Received: 21 November 2020 | Revised: 12 January 2021 | Accepted: 8 February 2021

DOI: 10.1111/tbed.14035

ORIGINAL ARTICLE

Transboundary and Emerging Diseases WILEY

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

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Abstract

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 captive wild animals. 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. 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. The probability of exposure of bats to SARS-CoV-2 through fieldwork activities was estimated to range from negligible to high, 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 were 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. Disease risk management measures are suggested, including the use of personal protective equipment, good hand hygiene and following the existing government advice. 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.

KEYWORDS

Bats, Chiroptera, COVID-19, Fieldworkers, Risk Assessment, SARS-CoV-2

1 | 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, subgenus sarbecovirus, within the Coronaviridae family (Tan et al. 2020; Zhu et al. 2020). 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 (Groot et al., 2012; Masters, 2006). For example, SARS-CoV-2 is within the sarbecovirus subgenus alongside SARS-CoV (Zhu et al. 2020), and within the same genus as MERS-CoV. SARS-CoV and MERS-CoV are responsible for causing outbreaks

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of severe acute respiratory syndrome (SARS) and Middle East respiratory syndrome (MERS), respectively, in humans in recent years. Both viruses are considered to have originated from animal reservoirs (Gorbalenya et al. 2020; Lu, Zhao, Yu, 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.

The susceptibility of species to SARS-CoV-2 infection has been suggested to be associated with the angiotensin-converting enzyme two(ACE2) gene. 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 utilize ACE2 to gain entry into human cells, as had previously been discovered for SARS-CoV (Kuba et al. 2005; Li et al. 2003). The importance of ACE2 for infection by SARS-CoV-2 has been shown through a study by Bao et al. (2020) in which human ACE2 (hACE2) transgenic mice and wild type mice (*Mus musculus*) were intranasally inoculated with SARS-CoV-2. hACE2 transgenic mice showed clinical signs of body weight loss along with multiple histopathological changes including interstitial pneumonia, and (i) viral RNA was detected in the lungs by quantitative PCR, and (ii) infectious SARS-CoV-2 could be isolated from the lungs of transgenic mice.

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). Similarly, Olival et al. (2020) examined the risk of humans inadvertently infecting North American bats with SARS-CoV-2 and suggested that over 40 species of temperate-zone bats could be susceptible to SARS-CoV-2 infection and therefore measures should be taken to mitigate the risk.

TABLE 1 Interpretation of probability categories used in this risk assessment (table taken from EFSA Panel on Animal Health and Welfare.(2006), adapted from Murray (2004))

Probability Category	*Interpretation*
Negligible	Event is so rare that it does not merit to be considered
Very Low	Event is very rare but cannot be excluded
Low	Event is rare but does occur
Medium	Event occurs regularly
High	Event occurs very often
Very High	Event occurs almost certainly

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.

2 | 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 (2013) DRA method, developed using the foundation provided by the World Organization for Animal Health (OIE) (Murray, 2004), and modified by Bobadilla Suarez et al. (2017); Rideout et al. (2017), with further consideration of previous qualitative DRA methods (Davidson & Nettles, 1992; Leighton, 2002), was applied in this report. Disease risk assessment was carried out according to the method described by the OIE (Murray, 2004). The biological pathways that might permit bats to be exposed and infected with SARS-CoV-2 were assessed, as well as the probability of exposure and infection 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. Probability categories assigned to events in the exposure assessments and consequence assessments were chosen using the justifications outlined in Table 1. Using the method described in Murray (2004), results of the exposure and consequence

assessments were combined to qualitatively assess the risk from disease (Risk Estimation as defined by Murray (2004)) associated with SARS-CoV-2 to bat species in England. Information used to assign probability categories was gathered via a thorough literature search using relevant keywords (SARS-CoV-2, COVID-19, animals, bats, Chiroptera). This was undertaken utilizing the search engines of Google Scholar, PubMed and Science Direct and eliciting expert opinion where necessary. All relevant papers were read and reviewed. Each time a probability category was concluded, the certainty level of this decision was indicated using the reasoning outlined in Table 2.

3 | RESULTS

3.1 | Hazard identification

3.1.1 | 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.

3.1.2 | 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 (August et al. 2012; Chen et al. 2014; Dominguez et al. 2007; Gloza-Rausch et al. 2008; Hashemi-Shahraki et al. 2013; Lau et al. 2005). 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 (Ge et al. 2013; Guan et al. 2003; Hashemi-Shahraki et al. 2013; Hu et al. 2017; Lau et al. 2018; Memish et al. 2013; Tang et al. 2006; 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, 2010; Lelli et al. 2013; Munster et al. 2016; Poon et al. 2005; Watanabe et al. 2010). 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 bat cells persistently infected with human SARS-CoV were higher when compared to uninfected cells and viral replication increased when this interferon response was disrupted. That being said, no bat coronaviruses have been successfully isolated at present and so no experimental studies involving bat coronaviruses have been undertaken to date. No signs of disease associated with coronaviruses have been reported in bats in England or the UK.

TABLE 2 Interpretation of Certainty categories used in this risk assessment (table adapted EFSA Panel on Animal Health and Welfare.(2006))

Certainty Category	*Interpretation*
Low	There are scarce or no data available on the species and/or event in question; evidence is not provided in references but rather in unpublished reports or based on observations, or personal communication; authors report conclusions that vary considerably between them
Medium	There are some but no complete data available on the species and/or event in question; conclusions have been extrapolated from closely related species; evidence is provided in small number of references; authors report conclusions that vary from one another.
High	There are solid and complete data available for the species and/or event in question; strong evidence is provided in multiple references; authors report similar conclusions

3.1.3 | Mammalian origin of SARS-CoV-like coronaviruses

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. Indeed, SARS-CoV is considered to be a virus of animal origin; several species of horseshoe bats (within the *Rhinolophus* genus) have been identified as a natural reservoir of SARS-CoV. In a study by Li et al. (2005), a SARS-CoV seroprevalence of between 28% and 71% was noted in three species (*R. pearsoni*, *R. pussilus* and *R. macrotis*). The virus was identified as having 92% sequence identity with the SARS-CoV identified in humans. Further supporting evidence was provided by Lau et al. (2005) who found genetic material closely related to SARS-CoV in 39% (23/59) of anal swabs taken from free-living Chinese horseshoe bats (*R. sinicus*) and a seroprevalence of 84% in the sampled bats. The seroprevalences found in both studies alongside the absence of clinical disease in these animals reported by numerous other studies are sufficient evidence to suggest that these species of bat form a wildlife reservoir of SARS-CoV (Cheng et al. 2007; Guan et al., 2003; Li et al. 2005; Wassenaar & Zou, 2020).

The palm civet (*Paguma larvata*) is widely considered to be the intermediate host facilitating and amplifying the spillover of SARS-CoV from horseshoe bats to humans (Shi & Hu, 2008; Wang & Eaton, 2007). Guan et al. (2003) isolated SARS-CoV-like viruses from civets and racoon dogs (*Nyctereutes procyonoides*) in a wet market in China, but the proportionately larger number of civets being traded led to a focus upon this species (Wang & Eaton, 2007). Civets were ruled out as a reservoir host after several surveillance studies of free-living and farmed civets did not find evidence of SARS-CoV antibodies on serology (Poon et al. 2005; Tu et al. 2004). However, when experimentally infected with two separate human isolates of SARS-CoV, civets displayed clinical signs of lethargy and fever highlighting their susceptibility to disease (Wu et al. 2005).

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

Preliminary reports have described the ability of SARS-CoV-2 to infect 18 non-human mammalian hosts: domestic cats (*Felis catus*), domestic dogs (*Canis familiaris*), racoon dogs, transgenic house mice (*Mus musculus*), North American deer mice (*Peromyscus maniculatus*), domestic ferrets (*Mustela putorius furo*), American mink (*Neovsion vison*), Egyptian fruit bats (*Rousettus aegyptiacus*), Syrian hamsters (*Mesocricetus auratus*), Malayan tigers (*Panthera tigris jacksoni*), Amur tigers (*Panthera tigris altaica*), African lions (*Panthera leo*), snow leopards (*Panthera unicia*), pumas (*Puma concolor*), rhesus macaques (*Macaca mulatta*), long-tailed macaques (*Macaca fascicularis*), African green monkeys (*Chlorocebus aethiops*) and common marmosets (*Callithrix jacchus*) (Bao et al. 2020; Chan et al. 2020; Deng et al. 2020; Goumenou et al. 2020; Lu, Zhao, Yu, et al., 2020; McAloose et al. 2020; ProMed International Society for Infectious Diseases., 2020a, 2020b; Schlottau et al. 2020; Shi et al. 2020; Speranza et al., 2020; Wang et al. 2020; World Organisation for Animal Health (OIE) (2020) ; Zhang et al., 2020). In 16 of these mammalian species (racoon dogs, Malayan tigers, Amur tigers, African lions, snow leopards, pumas, domestic cats, Syrian hamsters, North American deer mice, American mink, domestic ferrets, transgenic house mice, rhesus macaques, long-tailed macaques, common marmosets and African green monkeys), infection has been associated with disease (Bao et al. 2020; Chan et al. 2020; Freuling et al. 2020; ProMed International Society for Infectious Diseases., 2020b; Schlottau et al. 2020; Shi et al. 2020; World Organisation for Animal Health (OIE) (2020). Domestic pigs (Sus scrofa domesticus) are not thought to be susceptible to infection with SARS-CoV-2 (Schlottau et al. 2020).

3.1.5 | 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 highlight 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 et al., 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. An experimental challenge study was undertaken by Hall et al (2020) and suggested that big brown bats (*Eptesicus fuscus*), a North American species, are resistant to infection with SARS-CoV-2. Seven bats were intranasally inoculated and remained negative for SARS-CoV-2 DNA on PCR of rectal and oropharyngeal swabs taken for 20 days post-inoculation. Conversely, Schlottau and colleagues (2020) experimentally inoculated nine Egyptian fruit bats intranasally with SARS-CoV-2, which resulted in a 'transient respiratory tract infection' (Schlottau et al. 2020). Viral RNA 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 both experimental studies undertaken by Schlottau et al. (2020) and Hall and colleagues (2020) were 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 utilized by the SARS-CoV-2 alongside ACE2.

3.2 | Disease Risk Assessment

3.2.1 | Bat fieldworker exposure assessment

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 (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 hr on stainless steel and plastic (van Doremalen et al., 2020). SARS-CoV-2 has also been detected in the faeces of humans (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 the prevalence in bat fieldworkers is not expected to differ, that SARS-CoV-2 can be transmitted directly and that the virus is persistent in the environment, there is a high likelihood of exposure of bat fieldworkers 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, Zhao, Yu, 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 and a degree of certainty.

3.2.2 | 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 (e.g. 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 hr on plastic and stainless steel, and for shorter time periods on copper (24 hr) 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 negligible 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. (Anthony et al. 2013; August et al. 2012; Rizzo et al. 2017; Woo, Lau, Li, et al., 2006), *Barbastella* spp. (Tang et al. 2006), *Plecotus* spp. (Rizzo et al. 2017), *Nyctalus* spp. (Lelli et al. 2013; Tang et al. 2006), *Pipistrellus* spp. (Lelli et al. 2013; Woo, Lau, Li, et al., 2006), *Eptesicus* spp. (Anthony et al. 2013; Dominguez et al. 2007; Donaldson et al. 2010) and *Rhinolophus* spp. (Hu et al. 2017; Lau et al. 2005; Li et al. 2005; Rizzo et al. 2017; Tang et al. 2006; Woo, Lau, Li, et al., 2006; 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. The apparent lack of pathology associated with coronaviruses in bats could be due to long-term co-evolution of the host–parasite relationship, although since SARS-CoV-2 is a completely new betacoronavirus it is not possible to rule out associated infection and disease. There is experimental evidence to suggest that if bats from the genus *Rousettus* are exposed to SARS-CoV-2, they will become infected (Schlottau et al. 2020) but no bats from this genus reside in England. That being said, Big brown bats have been shown experimentally to be resistant to infection with SARS-CoV-2 and belong to the same genus as the serotine bat (*Eptesicus serotinus*) which is native in England, suggesting this genus may be resistant. 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.), but that bats of the *Eptesicus* genus appear to be resistant to infection, 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 felids, canids, rodents and mustelids (Chan et al. 2020; Freuling 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 among bat populations in England.

3.2.3 | 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 (Schlottau et al. 2020). In Schlottau et al.'s (2020) study, no clinical signs were noted in infected bats, and in a further experimental study by Hall et al. (2020), big brown bats were resistant to infection. 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 and resistance of big brown bats have 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, 2010; Lelli et al. 2013; Munster et al. 2016; Poon et al. 2005; Watanabe et al. 2010). 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 very 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.

3.3 | Risk estimation

Table 3 outlines each step in the risk estimation. 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 negligible to high 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 (Table 4). 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 very 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, with low certainty.

3.4 | Risk management

3.4.1 | Risk evaluation

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

TABLE 3 Table to show the estimated likelihood of occurrence of each event within the disease risk assessment and the associated certainty level

Event	*Likelihood of Occurrence*	*Certainty Level*
Exposure of bat fieldworkers to SARS-CoV–2	High	High
Infection of bat fieldworkers	High	High
Dissemination of SARS-CoV–2 through groups of bat fieldworkers and other people	High	High
Exposure of bats to SARS-CoV–2 as a result of fieldwork activities	Variable (See Table 4)	Variable (See Table 4)
Infection of bats if exposed to SARS-CoV–2	Medium	Low
Dissemination of SARS-CoV–2 through free-living bat populations and other mammals	Medium	Low
Clinical disease in bats after infection has occurred	Low	Low
Decline in bat populations as a result of infection with SARS-CoV–2	Very Low	Low
Biological, environmental or economic consequences as a result of declining bat populations	Very Low	Low

TABLE 4 Table to estimate the likelihood of exposure of bats to SARS-CoV-2 after specific fieldwork activities (prior to mitigation measures). A certainty level is also given for each likelihood estimation

Field/Conservation Activity	*Likelihood of Exposure*	*Certainty Level*
Catching bats in field/mist nets	High	Medium
Physical examination of bats	High	Medium
Entering small, enclosed roost sites to detect bats	Medium	Medium
Entering larger spacious roost sites to detect bats	Low	Medium
Using endoscopes to detect bat presence	Medium	Medium
Use of bat detectors in outdoor spaces	Negligible	High

3.4.2 | Option evaluation

Disease mitigation guidelines are already in place for bat workers in England, for example, to reduce the risk of transmission of European bat lyssavirus (EBLV) from bats to humans. The Bat Conservation Trust advises that any person handling a bat should wear disposable gloves, which are to be changed between individual animals, and handling of bats should be kept to a minimum to avoid stress (Bat Conservation Trust, 2016). Moreover, decontamination procedures are recommended if fieldworkers observe clinical signs associated with white nose syndrome (WNS) in bats (Bat Conservation Trust., 2019) but are not recommended as blanket guidelines (Bat Conservation Trust, 2016). We advise that further measures are required 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 minimizing travel and avoiding public transport. Contact of fieldworkers with minimal other people should also be practised, 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. This advice is in line with the advice published by the IUCN Species Survival Commission (SSC) Bat Specialist Group (BSG) (Nunez et al. 2020).

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). Indeed, several mitigation measures revolving around PPE have already been recommended to reduce the exposure of bats by infected fieldworkers, for example by the United States Geological Society (USGS) (Runge et al. 2020), The IUCN SSC BSG (Nunez et al. 2020) and EUROBATS (EUROBATS, 2020). Personnel undertaking fieldwork activities should therefore adhere to strict biosecurity principles in line with the aforementioned reports. It is recommended that a disposable overall (e.g. 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 s (following the World Health Organization (WHO) guidelines (World Health Organization, 2020a)), or cleaned by liberally using a hand sanitizer with at least 70% alcohol as an active ingredient, since this has been shown to be effective at killing SARS-CoVs in 30 s (Pittet et al. 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.

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. Filtering facepiece (FFP) respirators have been discussed in the context of the SARS-CoV-2 outbreak. These masks are highly effective at filtering particles in inhaled air—the highest protection is offered by the FFP3 respirator which filters at least 99% of aerosols with a total inward leakage of less than two percent (Lepelletier et al. 2020). This standard of respirator is recommended in certain situations in which the wearer may require additional protection. However, several FFP respirators have exhalation valves including the FFP3 respirator. This means that air exhaled by the wearer is not filtered, and therefore, this sort of mask is not appropriate for use in situations in which environmental protection is required. Alternatively, medical grade face masks, made from a minimum of three layers of synthetic, non-woven materials with filtration layers between, offer environmental protection against exhalation of viral particles and droplets by the wearer (Lepelletier et al. 2020). Although medical grade face masks have been recommended by WHO (World Health Organization, 2020b), 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 minimizing 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, 2020b).

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 s or by using a 70% alcohol-based hand sanitizer.

Fieldworkers who find a sick bat should seek further advice from within their conservation organization 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.

4 | 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 assessment, 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 considerable uncertainty in the pathogenicity of SARS-CoV-2 and the consequences of infection in bats, whilst 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. Currently, there are several important gaps in the knowledge associated with the virus, disease and dissemination in bat species, meaning that the authors have been forced to rely on extrapolation from other species and related viruses to draw uncertain conclusions. 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 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 when clinical signs are observed, such as disinfection of boots and equipment (Bat Conservation Trust., 2019). 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 sanitizer by all personnel before entering great ape habitats (Gilardi et al. 2015; Macfie & Williamson, 2010).

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 minimized 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, but another has been shown to be experimentally resistant. There is a lack of evidence, and hence considerable uncertainty, on the ability of SARS-CoV-2 to cause disease in bats. There is a need to mitigate the risk from SARS-CoV-2-associated disease in bats, particularly from those fieldwork activities which are estimated to pose a medium to high risk of exposure of bats to SARS-CoV-2 from infected fieldworkers. The probability of infection can probably be effectively reduced if fieldworkers follow routine government guidance, and minimum precautions have been set out in advice provided by DEFRA to Natural England (Nature 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.

ACKNOWLEDGEMENTS

The authors would like to thank Suzanne Crutchley, Andrew Cunningham, Claire Howe and Madeleine Ryan for their involvement in the project.

ETHICAL STATEMENTS

An ethical statement is not applicable for this study. The Authors declare no conflict of interest. A data availability statement is not applicable for this study; all data are within the manuscript.

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How to cite this article: Common SM, Shadbolt T, Walsh K, Sainsbury AW. The risk from SARS-CoV-2 to bat species in england and mitigation options for conservation field workers. *Transbound Emerg Dis*. 2021;00:1–12. https://doi.org/10.1111/tbed.14035