Dermacentor (*Indocentor*) *auratus* Supino 1897: potential geographic range, and medical and veterinary significance

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Abstract

Dermacentor (*Indocentor*) *auratus* Supino, 1897 occurs in many regions of Southeast Asia and South Asia. In many regions of Southeast Asia and South Asia, targeted tick sampling and subsequent screening of collected *D. auratus* ticks have detected pathogenic bacteria and viruses in *D. auratus*. These disease-causing pathogens that have been detected in *D. auratus* include *Anaplasma*, *Bartonella*, *Borrelia*, *Rickettsia* (including spotted fever group rickettsiae), African swine fever virus, Lanjan virus, and Kyasanur forest disease virus. Although *D. auratus* predominantly infests wild pigs, this tick is also an occasional parasite of humans and other animals. Indeed, some 91% of human otoacariasis cases in Sri Lanka were due to infestation by *D. auratus*. With the propensity of this tick to feed on multiple species of hosts, including humans, and the detection of pathogenic bacteria and viruses from this tick, *D. auratus* is a tick of medical, veterinary, and indeed zoonotic concern. The geographic range of this tick, however, is not well known. Therefore, in the present paper, we used the species distribution model, BIOCLIM, to project the potential geographic range of *D. auratus*, which may aid pathogen and tick-vector surveillance. We showed that the potential geographic range of *D. auratus* is far wider than the current geographic distribution of this tick, and that regions in Africa, and in North and South America seem to have suitable climates for *D. auratus.* Interestingly, in Southeast Asia, Borneo and Philippines also have suitable climates for *D. auratus*, but *D. auratus* has not been found in these regions yet despite the apparent close proximity of these regions to Mainland Southeast Asia, where *D. auratus* occurs. We thus hypothesize that the geographic distribution of *D. auratus* is largely dependent on the movement of wild pigs and whether or not these wild pigs are able to overcome dispersal barriers. We also review the potential pathogens and the diseases that may be associated with *D. auratus* and provide an updated host index for this tick.

Key words: Zoonoses, Disease, Public health, Species distribution model, BIOCLIM

1.0 Introduction

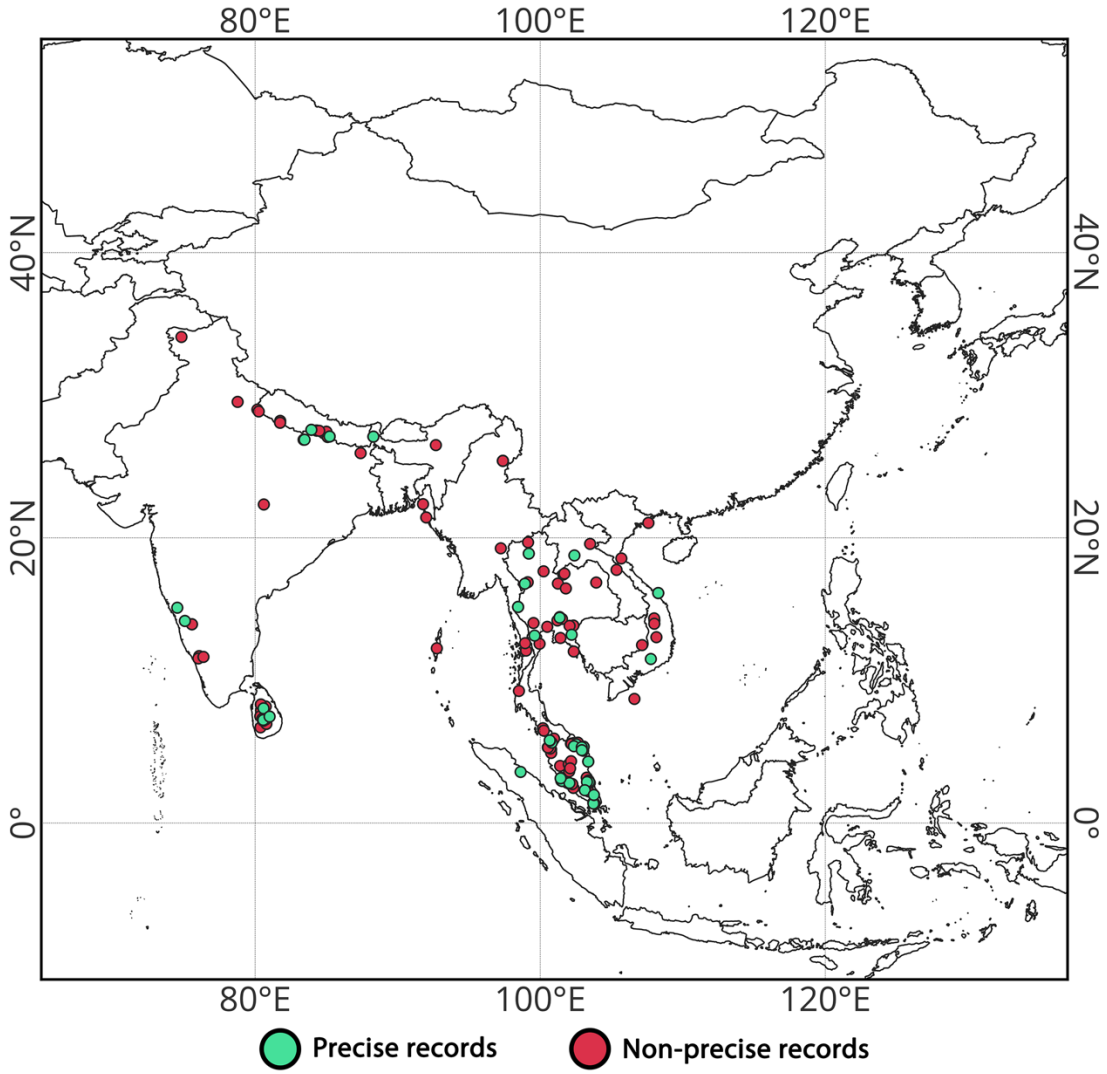

Figure 1. Records of *Dermacentor auratus*. In green, records that we considered to be precise (precision ≤ 5km) and in red, records that we considered to be non-precise (precision > 5km). Precise records were used for modelling the distribution of *D. auratus*.

Dermacentor (*Indocentor*) *auratus* Supino, 1897, is the most widely distributed *Indocentor* tick, occurring in much of Mainland Southeast Asia and South Asia (Petney and Keirans, 1996) (Fig. 1). Although *D. auratus* is predominantly a parasite of wild pigs (*Sus* spp.), periodic infestation of other animals and humans are common (Hoogstraal and Wassef, 1985; Parola et al., 2003; Liyanaarachchi et al., 2015) (Fig. 2). Moreover, there have been multiple detections of pathogenic bacteria and viruses of importance to human and animal health from *D. auratus*, and thus *D. auratus* is a tick of medical, veterinary, and indeed, zoonotic importance.

As with other ticks from Southeast Asia (Petney et al., 2007), the ecology, the vector competence, and the geographic distribution of *D. auratus* is not well established. This is of particular concern given the importance of *D. auratus* in human and animal health. Therefore, in the present paper, we project the potential geographic range of *D. auratus* with the species distribution model BIOCLIM. Species distribution models allow us to project the potential geographic range of a species when systematic surveys are not feasible and/or when presence data is sparse; such is the case for *D. auratus*. We also review the pathogens and the diseases that are associated with *D. auratus*, a tick that seems to be one of the most important ticks to human and veterinary medicine in parts of Asia.

2.0 Materials & Methods

2.1 Climate data

Mean near-surface air temperature (hereafter, mean temperature), vapor pressure deficit, and precipitation from CHELSA v2.1 (Karger et al., 2017; Brun et al., 2022) were used. We chose these variables because the activity, the abundance, and the geographic distribution and geographic range of ticks seem to be closely related to these climatic variables (Randolph and Storey, 1999; Zemtsova et al., 2016; Teo et al., 2021a; Teo et al., 2021b; Teo et al., 2023). [We use 'geographic distribution' to indicate where the tick has been found i.e., presences; whereas 'geographic range' describes where the tick may be found spatially i.e., range of suitable climate.] The climatic variables were available at a resolution of 30 arc seconds (< 1km), for each month of the year. Mean temperature and vapor pressure deficit were available as monthly averages whereas precipitation was available as the total precipitation for that month (Karger et al., 2017; Brun et al., 2022). For our analyses, we used these variables from the climatology of 1981-2010 and averaged these variables to obtain a snapshot of the average conditions from 1981-2010.

2.2 Occurrence records of *Dermacentor* (*Indocentor*) *auratus*

A Citation Report of publications of *D. auratus* was extracted from the Web of Science Core Collection (https://www.webofscience.com) in September 2023 using the search term: '*Dermacentor auratus*', using the default settings: 'all fields', and from 1900 to 2023. Additional publications were sought using the search terms: '*Indocentor auratus'*, '*Dermacentor* Asia, '*Dermacentor* Southeast Asia', '*Dermacentor* India', 'ticks Asia', 'ticks Southeast Asia', and 'ticks India'. Other pertinent publications that had been cited in the

publications from the Citation Report but were not available from the Web of Science Core Collection were also studied. These additional publications are henceforth referred to as 'supplementary publications' for ease of reference. Locality data for *D. auratus* from these publications took one of five forms: (i) precise GPS coordinates; (ii) collection sites plotted on a map; (iii) descriptive localities (e.g. 'tea plantation' in a village); (iv) coarse-scale descriptions (nature reserve/park, village, municipality, or country); and (v) not provided. Georeferencing was done for: (ii), by superimposing the figure provided in the publication on a map of the region; (iii), by studying historical satellite/aerial photographs of the region via Google Earth Pro 7.3.6 and locating the collection site with the provided descriptions; and (iv), by using the approximate center of the nature reserve, nature park, village, municipality, or country. We note that for (iii) and (iv), due to changes in the landscape (e.g. forest-clearing) and/or changes in the names of administrative divisions, some records could not be georeferenced confidently. For (v), when locality data was not provided, we attempted to retrieve information from the provided GenBank accession numbers, if they were available. The retrieved information was then georeferenced. For (i), we checked if the GPS coordinates provided in the respective publication tallied with the descriptors of the location, and if the provided coordinates did not tally with the descriptors provided in the respective publication (e.g. a different coordinate reference system was used), we georeferenced them using one or more of the aforementioned methods.

The georeferenced records were regarded as either 'precise' or 'non-precise'. Precise records were records where the coordinates provided in the respective publications indeed tallied with the location descriptors, records that were georeferenced by superimposing the figures onto a map, or records from regions such as, but not limited to, forests, towns and/or villages that we considered to be small (< 5 km, longest Euclidean distance). Non-precise records on the other hand were records from regions such as, but not limited to, forests, nature reserves, towns, cities and/or countries that we considered to be big (> 5 km). Records we were not confident about because of changes in landscapes and/or names were also regarded as 'non-precise'.

Records prior to the description of Wassef and Hoogstraal (1984) were removed because there was confusion regarding the identity of *D. auratus* prior to their description (Guglielmone et al., 2014). Additionally, records from Taiwan were removed since records from Taiwan need confirmation (Guglielmone et al., 2023). Records from China were also removed as sequences from these records clustered separately from *D. auratus* from India

and from Thailand, even though the latter two clustered together (see Fig. 2 in Wang et al., (2020)). Furthermore, the provided sequences indicated that the records from China were closely related to the records of *D. auratus* from Taiwan that were considered doubtful by Guglielmone et al. (2023) (Supplementary Materials). Hence, like the records from Taiwan, we propose that the records of *D. auratus* from China also require confirmation. We also used the records of and/or field collection sites of *D. auratus* that were available from the U.S. National Tick Collection (USNTC) in our study.

2.3 Potential geographic range of *Dermacentor auratus*

To predict the potential geographic range of *D. auratus*, we used the envelope model BIOCLIM (Nix, 1986). BIOCLIM describes the climatic profile of a species, and identifies locations with potentially suitable environments (Booth et al., 2014). We used BIOCLIM to project the geographic range of *D. auratus* because BIOCLIM only require presences (Nix, 1986; Booth et al., 2014); many of the records of *D. auratus* studied in the present paper were from targeted tick sampling, and therefore do not indicate the full geographic distribution of *D. auratus*. Moreover, envelope models like BIOCLIM are effective at estimating the potential geographic range of a species (Jiménez-Valverde et al., 2008).

Due to the low number of records of *D. auratus* that we considered to have precise locations, and that many of these records were from the same sites, the records were divided into two subequal groups, Subset A and Subset B, by latitude and by longitude for down-stream cross-validation (i.e. geographically structured cross-validation (Radosavljevic and Anderson, 2014)). Because BIOCLIM uses the percentile distribution of values of each variable to indicate the suitability of locations (Nix, 1986), multiple collections (i.e. clustering) from the same site or neighboring sites with similar climates may skew the percentile distribution of values, and subsequently affect the accuracy of the BIOCLIM model (spatial autocorrelation). Therefore, to account for spatial autocorrelation that may arise from clustering, mean temperature, vapor pressure deficit, and precipitation at locations where *D. auratus* were recorded were extracted, and step-wise Moran's *I* statistics were computed for each of the climate variables at Euclidean distances between 0 to 100 km, at an interval of 1 km with *spdep* (Bivand and Wong, 2018). Informed by the calculated Moran's *I* statistic, we thinned each subset by the three climatic variables independently, with *spThin*, and created ten datasets for each climatic variable (Aiello-Lammens et al., 2015). 'Single-variable BIOCLIM models' were generated with *dismo* (Hijmans et al., 2023) for the sixty datasets (2 subsets × 3

variables × 10 datasets) with the respective climatic variable (e.g. a mean temperature BIOCLIM model was generated with a dataset that was thinned to reduce potential spatial autocorrelation of mean temperature). High (upper limit) and low (lower limit) temperatures were regarded to restrict the geographic range of *D. auratus* whereas only low moisture (high vapor pressure deficit and/or low precipitation), and not high moisture, was regarded to restrict to the geographic range of *D. auratus*. The resulting projections of suitability from the BIOCLIM models generated from the datasets were then averaged by climate variable for Subset A and Subset B. The subsequent six (2 subsets × 3 variables) projections were then used to generate a 'three-variable BIOCLIM model' per subset. This process allowed us to maximize the number of records used for species distribution modelling while reducing potential spatial autocorrelation due to clustering of records of *D. auratus*.

For each subset, records from the same location (i.e. duplicates) were removed; the remaining records from these subsets were used to evaluate the 'three-variable BIOCLIM model' generated with records from the other subset (i.e. cross-validation). Sensitivity, the proportion of presence records that were from regions projected to be suitable by the model, and the area under the curve of the receiver operating characteristic (AUC) (Fielding and Bell, 1997), was calculated as a measure of model fit. AUC was calculated using presence and background points with *modEvA* (Márcia Barbosa et al., 2013). Since the models were evaluated with records from a geographically separated set of data, sensitivity and AUC may be interpreted as the model's transferability to other regions (Radosavljevic and Anderson, 2014).

The 'three-variable BIOCLIM models' generated from the two subsets were then averaged to produce a final model and to produce a map of 'consensus suitability'. Nix (1986), in the context of BIOCLIM, considered environments bound between the 5^{th} and 95^{th} percentile range to indicate 'core environments' of a species, and values that fall outside this range to indicate 'marginal environments'. Although Nix (1986) also considered the 25^{th} to 75^{th} percentile range, no labels were designated to the 25^{th} to 75^{th} percentile range. In the present paper, we considered the minimum value (i.e. 0^{th} percentile) to the 5^{th} percentile, and the 95^{th} percentile to the maximum value (i.e. 100^{th} percentile) to indicate marginal environments; the 5^{th} to the 25^{th} percentile, and the 75^{th} to the 95^{th} percentile to indicate favorable environments; and the 25^{th} to the 75^{th} percentile to indicate optimal environments. By comparing the distribution of values of our variables with the BIOCLIM algorithm implemented in *dismo*

(Hijmans et al., 2023), regions were considered to be unsuitable for *D. auratus* at a suitability of 0, marginal: > 0, but < 0.14; favorable: 0.14 – 0.52; and optimal: 0.52 – 1. All analyses were done in R 4.3.1 (R Core Team, 2023), and in QGIS (QGIS Development Team, 2023).

2.4 Disease-causing pathogens associated with *Dermacentor auratus*

Many of the publications we reviewed for the present paper were on the detection and identification of disease-causing pathogens that were associated with *D. auratus*. In the present paper, we summarize these findings. We also present a map of where *D. auratus* have been found with the specific disease-causing pathogens.

3.0 Results & Discussion

3.1 Records of *Dermacentor auratus*

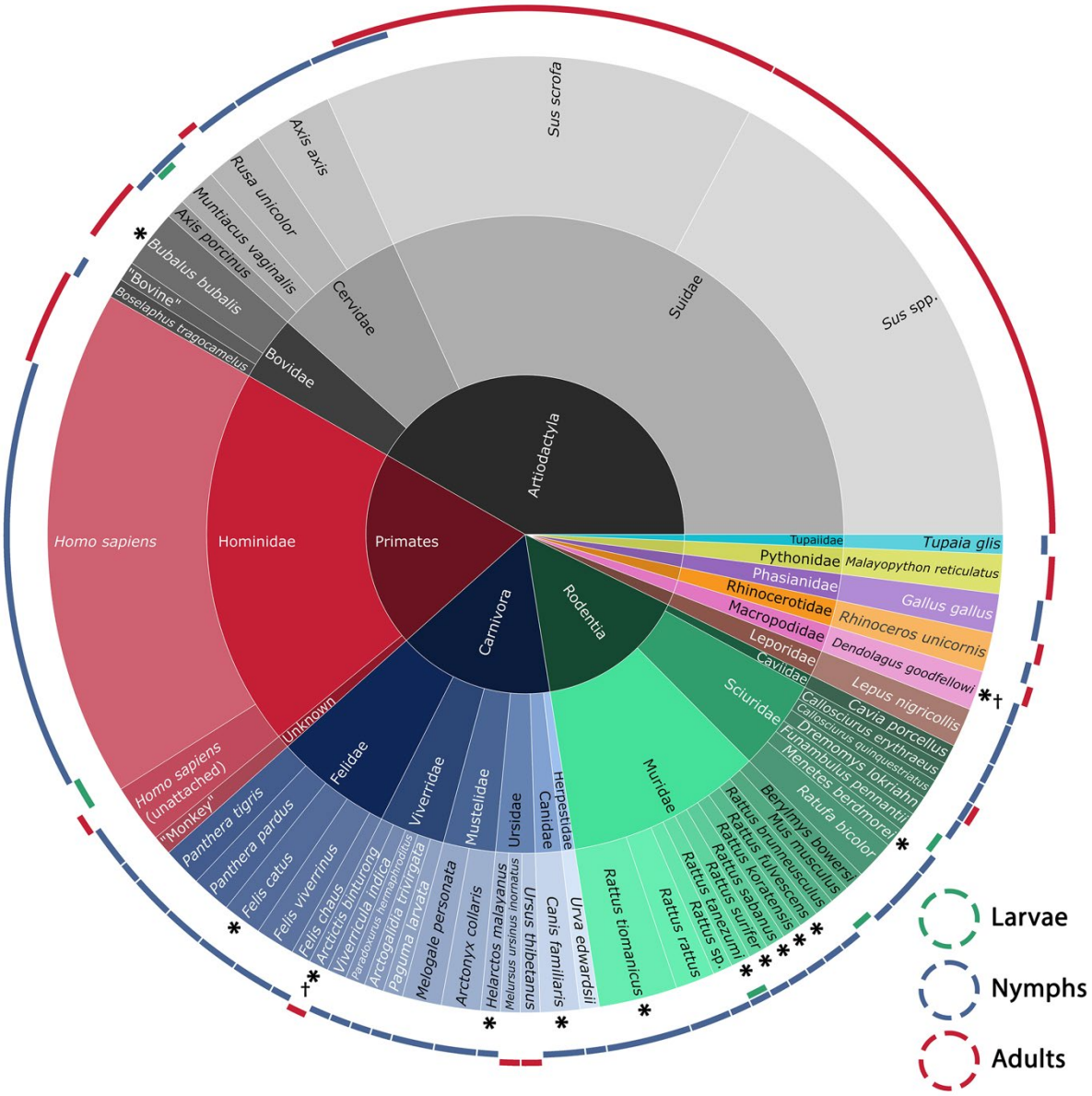

Figure 2. Host records of *Dermacentor auratus* from 151 records that were associated with host species. The three outer disjointed circles indicate the life-stages of *D. auratus* that were associated with the infestation and is shown as a proportion of records that had information of life-stages. Overlaps of the circles indicate host(s) that were infested by multiple life-stages of *D. auratus*. * indicates new host records since Hoogstraal and Wassef (1985) and † indicates that the host was held in captivity. Records of *Sus* spp. were either from *S. scrofa* or *S. barbatus* (Hoogstraal and Wassef, 1985).

Two-hundred and forty-four records of *D. auratus* and/or coordinates of collection sites were retrieved from 28 publications from the Web of Science Core Collection; 13 'supplementary publications'; and from the USNTC. These 244 records were from 1935 to 2023 and 25 of these records (10%) that had detected pathogens in *D. auratus* (Tan et al., 1967; Boshell et al., 1968; Sumrandee et al., 2016; Nooroong et al., 2018; Asyikha et al., 2020; Misra et al., 2021; Chaloemthanetphong et al., 2023; Koh et al., 2023). Sixteen of the 244 records were considered doubtful because they were records identified prior to Wassef and Hoogstraal (1984) (n = 8); or were records from Taiwan (Guglielmone et al., 2023) (n = 1) or from China which we considered to be doubtful (n = 7) (Supplementary Materials). Eighty-three of the remaining 228 records were considered to have precise locations (precision ≤ 5km), and these records were used for our BIOCLIM models (Fig. 1). Also, one hundred and fifty-one of the 228 records were associated with 52 host species; the three most common hosts were: pigs (48/151; 32%), humans (29/151; 19%), and murine rodents (15/151; 10%) (Fig. 2). Thirteen of the 52 host species were new host-parasite associations since Hoogstraal and Wassef (1985) (Fig. 2). Of the three most common hosts, life-stages were recorded for 84% of the records (77/92). Of the 44 records from pigs (Suidae) that had information on the life-stage of the ticks, 42 recorded adults and 3 recorded nymphs (two pigs were infested by adults and by nymphs) (Fig. 2). For humans, of the 21 records that had information on the life-stage of the ticks, 4 recorded adults (3 attached, 1 not attached), 16 recorded nymphs (14 attached, 2 not attached), and 1 recorded an attached larva (Fig. 2). Last, for murine rodents, of the 12 records that had information on the life-stage of the ticks, 11 recorded nymphs, and 2 recorded larvae (one rodent was infested by nymphs and by larvae) (Fig. 2).

3.2 Potential geographic range of *Dermacentor auratus*

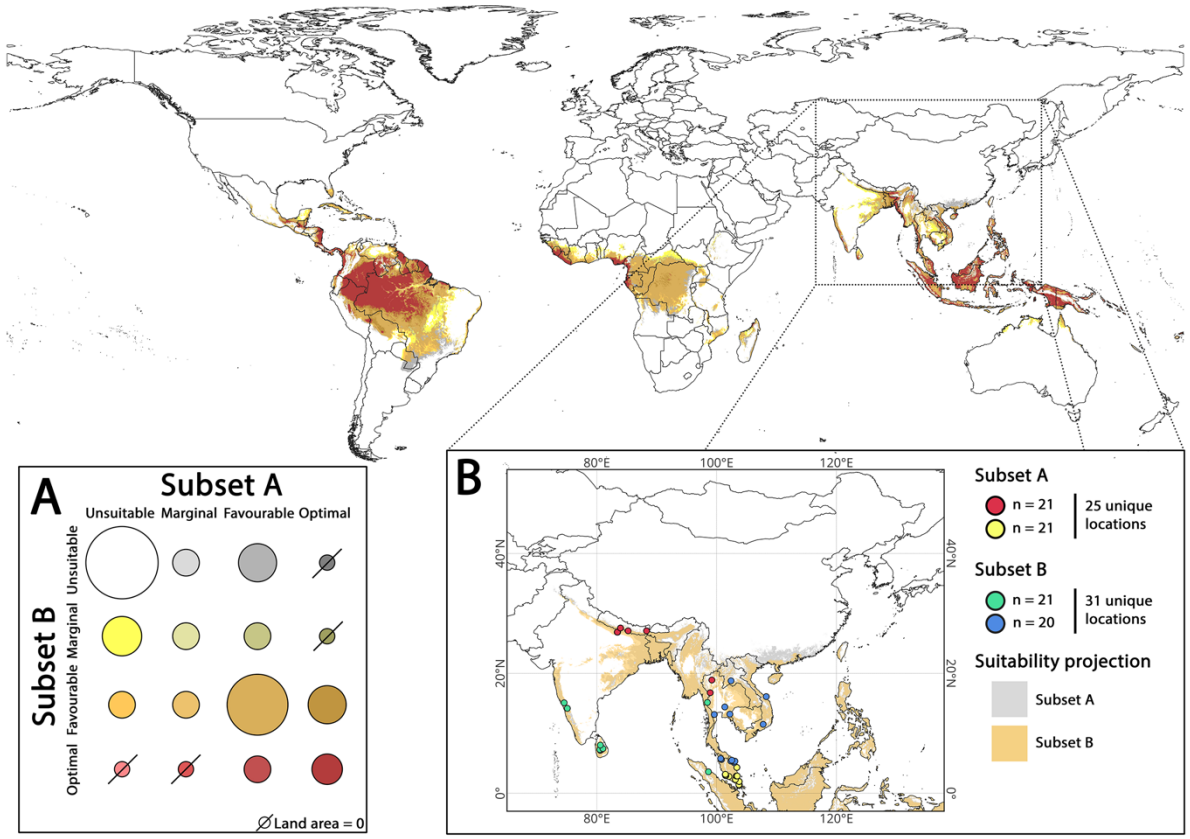

Figure 3. Consensus map of potential geographic range of *Dermacentor auratus* projected by the two BIOCLIM models. Insert A, legend to the main figure and the land area (i.e. number of ~1 km^2 pixels) by suitability for *D. auratus* by the two BIOCLIM models. Suitable land area was sorted by Jenks natural breaks classification with five breaks. Insert B, geographic distribution of records from Subset A, and from Subset B which were used to generate the two BIOCLIM models. Also, in Subset B, the potential geographic range of *D. auratus* (i.e. range of suitable climates) projected from the two subsets and how well these projections accounted for the records from the other subset.

Some 88% (22/25) of records of *D. auratus* from Subset A (Fig. 3B) were accounted for by the 'three-variable BIOCLIM model' of Subset B. The three records that were not accounted for by the model were between 0.70 to 1.60 km away from the nearest suitable area (mean ± s.d. of 0.94 ± 0.47 km). The AUC for the 'three-variable BIOCLIM model' of Subset B was 0.85. On the other hand, some 87% (27/31) of records of *D. auratus* from Subset B (Fig. 3B) were accounted for by the BIOCLIM model generated with records from Subset A. The four records that were not accounted for by the model were 0.85 to 9.89 km away from the nearest suitable area (7.31 ± 3.74 km). The AUC for the 'three-variable BIOCLIM model' of Subset

A was 0.86. The AUC of the models generated from Subset A and Subset B were 0.86 and 0.85 respectively, which indicated that the models performed better than random (AUC > 0.5) (Fielding and Bell, 1997). There was much consensus between the two models: 89% of the land area projected to be suitable (suitability > 0) by the BIOCLIM model of Subset A was also projected to be suitable by the BIOCLIM model of Subset B. The reverse was also true, with a consensus of 85%. Furthermore, all of the regions projected to be optimal by the BIOCLIM model of one subset was projected to either be favorable or optimal by the BIOCLIM model from the other subset (Fig. 3).

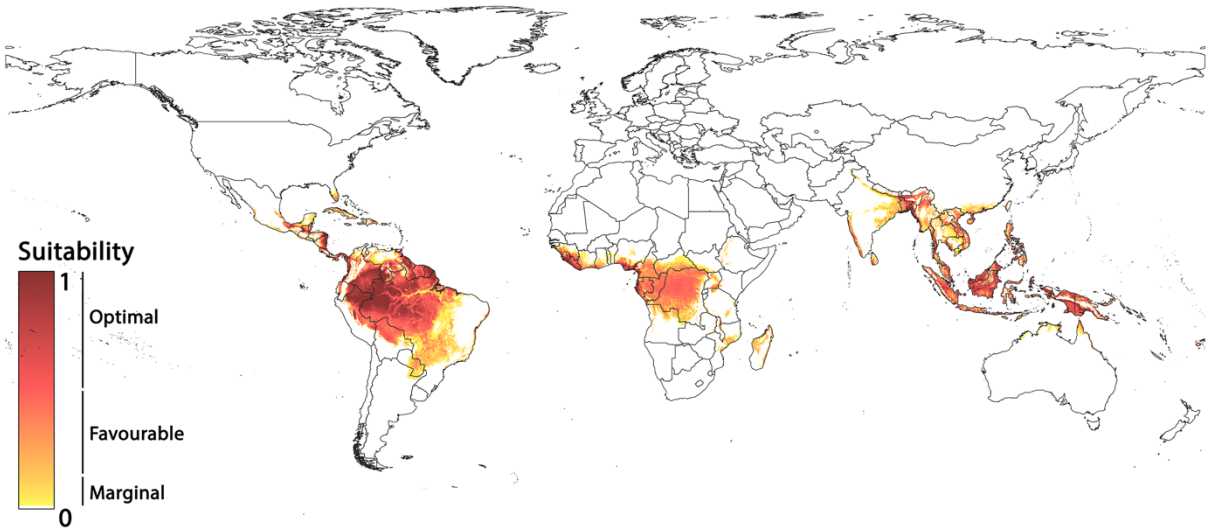

Figure 4. Potential geographic range of *Dermacentor auratus* from the final model. Suitability was averaged from the two BIOCLIM models. White indicates regions which were projected to be unsuitable by both BIOCLIM models (suitability of 0). Regions projected to be suitable (suitability > 0) by at least one BIOCLIM model on the other hand, are shaded, with darker colors indicating higher suitability.

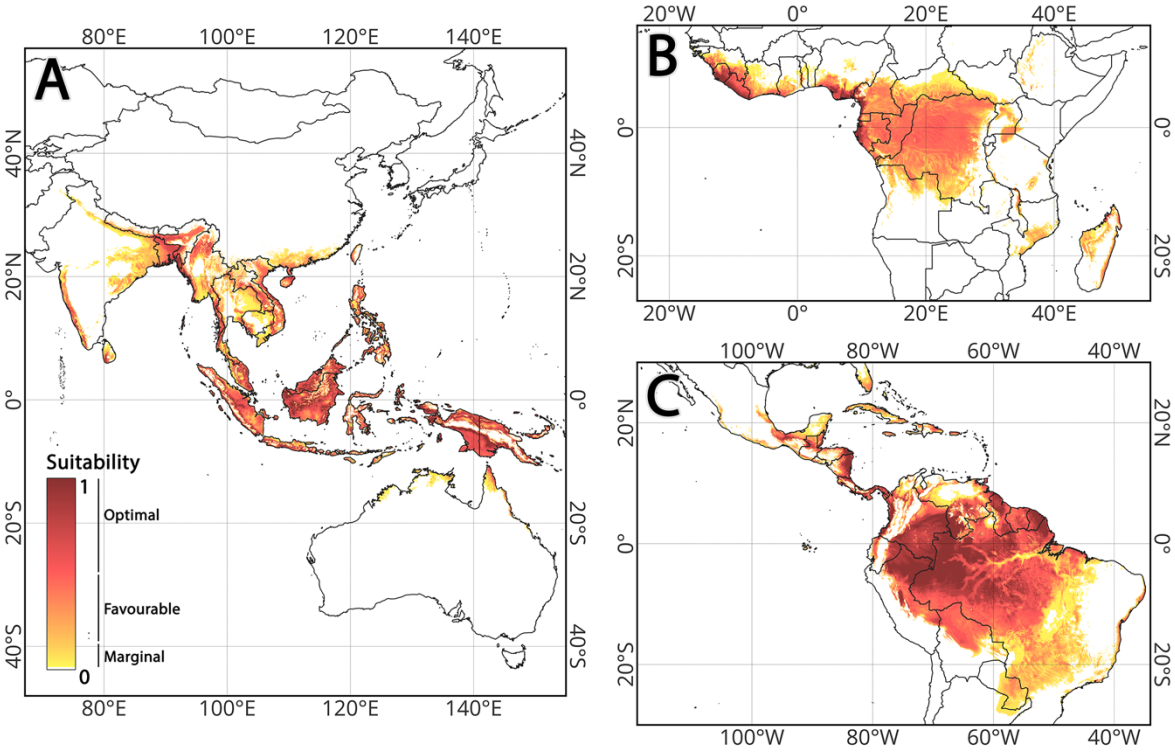

Figure 5. Potential geographic range of *Dermacentor auratus* in three regions. A, parts of Asia and Australia; B, parts of Africa; and C, parts of North and South America.

Although the geographic distribution of *D. auratus* is more-or-less constrained to South East Asia and parts of South Asia (Fig. 1 & 3), the potential geographic range of this tick (i.e. extent of regions with suitable climates) is much greater, with the northern parts of Australia, parts of Africa, parts of North America and parts of South America projected to be climatically suitable for *D. auratus* (Figs. 3, 4 & 5). We note with interest that *D. auratus* has only been recorded on Mainland Southeast Asia and South Asia, and from islands and island countries that are in very close proximity to Mainland Southeast Asia and South Asia (e.g. Singapore, Sri Lanka, and a single record from Sumatra) (Fig. 1). To our knowledge, *D. auratus* has not been recorded from other parts of Sumatra or from the other islands of Indonesia. *D. auratus* has also not been recorded from Borneo, or from Philippines even though these regions were projected to be suitable by our model and even though these regions are close to Mainland Southeast Asia (Figs. 3, 4 & 5). The possible reintroduction of *D. auratus* into the island country of Singapore by wild pigs were discussed by Kwak et al. (2021). Following studies on the movement of wild pigs into Singapore (Lamperty et al., 2023) and because wild pigs seem to be the predominant as well as a very important host in the life-cycle of *D. auratus* (Hoogstraal and Wassef, 1985), we hypothesize that the dispersal

of *D. auratus* is largely dependent on the movement of wild pigs and the ability of wild pigs to overcome dispersal barriers (e.g. water bodies, hills, and mountain ranges). Moreover, in contrast to other *Indocentor* species whose immatures seem to feed chiefly on rodents (Hoogstraal and Wassef, 1985; Wassef and Hoogstraal, 1988; Apanaskevich and Apanaskevich, 2015) and occasionally, on other medium-sized mammals (e.g. Leporidae, Mustelidae, and Viverridae) (Hoogstraal et al., 1986), immature *D. auratus* have been also been recorded on pigs and other large-sized mammals (e.g. Bovidae, Cervidae, Rhinocerotidae, Ursidae, and Felidae: *Panthera* spp.) (Hoogstraal and Wassef, 1985) (Fig. 2). Compared to other *Indocentor* species, the indiscriminate parasitism of large-sized mammals, which have larger home ranges (Swihart et al., 1988), by immature *D. auratus* may explain why *D. auratus* is the most widely distributed *Indocentor* species (Petney and Keirans, 1996).

Although we hypothesize that the dispersal of *D. auratus* is largely dependent on the movement of wild pigs, *D. auratus* have been imported into the United Kingdom and the United States by travelers and on plants (Keirans and Durden, 2001; Gillingham et al., 2020). There is therefore a possibility that, in the absence of 'wild pig connectivity' to Mainland Southeast Asia and South Asia, the geographic distribution of *D. auratus* may expand to other regions that were projected to be suitable by our model.

In the present paper, we used the climatology from 1981-2010 to project the potential geographic range of *D. auratus* using the envelope model, BIOCLIM. We note that our use of the 1981-2010 climatology may not have captured, accurately, the climatic conditions from older (1966-1981) and newer (2010-2023) records of *D. auratus*. The climatology of 1981-2010, however, describes the average conditions over 30 years, and should indicate, to some degree or another, the climate that these older and newer records of *D. auratus* could have been exposed to.

As an envelope model, BIOCLIM performs well in projecting the potential geographic range of a species (Jiménez-Valverde et al., 2008; Booth et al., 2014). The realized geographic range of a species is often smaller than the potential geographic range, and thus, it is likely that the actual potential geographic range of *D. auratus* is smaller than projected. On the contrary, because BIOCLIM uses the percentile distribution of each variable to inform suitability, the range of potential suitable area projected by our model may be smaller than the actual potential geographic range of *D. auratus*. This is because BIOCLIM does not account

for possible interactions between variables e.g. the effects of high mean temperatures may be mitigated by high precipitation (Nix, 1986). In the present paper, however, we used climatic variables that relate well to the biology of ticks (Randolph and Storey, 1999). Moreover, using similar envelope modelling approaches, we have previously shown that these climatic variables were able to account for the presences as well as the absences of other species of ticks to a remarkable extent (Teo et al., 2021a; Teo et al., 2021b).

3.3 Medical and veterinary significance of *Dermacentor auratus*

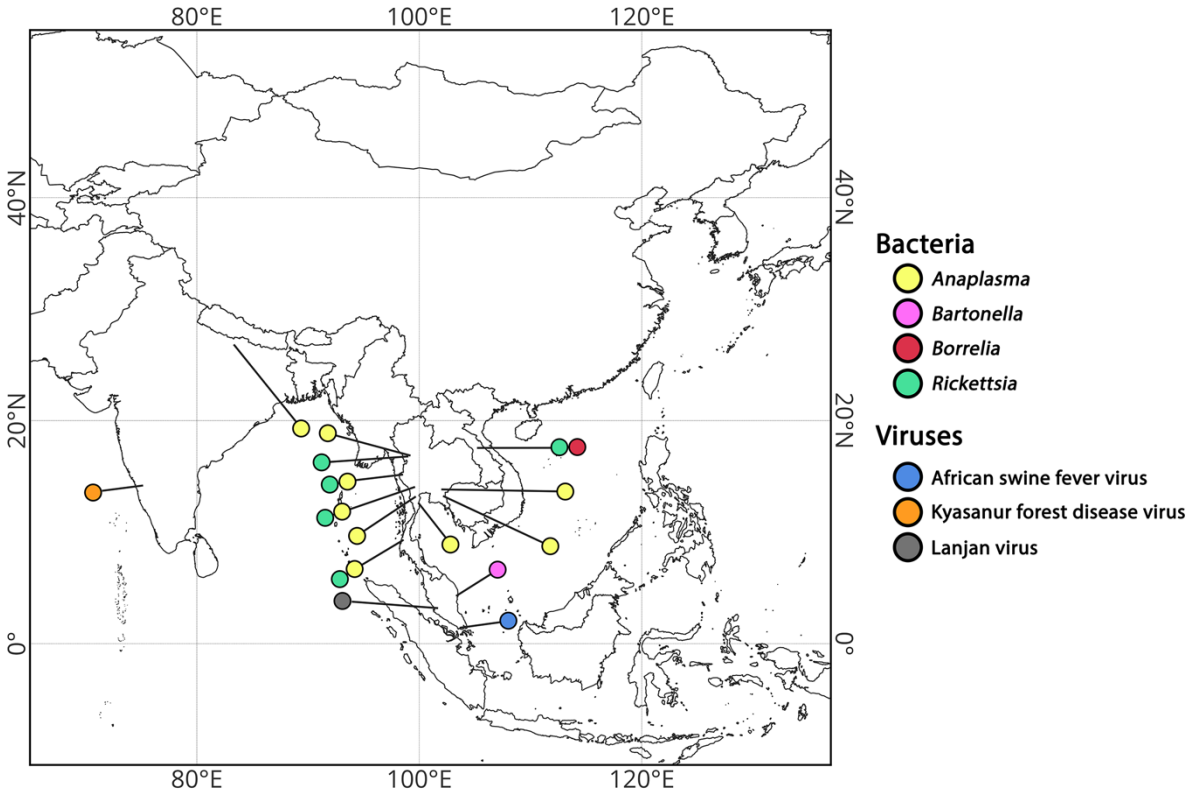

Figure 6. Geographic locations where disease-causing pathogens were detected from *Dermacentor auratus* ticks. Data from Tan et al. (1967); Boshell et al. (1968); Parola et al. (2003); Sumrandee et al. (2016); Taylor et al. (2016); Nooroong et al. (2018); Asyikha et al. (2020); Chaloemthanetphong et al. (2023); and Koh et al. (2023).

3.3.1 Human infestation

Human infestation by *D. auratus* is normally associated with otoacariasis. Indeed, some 91% of otoacariasis cases in Sri Lanka were due to *D. auratus* and majority of these patients were < 10 years old (Ariyarathne et al., 2016; Bandaranayaka et al., 2021). The most common symptoms associated with otoacariasis is 'ear fullness', and tinnitus, with 98-100% and 60-81% of the patients reporting these symptoms respectively (Bandaranayaka et al., 2021).

Other complications of otoacariasis may also include otalgia, secondary bacterial infections, and temporary deafness (Ariyarathne et al., 2016; Bandaranayaka et al., 2021). Analyses of associated risk factors of human infestation by ticks and otoacariasis in Sri Lanka showed that outdoor activities, the presence of wildlife, and the location of the house to be significantly correlated with human infestation by ticks and significantly correlated with otoacariasis (Ariyarathne et al., 2016; Bandaranayaka et al., 2021). Apart from infestation of the ear canal in humans, various feeding life-stages of *D. auratus* has also been recovered from the eyelid as well as other parts of the body from different regions of the world (Kirwan, 1935; Hoogstraal and Wassef, 1985; Ajithkumar et al., 2012; Chitimia-Dobler et al., 2021).

An additional complication of human infestation by *D. auratus* is tick paralysis (Gothe et al., 1979; Hoogstraal and Wassef, 1985). Although the mechanisms of tick paralysis caused by *D. auratus* has not been fully elucidated, a correlation study between otoacariasis and facial nerve palsy has suggested that *Rickettsia* transmitted by the tick could be the causative agent of paralysis associated with feeding *D. auratus* (Kularatne et al., 2018). With high prevalence of human infestation by *D. auratus*, the reason why *D. auratus* may cause paralysis warrants further study.

3.3.2 Bacteria

3.3.2.1 *Rickettsia*

Since Hoogstraal and Wassef (1985), there have been multiple detections of *Rickettsia* spp. from *D. auratus*. Parola et al. (2003) detected *Rickettsia* sp. closely related to *R. bellii* and *Rickettsia* sp. closely related to *R. conorii* subsp. *raoultii*, a spotted fever group rickettsiae (SFGR) from Kanchanaburi province, Thailand (Fig. 6). Similarly, *Rickettsia* sp. that was closely related to *R. conorii* subsp. *raoultii* was also detected in Phang Nga Province, Thailand (Sumrandee et al., 2016) (Fig. 6). From Tak Province, Thailand, *Candidatus* Rickettsia laoensis was detected from questing *D. auratus* (Chaloemthanetphong et al., 2023). Last, there have also been isolations of unidentified *Rickettsia* sp. from Kanchanaburi, Thailand (Nooroong et al., 2018) and from Khammouan Province, Laos from *D. auratus* (Taylor et al., 2016). Despite the numerous isolations of *Rickettsia* and indeed, SFGR, from *D. auratus*, the prevalence of *Rickettsia* spp. seems to be low, at 0 – 27%. We note that like Marchette (1966), none of these studies detected typhus-group *Rickettsia* from *D. auratus*.

Further, a correlation study in Sri Lanka has suggested that SFGR transmitted by ticks could be the causative agent of facial nerve palsy in otoacariasis patients (Kularatne et al., 2018). SFGR, however, was not detected from the single *D. auratus* that was recovered from a patient with facial nerve palsy (Kularatne et al., 2018). SFGR was also not detected in eight *D. auratus* from Sri Lanka in another study (Liyanaarachchi et al., 2016). *D. auratus*, however, is the tick most commonly associated with otoacariasis in Sri Lanka (91%) (Bandaranayaka et al., 2021), where facial nerve palsy associated with otoacariasis is commonplace (Kularatne et al., 2018). The association of *D. auratus* with SFGR in other regions of the world, and the correlation of *D. auratus* with facial nerve palsy associated with SFGR warrants further study since *D. auratus* is an occasional parasite of humans (Fig. 2).

3.3.2.2 *Anaplasma*

There have been multiple detections of *Anaplasma* spp. from *D. auratus*. From Uttar Pradesh, India, *Anaplasma* sp. closely related to *A. centrale* was detected in *D. auratus* that were collected from buffalos (Bovidae) (Misra et al., 2021). From Kanchanaburi province and from Phang Nga Province, Thailand, *Anaplasma* sp. closely related to *A. platys* was detected in *D. auratus* that were collected from dogs and a wild pig respectively (Parola et al., 2003; Sumrandee et al., 2016). Last, Nooroong et al. (2018) detected *Anaplasma* from *D. auratus* collected from vegetation in multiple regions of Thailand. Amongst the detected *Anaplasma,* Nooroong et al. (2018) reported that *Anaplasma* sp. closely related to *A. phagocytophilum* was detected from Prachuap Khiri Khan Province, Thailand (Nooroong et al., 2018). We note with interest that the *Anaplasma* spp. detected in these studies were all closely related to pathogenic *Anaplasma* spp. which are zoonotic, and is of concern (Stuen et al., 2013; Arraga-Alvarado et al., 2014).

3.3.2.3 *Bartonella*

A strain of *Bartonella*, closely related to *B. phoceensis* was detected from *D. auratus* parasitizing *Rattus tiomanicus*, the Malayan field rat, from Terengganu, Malaysia (Asyikha et al., 2020). Apart from Malaysia, *B. phoceensis* has also been detected from rodents in Indonesia, Laos, Nepal, and Thailand (Jiyipong et al., 2014), where *D. auratus* occurs. Although *B. phoceensis* has also been detected from non-rodent hosts such as dogs and cats (Tsai et al., 2011; Dybing et al., 2016), *B. phoceensis* is, at the present moment, not considered to be of zoonotic importance (Jiyipong et al., 2014; Dybing et al., 2016).

3.3.2.4 *Borrelia*

There was a single detection of an unidentified *Borrelia* sp. from a nymphal *D. auratus* from Khammouan Province, Laos (Taylor et al., 2016). Similarly, a study in Khao Yai National Park, Thailand, detected *B. theileri*, the causative agent of bovine borreliosis, in unidentified questing larval *Dermacentor* (Takhampunya et al., 2021). Takhampunya et al. (2021), however, did not detect any *Borrelia* from any of the adult *Dermacentor* spp., including *D. auratus*. It is thus not fully known whether or not *D. auratus* is indeed a vector of (i.e. able to transmit) *Borrelia* spp..

3.3.3 Viruses

3.3.3.1 African swine fever virus

African swine fever (ASF) virus (ASFV) (*Asfarviridae*) was detected for the first time from an adult male and an adult female *D. auratus* collected from the carcass of a wild pig (*Sus scrofa*) that was infected with ASFV in Singapore (Koh et al., 2023). It is not known, however, whether or not *D. auratus* is a competent vector of ASFV since both ticks had been attached i.e., whether or not the detected ASFV was from the bloodmeal of the infected wild pig (Koh et al., 2023). We note with interest that ASFV was also detected in *Dermacentor nuttalli*, *Dermacentor niveus*, and *Dermacentor silvarum* in Xinjiang, China (Chen et al., 2019). In the same study, it was shown that *D. niveus* may be considered a reservoir for ASFV since there was transovarial transmission of ASFV; *D. nuttalli* and *D. silvarum* were not tested (Chen et al., 2019). Contrastingly, a study of the replication of ASFV in artificially fed *Dermacentor reticulatus* concluded that although the virus may continue to persist in *D. reticulatus* for weeks, *D. reticulatus* was not considered a reservoir for ASFV because ASFV did not replicate in *D. reticulatus* (de Carvalho Ferreira et al., 2014). It is thus not known whether or not *D. auratus* could be a reservoir of ASFV like *D. niveus*, or whether *D. auratus* is not considered to be a reservoir for ASFV like *D. reticulatus*. The findings from the two studies (de Carvalho Ferreira et al., 2014; Chen et al., 2019) indicate that ASFV may continue to persist in *Dermacentor* ticks. There is thus the possibility that *D. auratus*, especially adult males, may serve as mechanical vectors for ASFV like other hematophagous arthropods (Mellor et al., 1987). Indeed, adult male *Dermacentor* may change their attachment sites even after attachment (Bartosik et al., 2019) which at least to us, indicate that male *Dermacentor* may feed on multiple hosts, resulting in ASFV transmission. On the other hand, although adult female *Dermacentor* will not change their attachment sites if undisturbed (Bartosik et al., 2019), they may attach to another host to feed to repletion if feeding is disturbed (Chen et

al., 2019). Whether or not *D. auratus* does indeed serve as a reservoir of ASFV and/or whether or not *D. auratus* is able to transmit ASFV warrants further study with ongoing outbreaks of ASFV in regions which we projected to be suitable for *D. auratus*.

3.3.3.2 Kyasanur forest disease virus

Kyasanur forest disease (KFD) virus (KFDV) (*Flaviviridae*), the causative agent of KFD or 'monkey fever' is a zoonotic pathogen with a human case-fatality rate of 3-10% (Work et al., 1959). *D. auratus* is not considered to be a primary vector of KFDV as there has only been one documented isolation of KFDV from *D. auratus* (Boshell et al., 1968). It was shown in experimental infections, however, that *D. auratus* is a competent vector for KFDV, where transmission of the virus occurred even after moulting to the next life-stage (i.e. transstadial transmission) (Sreenivasan et al., 1979). Furthermore, it was shown that larval and nymphal *D. auratus* are common parasites of rodents (Rajagopalan et al., 1968), and of non-human primates (Trapido et al., 1964) which are the natural hosts for KFDV (Shah et al., 2018). The propensity of immature *D. auratus* to feed on the natural hosts for KFDV; the ability of KFDV to be transmitted transstadially by the tick; the ability of *D. auratus* to transmit the virus to vertebrates; and the propensity of *D. auratus* to feed on humans is thus of concern regarding KFDV transmission to humans by *D. auratus*. We note with interest that the identification of *D. auratus* in KFDV endemic regions (Trapido et al., 1964; Boshell et al., 1968; Rajagopalan et al., 1968; Sreenivasan et al., 1979) precedes the redescription by Wassef and Hoogstraal (1984). *D. auratus*, however, is the only *Dermacentor* known to occur in Karnartaka state, India, where these studies were done (Geevarghese et al., 1997).

3.3.3.3 Lanjan virus

Lanjan virus (*Bunyaviridae*) was isolated from nymphs of the '*D. auratus*-group' in Bukit Lanjan, Selangor, Malaysia in 1960 and 1961 (Tan et al., 1967). When inoculated intracerebrally, the virus is pathogenic to suckling and adult mice and results in paralysis and subsequently, death. Although the virus is not pathogenic to adult mice if the mice were inoculated intraperitoneally, it is not known if this route of inoculation is pathogenic to suckling mice because this route of inoculation was not tested (Taylor, 1968). The virus was also not pathogenic to other animals regardless of the route of inoculation (Tan et al., 1967). Via serosurveys in neighbouring forest reserves, antibodies against Lanjan virus were detected from rodents (Muridae) in Ulu Langat Forest Reserve. We note with interest that Hoogstraal and Wassef (1984) indicated that the nymphs found to have Lanjan virus in Tan et

al. (1967) were probably *D. compactus* or *D. atrosignatus* (the latter now referred to as *D. tricuspis* (Apanaskevich et al., 2021)); this cannot be confirmed because the ticks were homogenized in Tan et al. (1967). In their review of the medical significance of *D. auratus*, however, Hoogstraal and Wassef (1985) associated Lanjan virus with *D. auratus*. It is therefore not completely clear whether or not *D. auratus* is a vector of Lanjan virus. We have included Lanjan virus in the present paper as many authors implicate *D. auratus* as the vector of this virus, citing Tan et al. (1967); this will need further clarification.

4.0 Conclusion

Many of the reports of human infestation and/or the detection and isolation of pathogens associated with *D. auratus* were clustered, with most reports of otoacariasis from Sri Lanka, and most detections of disease-causing bacteria from Thailand. Hence, the map of locations where pathogens have been detected from *D. auratus* that we present here may not be comprehensive; that it is likely that other populations of *D. auratus* may also harbor disease-causing pathogens, but they have not been studied in such detail. We note that all the records of *D. auratus* and disease-causing pathogens in the present study are from scientific publications and that each of these publications may or may not have had restrictions pertaining to the sharing of scientific findings prior to the submission of the manuscript. Hence, it is likely that at least some details pertaining to the distribution of *D. auratus* and the pathogens associated with *D. auratus* is under-represented in this paper. The detection of some of these pathogens in *D. auratus* also do not indicate the capacity of *D. auratus* to transmit these pathogens: this warrants further study.

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