Personnel undertaking fieldwork activities should therefore adhere to strict biosecurity principles. It is recommended that a disposable overall (for example Tyvek®) is donned before entering the conservation site/roost to protect bats from possibly contaminated clothing. Hand cleaning should be undertaken at the start and at regular intervals throughout fieldwork activities, either washed with soap and water for a minimum of 20 seconds (following the World Health Organisation (WHO) guidelines (World Health Organization 2020a)), or cleaned by liberally using a hand sanitiser with at least 70% alcohol as an active ingredient, since this has been shown to be effective at killing SARS-CoVs in 30 seconds (World Health Organization 2009, Siddharta et al. 2017). Hand cleaning should particularly be undertaken before entering a field site, before and after touching any monitoring equipment and if the fieldworker touches their face.

Disposable gloves should be worn whenever possible. The effectiveness of face masks as a means of preventing exposure of bats to SARS-CoV-2 is currently unclear, however there appears to be some support for the wearing of masks by potentially infected humans to prevent respiratory droplet spread of virus particles (del Rio & Malani 2020). Given the possibility that a fieldworker could be infectious whilst asymptomatic, it is recommended that face coverings are worn to convey additional protection against introducing SARS-CoV-2 to bat populations. Although medical grade face masks, made from a minimum of three layers of synthetic, non-woven materials with filtration layers between, have been recommended by WHO (World Health Organization 2020c), the risk of shortage of these masks means that they should be reserved for use in healthcare settings; it has been suggested that these masks are more important in situations where self-protection is the priority (Greenhalgh et al. 2020). When considering the use of protective equipment to reduce the risk of exposing others, including bats, to SARS-CoV-2, for example from an infected fieldworker, a cloth face covering should suffice (Cheng et al. 2020). Cloth face coverings have been recommended by the Centers for Disease Control (CDC) as a method of minimising transmission from infected individuals (Centers for Disease Control 2020), and are suggested to be an appropriate alternative to medical grade face masks in the contexts of reducing transmission (Greenhalgh et al. 2020). Any face covering should be worn tightly around the chin and top of the nose and hand cleaning should be undertaken before placing the mask (World Health Organization 2020c).

Any fomites, including endoscopes, nets, traps or other examination equipment, should be appropriately disinfected before contact with the bat, between bats, and after any contact with a fieldworker who is not wearing gloves or a mask. Disinfectants containing 0.1% sodium hypochlorite or 62-71% ethanol lead to effective inactivation of the SARS-CoV-2 (Kampf et al. 2020) however the safety of products containing these chemicals has not been evaluated for use on bats. At present, Safe4 is considered the disinfectant of choice as it is safe for animal contact even when surfaces remain damp with the product. Safe4 is also biodegradable and considered to be safe for the environment. The efficacy of Safe4 against SARS-CoV-2 has been evaluated and this product is considered effective against the virus at a dilution of 1:50 (safe4disinfectant.com 2020).

To avoid transfer of SARS-CoV-2 via other fomites, personal items such as watches and mobile phones should not be touched whilst carrying out fieldwork activities. At the end of the fieldwork site visit all potentially contaminated items including disposable overalls, gloves and masks should be removed in a manner to avoid contact with their outer surfaces, placed in a clinical waste bin bag secured with a cable tie and decontaminated appropriately. Hands should once again be cleaned with soap and water for a minimum of 20 seconds or by using a 70% alcohol-based hand sanitiser.

Fieldworkers who find a sick bat should seek further advice from within their conservation organisation or a wildlife veterinarian. Any bats found dead by fieldworkers should be submitted for pathological examination at the Animal & Plant Health Agency (APHA) (Bat Conservation Trust, 2020b). Health surveillance of populations of bats exposed to fieldworkers should be considered; interventions should be motivated by increasing our understanding of SARS-CoV-2 epidemiology.

Discussion

In this DRA, we evaluated the risk of disease induced by SARS-CoV-2 to free-living bats within England as a result of contact with humans undertaking conservation activities. Using a qualitative method of disease risk analysis, involving an extensive literature review, the risk of disease was predicted to be low, indicating the value of the implementation of disease risk management measures when conducting field conservation activities in the future. Given the rapid and recent emergence of SARS-CoV-2, there is uncertainty in the pathogenicity of SARS-CoV-2, and the consequences of infection, in bats, while evidence to estimate the probability of exposure was relatively better. Thus, extrapolation on the interaction between closely related viruses and bats was required to inform the analysis. As further research on SARS-CoV-2 epidemiology is published our understanding of pathogenicity will improve and the disease risk analysis can be re-evaluated. In addition, the epidemiology of the virus in the human population and its genetic make-up will probably rapidly change over the ensuing months and years. Our disease risk analysis methods are transparent, each stage of the assessment has been made in a logical, reasoned approach and therefore, given new data, the way in which risk changes can be made clear.

Guidelines were produced by the Bat Conservation Trust to reduce the risk to bat species in England from disease precipitated by the fungus *Pseudogymnoascus destructans*, the infectious agent responsible for white nose syndrome (WNS), a group of clinical signs associated with the deaths of millions of bats in North America since 2006 (Turner et al. 2011). These guidelines focussed on surveillance for signs of WNS in UK bats, since the disease has not been reported, as well as recommendations on appropriate measures to reduce potential transfer between field sites, such as disinfection of boots and equipment. However, WNS is not a zoonotic disease, and therefore fieldworkers need only consider themselves as fomites for the fungus, rather than a continuous infection source. Consequently, the management measures recommended to combat the risk from SARS-CoV-2 are more stringent and robust. Unlike WNS, the hazard originates from an infected fieldworker and therefore fieldworkers are a sustained risk of exposure and infection through their respiratory secretions to bats. Fieldworkers could also ‘create’ fomites by handling equipment or surfaces which could contact bats. Recommendations for preventing the exposure of bats to SARS-CoV-2 are akin to those produced for fieldworkers working with great apes, for which there are several zooanthroponoses which could lead to disease. For example, in such cases the addition of facemasks is considered to be important, as well as the use of hand sanitiser by all personnel before entering great ape habitats (Macfie & Williamson 2010, Gilardi et al. 2015).

In the future, it may be prudent to consider health surveillance of bat populations for which contact with fieldworkers is considerable. Health surveillance could help to inform further decision making and advice regarding future fieldwork activities around bats and provide information regarding SARS-CoV-2 epidemiology within free-living bat populations in England. That being said, surveillance interventions should not place bats at increased probability of exposure. The epidemiology of the SARS-CoV-2 in people should be carefully monitored, and activities which may necessitate increased contact with bats should be minimised until the probability of exposing bats to SARS-CoV-2 is reduced, for example when the infection rate of humans in the UK is reduced. Other mitigation methods advised in this report should still be followed during these activities.

In conclusion, our disease risk analysis has shown that SARS-CoV-2 has been demonstrated experimentally to infect one species of bat and that there is a lack of evidence, but uncertainty, on the ability of SARS-CoV-2 to cause disease in bats. Since there is a high to very low probability of exposure of free-living bats in England to humans infected with SARS-CoV-2 from the plethora of surveying, monitoring and intervention activities, there is a need to mitigate the risk from SARS-CoV-2-associated disease in bats during fieldwork activities. The probability of infection can probably be effectively reduced if fieldworkers follow routine government guidance, minimum precautions have been set out in advice provided by DEFRA to Natural England, Natural England (2020) and in addition follow strict biosecurity measures when contacting bats or possible fomites which may expose bats to the virus, including the use of disposable gloves, cloth face coverings, effective hand cleansing and appropriate disinfecting of equipment.

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