

A research hypothesis: Considering Traavik findings (1973-1980), during a SARS-CoV-2 pandemic.

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Abstract

The pandemic has triggered worldwide social and economic disturbance, with the leading economic depression from the time when there was a Great Depression. Moreover, misleading information about the virus has spread far and wide; even some public members have raised direct questions about the possibilities of ticks to transmit the virus. These questions have not received a simple solution so far. Thus, the key idea of this paper is to provide hints and hypothesis about the publicly raised questions about the possibilities of ticks transmitting SARS-CoV-2. The approach of the mentioned questions was based on the broader perspective of using the systemic review, where this newly discovered virus (SARS-CoV-2) was put into context with respect to the once mentioned ticks coronavirus-like of Traavik et al., during the 1973-1980 period. The possibilities of ticks to transmit the virus was hypothesized. Proving or disproving this hypothesis for the emergence of SARS-CoV-2 might be possible. Therefore, the role of ticks to transmit the virus needs more attention. This could lead to more efficient measures, to block the rise of another coronavirus epidemic with persistent transmission in humans.

KEYWORDS

SARS-CoV-2, ticks, virus and hypothesis.

1 INTRODUCTION

On the 30th January 2020, World Health Organization affirmed the outbreak of coronavirus disease (COVID-19) as a health crisis of global concern and on the 11th March 2020, as a pandemic (World Health Organization [WHO], 2020a, 2020b). The outbreak was initially detected in China, Wuhan, around December 2019 (WHO, 2020c; Huang et al., 2020). Currently, COVID-19 is a persisting pandemic, triggered by severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) (WHO, 2020d). Before we proceed, it is interesting to briefly review the current problem. As of 21st June 2020, more than 8,815,743 cases of SARS-CoV-2 have been conveyed in 188 different countries, ensuing 464,895 mortalities (COVID-19 Dashboard by Center for Systems Science and Engineering [CSSE], 2020). The pandemic has triggered worldwide social and economic disturbance, with the leading economic depression from the time when there was a Great Depression (International Monetary Fund [IMF] Blog, 2020). Moreover, misleading information about the virus has spread far and wide (Clamp, 2020); even some public members have raised direct questions about the possibilities of ticks to transmit the virus (Annapolis, 2020). These questions have not received a simple solution so far. The Entomological Society of America by the U.S. Centers for Disease Control and Prevention's Division of Vector-Borne Diseases, have provided information that there is no evidence to support the fact that ticks can transmit SARS-CoV-2 (Entomological Society of America, 2020). A closer look at the literature reveals a few gaps and shortcomings. With that in mind, I raise more questions about the findings of Traavik and his colleagues, reported four decades ago, during the 1973-1980 period; can their work be considered to provide hints and hypothesis that can be tested to answer the above mentioned questions?

1.1 Objective and scope of the paper

The key idea is to provide hints and hypothesis concerning the publicly raised questions about the possibilities of ticks to transmit SARS-CoV-2. The provided hints and hypothesis can be tested by targeted audience mentioned below. The approach of the mentioned questions was based on the broader perspective of using the systemic review, where this newly discovered virus (SARS-COV-2) was put into context with respect to the once mentioned tick coronavirus-like of Traavik et al., during the 1973-1980 period.

1.2 Targeted audience

This paper is developed as a complementary and informative document for voluntary adoption by participating users, including academics, researchers, decision makers, veterinary and healthcare professionals.

2 METHODOLOGY FOR RETRIEVAL OF THE EVIDENCE

To provide hints and hypothesis about the possibilities of ticks to transmit SARS-CoV-2, the evidence within a systematic review was captured. The considered evidence was the 1st January 1970 to the 1st June 2020. Medline; Scopus; EMBASE; Google Scholar, Scifinder and the WHO Institutional Repository databases were analysed. Information sharing was achieved by using variations of the following search strategy:

Transmission: “coronavirus/ Runde coronavirus-like transmitted by ticks” or “SARS-CoV transmitted by ticks” or “SARS-CoV-2 transmitted by ticks” or “Covid-19 transmitted by ticks”.

Structure: “coronavirus/ Runde coronavirus-like structure ticks” or “SARS-CoV structure ticks” or “SARS-CoV-2 structure ticks” or “Covid-19 structure ticks”.

Host range: “coronavirus/ Runde coronavirus-like host range ticks” or “SARS-CoV host range ticks” or “SARS-CoV-2 host range ticks” or “Covid-19 host range ticks”.

Distribution: “coronavirus/ Runde coronavirus-like distribution ticks” or “SARS-CoV distribution ticks” or “SARS-CoV-2 distribution ticks” or “Covid-19 distribution ticks”.

Cross-referencing was done to find extra studies meeting the inclusion criteria. The published articles were evaluated by reading the full text. The Integrated quality criteria for review of multiple study designs (ICROMS) scoring system was used to assess the standard of articles (Zingg et al., 2016). The standard of appropriate studies was ranked as ‘low’, ‘moderate’ or ‘high’. The hypothesis was then formulated based on the appropriate evidence of each study.

3 RETRIEVED EVIDENCE

Several studies were examined, and 31 citations were found from all the databases: based on the inclusion and exclusion criteria, 8 experimental articles were found relevant for systematic review (Figure 1). The evidence from these 31 studies was identified to be of low (24 articles), moderate (1 article) and high (7 articles) standards. Eight experimental studies were specific and relevant about providing hints about the possibilities of ticks transmitting coronavirus like. The seven experimental studies were sourced from Traavik and colleagues, from the 1973s to 1978s, while one was obtained from Saikku and colleagues, reported in the 1980s (Figure 1).

Studies by Traavik and colleagues at Runde Island, Norway during the 1973s, were initiated in the attempt to solve the mystery of unusually high chick mortalities from seabird colonies reported. In the first study efforts were made in the 1973s, where a collection of *Ixodes uriae* samples from the seabird colonies and isolations of potential tick-borne arboviruses were conducted. During the 1975s, the second study was reported, where apart from the viruses isolates namely, Tick-borne encephalitis and Uukuniemi group viruses, additional two same strains of a coronavirus-like were found from *I. uriae* ticks collected during the 1973s. This latter result leads to the collection of Seabird sera samples, early May from Hernyken, RØst Island, Norway (Traavik, Meel, & Kjeldsberg, 1977). During the 1977s, the third study was reported, where the coronavirus like strain was tentatively named Runde virus linked with Seabirds and *I. uriae*. The virus was termed Runde virus after the island name where the seabird colonies were situated (Traavik, Meel, & Kjeldsberg, 1977; Traavik & Brunvold, 1978). Several more landmark studies (Traavik, 1977; Traavik & Brunvold,

1978; Traavik, 1978,1979) were conducted and reported in the 1977s and 1978s in the attempt to back up the evidence of Traavik, Meel and Kjeldsberg (1977). Evidence from the cohort study indicated that the isolation of a coronavirus like agent transmitted transstadially and sustained for six months in *I. uriae* , was thought-provoking (Saikku, Main, Ulmanen, & Brummer-Korvenkontio, 1980). There evidence is available, however Saikku, Main, Ulmanen and Brummer-Korvenkontio (1980), work does not overwhelmingly support the findings of Traavik, Meel and Kjeldsberg (1977); due to the lack of resources (for example, RT-PCR, RT-qPCR molecular analysis and metagenomic sequencing) four decades ago. Nonetheless, the ecological conditions of the isolations designated a coronavirus circulating among the *I. uriae* and its seabird hosts.

3.1 Significance of the previous research by Traavik and colleagues

The previous prospective research by Traavik and colleagues has made innovative contributions in several areas, especially in Acarology, Ecology and Virology. The knowledge about the coronavirus circulating among the *I. uriae* and its seabird hosts provide a hint about the possibilities of ticks to harbour and transmit coronavirus. Although, their results cannot be claimed to universally be the case for all different kinds of tick species and coronavirus. It is hard to comprehend why this knowledge should be excluded from the raised questions about the possibilities of any tick species be able to harbour and circulate coronavirus like SARC-CoV-2. Thus, the information is vital since there is ample of evidence about the different kinds of tick species that share ecological niches with potential vertebrate reservoir, such as bats, seabirds and pangolins (Olival et al., 2017; Fagre & Kading, 2019; Málková et al., 1985; Dietrich, Go´mez-Dı´az, & McCoy, 2010; Ramos et al., 2001; Gao et al., 2020; Khatri-Chhetri et al., 2016; Mohapatra, Panda, Nair, & Acharjyo, 2016; Robinson, 1983).

Classification of ticks is well done in pangolins consisting of eight genera and twenty species of ticks described from six species of pangolins namely, *Manis pentadactyla*, *M. javanica*, *M. crassicaudata* , *M. gigantea*, *M. tricuspis* and *M. temminckii* . The most intriguing finding is that unassigned ticks that were described from *M. tetradactyla* by Robinson (1983). *Amblyomma* , *Rhipicephalus* and *Aponomma* genera of ticks have been described from the above mentioned Asian and African pangolin species. Asian pangolins namely, *M. pentadactyla*, *M. javanica* and *M. crassicaudata* have been associated with *Amblyomma javanense* . While, African pangolins namely, *M. temminckii*, *M. tricuspis* and *M. gigantean* have been associated with *Amblyomma compressum* (Sanyal, De, Rao, & Acharjyo, 1987; Parola et al., 2003; Mohapatra, Panda, Nair, & Acharjyo, 2016). Possible geographic distribution of hard ticks linked with pangolins is provided in figure 2. The geographic distribution was developed from different research work of Hassan, Sulaiman and Lian (2013), Kollars and Sithiprasasna (2000), Parola et al. (2003), Li, Lin, Lan, Pei and Su (2011), Mediannikov et al. (2012) and Njiokou et al. (2006).

Different reviews of the literature undertaken by Nuttall (1984) and Chastel (1980), reported that seabird ticks harbour approximately 60 viruses or variants. Evidence about viraemic transmission to seabirds has been provided by Nunn et al. (2006). Moreover, Dietrich et al. (2010), reported that hard ticks prefer to infest seabird colonies in higher latitudes. The main example is *I. uriae* , which is the most significant species when focusing on its host species assortment and geographical distribution (Pettersson et al., 2020). Possible geographic distribution of hard ticks linked with seabirds is provided in figure 3. The geographic distribution was developed from the research work of Dietrich et al. (2010).

Several landmark studies observed associate phylogenetically viruses in bats with various arboviruses which can be transmitted by ticks (Fagre & Kading, 2019). Isolation results are providing evidence of bats being responsible for viruses isolated from either soft ticks or hard ticks. For instance, a study of Málková et al. (1985), provides evidence, where *Ornithodoros tadaridae* ticks obtained from a palm tree colonized by Cuban bats were found to be infected with Estero real virus. Recently, different kinds of Ixodes species (i.e. *Ixodes ariadnae* , *I. simplex* and *I. vespertilionis*) and *Dermacentor reticulatus* have been associated with bats (Sándor et al., 2019). Possible geographic distribution of hard ticks linked with bats is provided in figure 4. The geographic distribution was developed from different research work of Zahn and Rupp (2004), Hornok et al. (2014) and Hornok et al. (2016).

3.2 Implications for human health

In the light of reported evidence by Traavik and Brunvold, (1978), where the isolated Runde coronavirus agent from virus families that have RNA genomes, it is conceivable that this RNA virus may have “proofreading” systems deficiency than DNA viruses, and therefore it may be more inclined to develop and maintain genome mutations (Graepel et al., 2017). Thus, it would be reasonable to assume that this RNA virus is more likely to emerge, and for it to be capable to replicate in the cytoplasm is the best speculator of cross-species transmission from animals (for example, the above mentioned seabirds, bats and pangolins) to humans (Pulliam & Dushoff, 2009). Therefore, it is critical to consider this assumption since, bat ticks can also bite humans and they are capable to transmit viruses between bats and human (Socolovschi, Kernif, Raoult & Parola, 2012; Jaenson et al., 1994). The epidemiological importance for the transmission of diseases to humans from bats and bat associated ticks has become a major concern, although limited by lack of detailed information about bat ticks pathogen association and distribution (Loftis et al. 2005). However, growing urbanisation and bats adaptation to urban habitats has raised the chances for contact between domestic animals and humans with bat associated ticks and bats (Hornok et al., 2016; Krauel & LeBuhn, 2016). Moreover, Guglielmone et al. (2014) reported ten different types of tick species feeding on pangolins also feeding on unlikely animal hosts. Some of the pangolin’s ticks have been reported to bite humans (Estrada-Pena & Jongejan, 1999; Parola et al., 2013; Durden, Merker, & Beati, 2008; BurrIDGE, 2001; Audy, Nadchatram, & Lim, 1960). Limited reports of seabird tick bites to humans have been recognized (Gylfe et al., 1999; Duneau et al., 2008; Dietrich et al., 2010).

However, the fact that there are few reported cases of tick bites (ticks associated with seabird, bat and pangolin); it does not suggest that tick bites to humans do not occur. This can be due to unreported cases and undeveloped illness by the bitten person. Besides, areas where seabird, bat and pangolin ticks co-occur with other tick species that are significant vectors of animal and human pathogens signify likely contact areas for pathogen transmission. Anthroponotic factors related to the modern lifestyle can facilitate the emerging of tick-borne viruses. Today, we persistently recognize and obliged to deal with new cases of emerging viruses including tick-borne viral diseases (e.g. Wang et al. (2019), reported a new segmented virus associated with human febrile illness and ticks in China). Moreover, due to anthroponotic factors, it is not surprising that the outbreak of SARS-CoV-2 has been tentatively related with a seafood market in Wuhan, China, where the trading of wild animals may be the cause of zoonotic infection (Lu et al., 2020; Cohen, 2020). This assumption can be true since different kinds of mammalian species were purchase before SARS-CoV-2 outbreak at the Huanan seafood market as mentioned by Cohen (2020). Malayan pangolins (*Manis javanica*) smuggled into Southern China, are the only mammals except for *Rhinolophus affinis* bat (sampled from Yunnan in the year 2013) recognized to be affected by a SARS-CoV-2 related coronavirus (Lam et al., 2020; Zhou et al., 2020). This current finding by Lam et al. (2020), cannot be ignored, since the sampled pangolins independently acquired SARS-CoV-2 related viruses from bats or different animal host. However, their position as intermediate host in the development of human SARS-CoV-2 is still unclear. There is a clear dearth of consensus among researchers about the occurrence of coronaviruses, together with those associated to SARS-CoV-2, in different kinds of wild mammals found in Asia (Wang et al., 2005; Liu, Chen, & Chen, 2019; Wang et al., 2017). These are the most relevant findings and perhaps also the most significant, since, different tick species can be associated with both mammals (bats and pangolins), and they may also harbour coronavirus as proven by Traavik, Meel and Kjeldsberg (1977), Traavik and Mehl (1975) and Saikku et al., 1980.

All these above-mentioned findings are thought-provoking, and it could be hypothesized that ticks may possibly transmit SARS-CoV-2 to humans via different ways.

3.3 Possible hypothesis

The hypothesis was substantial enough necessitating a full descriptive cycle diagram. Therefore, figure 5 provides a hypothesis about the possible ways that *I. uriae* ticks can use to transmit SARS-CoV-2 to humans. In relation to the evolution of host specificity and local adaptation of ticks (Klompen, Black, Keirans, & Oliver, 1996), permits us to form the described potential hypothesis that remains to be scientifically proven.

4 FINAL REMARKS

The possibilities of ticks to transmit the virus was hypothesized. Proving or disproving this hypothesis for the emergence of SARS-CoV-2 might be possible. Since, such viruses may be asymptomatic in their hosts, but the balance may be tipped over, and overt disease or behavioural aberrations may occur due to ecosystem and climate alterations. In some instances, such viruses may cross a species barrier and affect other tick species, wildlife species, domestic animals and humans. Nonetheless, isolation of coronavirus-like from a range of animals, including ticks may possibly assist to clarify the steps to emergence in humans. Therefore, the role of ticks to transmit the virus needs more attention. These could lead to more efficient measures to block the rise of another coronavirus epidemic with persistent transmission in humans.

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CONFLICT OF INTEREST

No conflict of interest to be declared by the author.

AUTHORS CONTRIBUTION

Mkolo N.M. prepared wrote and revised the manuscript.

ETHICAL STATEMENT

Not applicable.

DATA AVAILABILITY

Data sharing not applicable to this review as no datasets were produced or analysed for this study.

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FIGURE LEGENDS

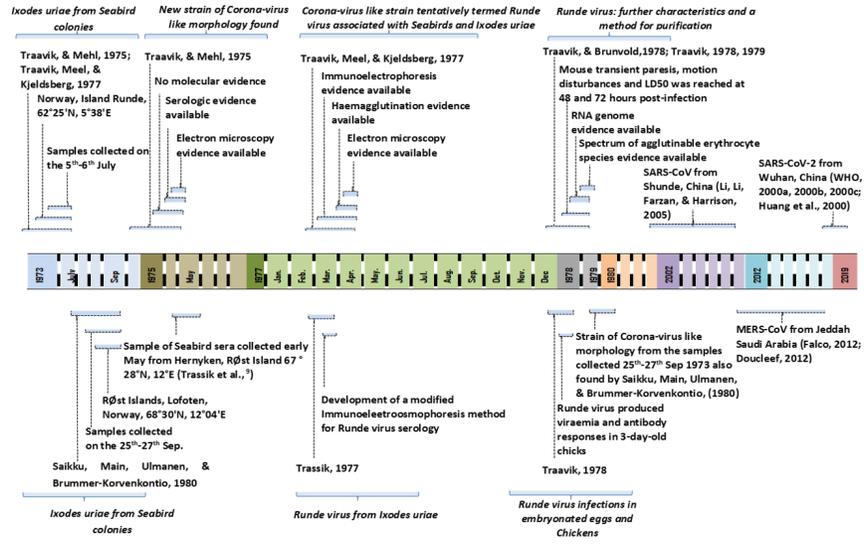
FIGURE 1 Evidence captured within a systematic review (from year 1973 to year 2020) to provide hints and more hypotheses on the origin of tick’s coronavirus and the possibilities of ticks transmitting coronavirus.

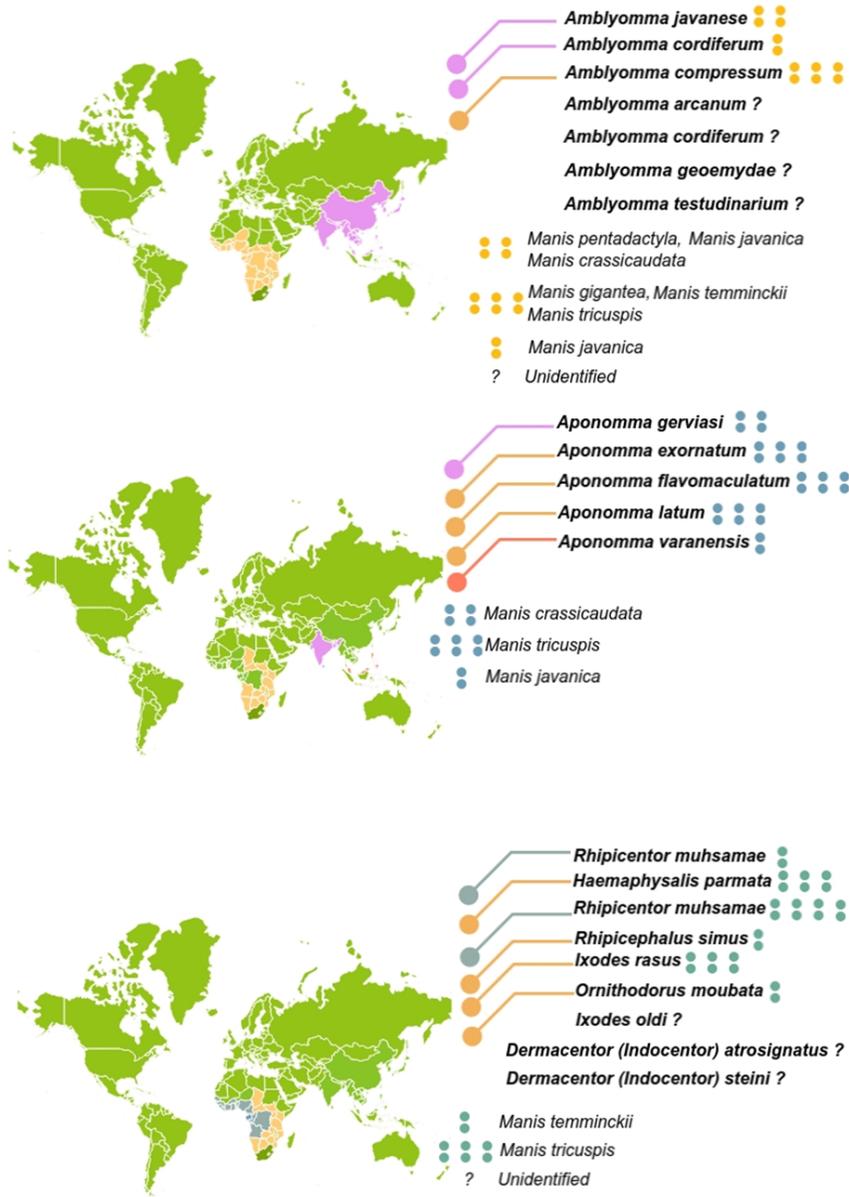
FIGURE 2 Possible geographical distribution of hard ticks linked with pangolins. **Note:** geographical distribution of some of the ticks linked with pangolins was unidentified. Map created with VIsME software.

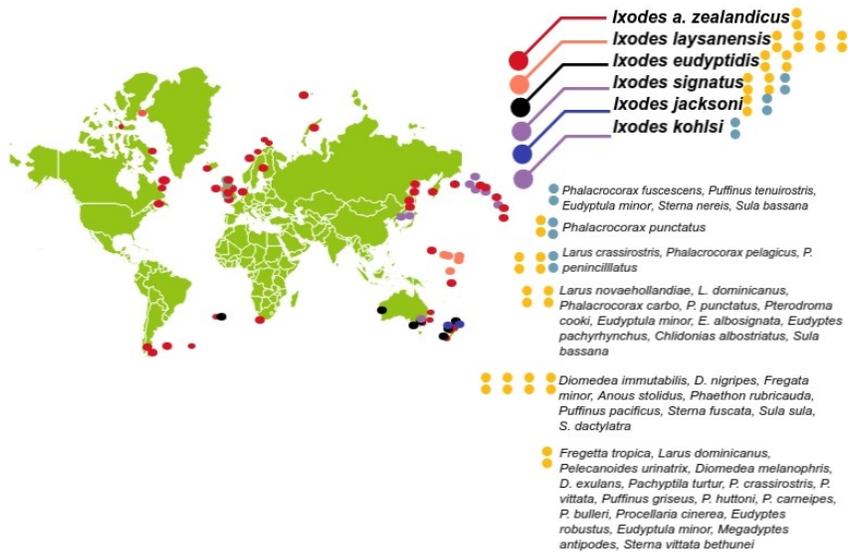
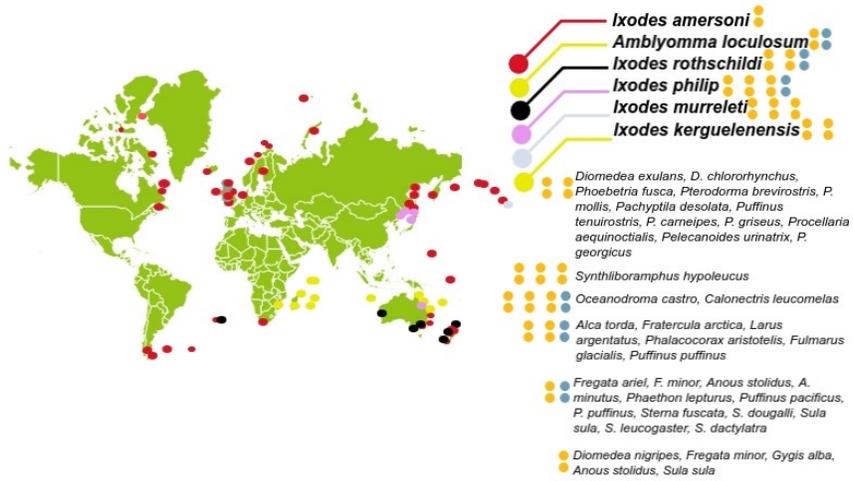
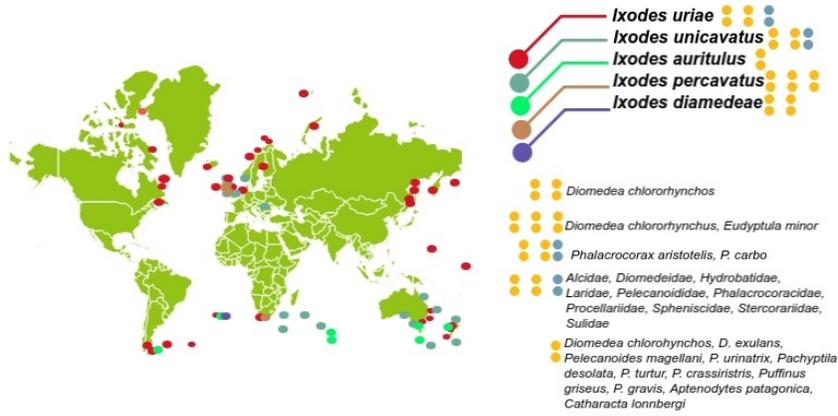
FIGURE 3 Possible geographic distribution of hard ticks linked with seabirds. Map created with VIsME software.

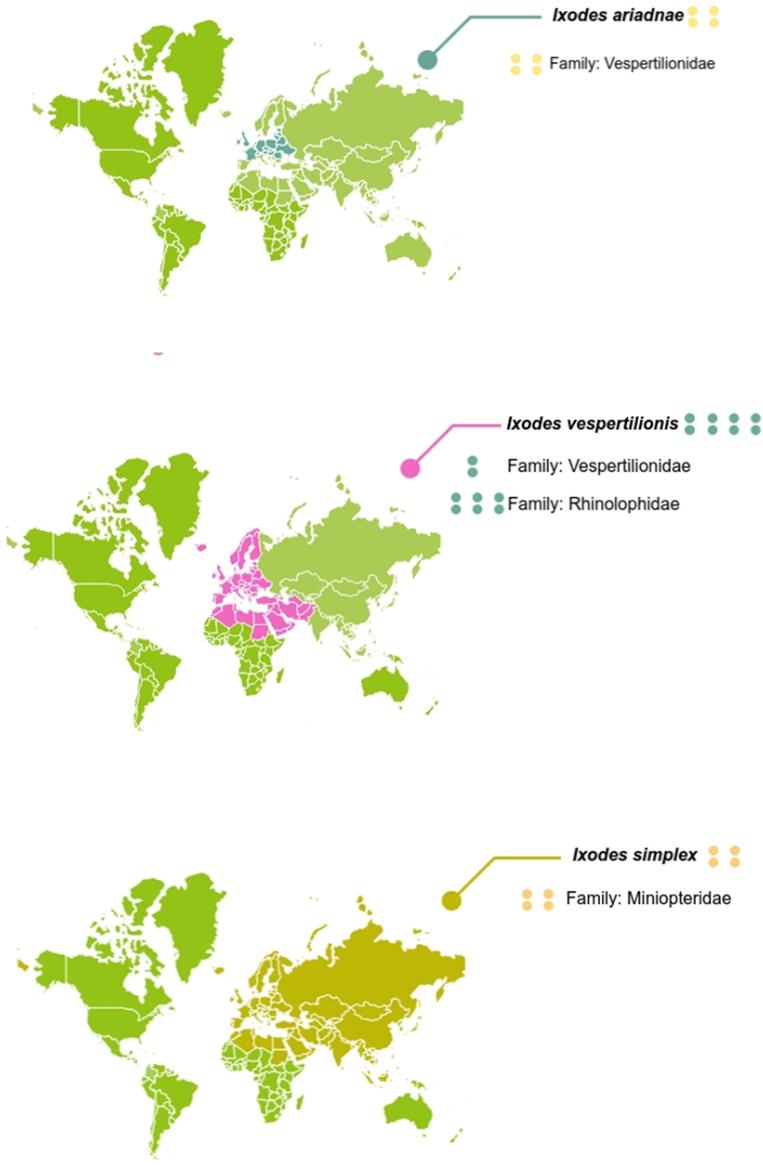
FIGURE 4 Possible geographic distribution of hard ticks linked with bats. Map created with VIsME software.

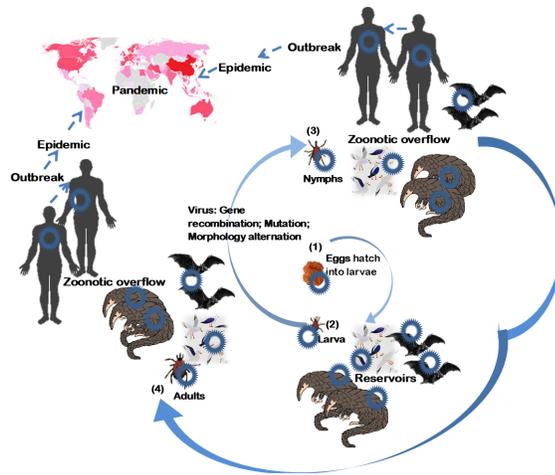
FIGURE 5 Hypothesis about the possible ways that *I. uriae* ticks can use to transmit SARS-CoV-2 to humans.











Key:

○ SARS-CoV-2

- (1) Eggs hatch into larvae
- (2) Larva feeds once on Seabirds, Bats or Pangolins infected with SARS-CoV-2 before moulting to Nymph. Ticks species co-feeding can also take place resulting to cross-infection.
- (3) Nymphs feed and may infect new hosts of Seabirds, Bats or Pangolins and may transmit SARS-CoV-2 to humans. It is this stage ticks are most likely to bite humans. Implication by human to human transmission may occur resulting to pandemic.
- (4) Nymphs moult to become adults female and male. The adult female feed and mate on new hosts of Seabirds, Bats or Pangolins and they may be infected with SARS-CoV-2 and human infection may occur also. Animal to human spill-over transmission of SARS-CoV-2 can occur resulting to pandemic, due to implication by human to human transmission. The engorged adult female ticks can drop on the ground and produce eggs then die. In this stage, eggs can also be infected with SARS-CoV-2 and the cycle may begin again.