

# Chapter 8

## Ticks: A Largely Unexplored Factor in Disease Transmission



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**Abstract** Tick species occur on most reptiles, birds, and mammals, including humans. They are major vectors of viral, bacterial, and protozoan pathogens of animals and humans worldwide. There is currently increasing interest in the tick species and the pathogens that ticks transmit in Southeast Asia, although substantial gaps in our knowledge remain. Here we provide an overview of the tick fauna of mainland and insular Southeast Asia, the pathogens that the ticks transmit, and likely future changes in the structure of tick communities.

**Keywords** Ixodidae · Argasidae · Southeast Asia · Biodiversity · Pathogens

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## 8.1 Introduction

Formal tick research in Southeast Asia dates from the final years of Western colonialism, which yielded seminal works by Toumanoff (1944, Vietnam), Anastos (1950, Indonesia), and Kohls (1950, the Philippines; 1957, Malaysia), to cite some noteworthy examples. It then underwent a period of minimal interest prior to the Vietnam War, when both American and Russian workers conducted major surveys in a number of Southeast Asian countries (Petney et al. 2007). This was followed by continuing efforts, particularly by Harry Hoogstraal and coworkers, until Hoogstraal's untimely death in 1986 (Petney et al. 2007). Recently there has been an upsurge of interest in both the taxonomy of Southeast Asian ticks (Apanaskevich and coworkers) and the pathogens that these ticks may transmit (Ahanatrig et al. 2008; Petney et al. 2019; Low et al. 2020; Sharifah et al. 2020). In this chapter we summarize current information on tick biodiversity in Southeast Asia, the role of ticks as disease vectors, and the rapidly changing dynamics of tick ecology in this part of the world.

Southeast Asia has been identified as a region with a higher extinction potential for many species than most other areas worldwide (Schipper et al. 2008; Hughes 2017); indeed, this region is undergoing a biodiversity crisis (Sodhi et al. 2004, 2010; Bickford et al. 2012). There are various factors responsible for this situation, predominantly habitat destruction and fragmentation (Crooks et al. 2017; Tölle et al. 2017; Imai et al. 2018); for example, the massive increase in oil palm and rubber plantations at the expense of natural forest areas (Ziegler et al. 2009; Yaap et al. 2010; Gatti et al. 2019), subsistence hunting, the exotic pet industry, and the Oriental “pharmaceutical” industry (Gray et al. 2017), all of which are exacerbated by rapid increases in the human population (Bickford et al. 2012).

Many of the wild reptile, bird and mammal hosts of parasites, including ticks, have been reduced in numbers and their populations restricted to fragmented habitats, increasing the risk of local extinction (Bordes et al. 2015; Fig. 8.1). Thus, some species of ticks with a limited host range are vulnerable to extinction along with their

**Fig. 8.1** A female *Amblyomma supinoi* from Myanmar. This is a relatively rare, endangered species found predominantly on tortoises in mainland Southeast Asia. Photo courtesy of James L. Occi, Center for Vector Biology, Rutgers University, New Jersey, USA (see Robbins and Platt 2001)



**Table 8.1** Endangered tick species in Southeast Asia. Modified and enlarged after Durden and Keirans (1996) and Mihalca et al. (2011)

Ixodidae	
<i>Amblyomma</i>	<i>babirusae</i>
	<i>clypeolatum</i>
	<i>crenatum</i>
	<i>javanense</i>
	<i>komodoense</i>
	<i>robinsoni</i>
	<i>supinoi</i>
<i>Haemaphysalis</i>	<i>borneata</i>
	<i>capricornis</i>
	<i>kadarsani</i>
	<i>palawanensis</i>
	<i>psalistos</i>
	<i>vietnamensis</i>

hosts. Durden and Keirans (1996) list six species (from a total of 48, 12.5%) from Southeast Asia as endangered, while Mihalca et al. (2011) list 10 (from 63, 15.9%) as co-endangered with their hosts (Table 8.1). Both estimates will probably have to be increased as escalating land use changes lead to destruction of natural habitats (Zhao et al. 2006).

By contrast, the increase in stock numbers (particularly cattle, Smith et al. 2018) has substantially increased the number of potential hosts for ticks, and tick-borne diseases, at least for those tick species that are able to utilize these animals as hosts. The large numbers of stray dogs (Traub et al. 2015) also provide suitable hosts for a variety of tick species capable of pathogen transmission (Irwin and Jefferies 2004; Petney et al. 2019).

## 8.2 The Tick Fauna

Southeast Asia has a substantial tick fauna. Petney et al. (2019) listed 97 species from continental Southeast Asia, to which a number of new or reinstated species have been added (*Dermacentor laothaiensis* and *D. pasteuri*, both found in Lao PDR and Thailand, Apanaskevich et al. 2019, 2020) (Table 8.2).

There is no similar summary of species for insular Southeast Asia; however, a list of species known only from islands within the region is provided in Table 8.3. A large number of endemic species occur in this area, some of which are found on specific islands or small island groups; for example, *Amblyomma robinsoni* and *A. komodoense* parasitize Komodo dragons (Guglielmone et al. 2014), large varanid lizards that are found on five small islands within the Lesser Sunda Islands of Indonesia (Ciofi et al. 1999).

In general, the tick fauna of Southeast Asia is strongly biased toward the genus *Haemaphysalis*, followed by substantial numbers of *Amblyomma* and *Dermacentor*.

**Table 8.2** Number of species per tick genus in continental Southeast Asia (modified after Petney et al. 2019)

Family/genus	Number of species
Argasidae	
<i>Argas</i>	3
<i>Ornithodoros</i>	2
Ixodidae	
<i>Amblyomma</i>	17
<i>Dermacentor</i>	12
<i>Haemaphysalis</i>	43
<i>Hyalomma</i>	2
<i>Ixodes</i>	14
<i>Nosomma</i>	1
<i>Rhipicephalus</i>	6
Total	101

**Table 8.3** Tick species found only on islands in Southeast Asia

Family/genus	Species
Ixodidae	
<i>Amblyomma</i> (4)	<i>komodoense</i>
	<i>kraneveldi</i>
	<i>robinsoni</i>
	<i>soembawense</i>
<i>Dermacentor</i> (1)	<i>confragus</i>
<i>Haemaphysalis</i> (13)	<i>bartelsi</i>
	<i>borneata</i>
	<i>celebensis</i>
	<i>hirsuta</i>
	<i>kadarsani</i>
	<i>luzonensis</i>
	<i>mjoebergi</i>
	<i>psalistos</i>
	<i>renschii</i>
	<i>rusae</i>
	<i>sumatraensis</i>
	<i>susphilippensis</i>
	<i>toxopei</i>
<i>Ixodes</i> (2)	<i>collocaliae</i>
	<i>cordifer</i>
Argasidae	
<i>Ornithodoros</i>	<i>collocaliae</i>

The genus *Ixodes* is poorly represented, and very few *Hyalomma* and *Rhipicephalus* have been found in this region (Table 8.2). There are also relatively few representatives of the soft tick family Argasidae.

The tick faunal community can be defined at different levels: region, country, ecosystem, host, and microhabitat, and in the case of maritime countries the island

(s) occupied. Although recent species lists for mainland Southeast Asian countries are available in Petney et al. (2019), no such up-to-date lists are available for the island countries (note: *Dermacentor laothaiensis* and *D. pasteuri* were described after Petney et al. (2019) in Apanaskevich et al. 2019, 2020).

There are numerous country lists, most of which are dated. The older works listed in the introduction to this chapter have recently been supplemented by Phan (1977, Vietnam), Tanskul et al. (1983, Thailand), Kolonin (1995, Vietnam), and Kwak (2018, Singapore).

There are also some local or province lists that provide an indication of the tick faunas present at smaller scales. For example, Vongphayloth et al. (2016) surveyed the tick fauna of two protected areas in Nakai District, Khammouane Province, Lao PDR. Sampling was carried out by dragging vegetation in two habitats (mountainous primary forest and valley secondary forest), thus providing an indication of the tick species present in certain natural/semi-natural tick habitats within a defined political jurisdiction. Vongphayloth et al. (2016) identified 11 species belonging to five genera (*Amblyomma*, *Dermacentor*, *Haemaphysalis*, *Ixodes*, and *Rhipicephalus*).

A number of other local surveys, often focusing on a restricted host spectrum, have provided valuable information on broad-scale, potentially non-interacting tick species within tick communities (Hoogstraal et al. 1968, 1972; Durden and Watts 1989; Durden et al. 2008; Mariana et al. 2008; Ishak et al. 2018).

Because national boundaries are artificial constructs that generally do not conform to ecological zones, they are of relatively little value in defining the distributions of tick species. Of more relevance are the ecosystem characteristics themselves, as these define both the hosts found in an area and the microclimate available to ticks when they are detached from their host. This is of vital importance because appropriate temperatures and relative humidities are critical for tick survival (Needham and Teel 1991). Nevertheless, many tick species found in the same habitat may not be part of, or may exist peripheral to, an interactive community. This is often the case with birds, which may range over vast, ecologically unrelated areas. For example, *Haemaphysalis megalaimae* is a parasite specific to the avian family Megalaimidae, the Asian barbets (previously classified in the Capitonidae, the New World barbets), which are widespread in Southeast Asia (Guglielmone et al. 2014).

Although the tick fauna of Southeast Asia is relatively well known morphologically, considerable molecular work will be required to confirm some morphological descriptions. This is particularly true of several recently described *Dermacentor* species, all of which parasitize the ubiquitous wild boar (*Sus scrofa*) (Petney et al. 2019), calling the concept of allopatric speciation into question. The value of modern molecular methods can be gauged by the example of *Rhipicephalus (Boophilus) microplus* sensu lato (s.l.), which a decade ago was thought to constitute a single taxon distributed widely throughout the tropics. In 2012, Estrada-Peña et al. showed that the Australian population in fact represented a previously described species, *R. (B.) australis*. Thereafter, Roy et al. (2018) showed that *R. (B.) microplus* (s.l.) (Fig. 8.2) consists of at least five species and that morphological methods alone cannot effectively distinguish these. A similar situation exists in the case of the brown dog tick *Rhipicephalus sanguineus* (Fig. 8.3), which consists of at least two



**Fig. 8.2** *Rhipicephalus microplus* sensu lato females in different stages of engorgement from cattle in northeast Thailand (photo by Weerachai Saijuntha)



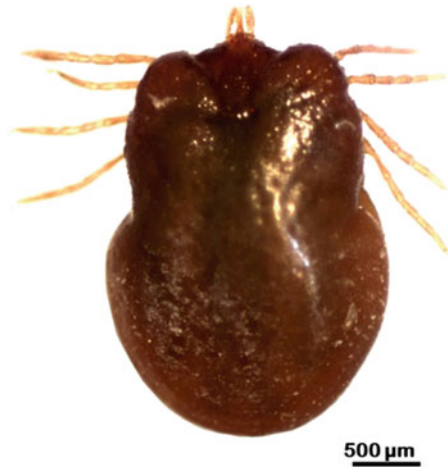
**Fig. 8.3** An engorged and an unengorged female *Rhipicephalus sanguineus* sensu lato from a dog in northeast Thailand (photo by Weerachai Saijuntha)

species (Nava et al. 2015; Sanches et al. 2016). As these species are frequently encountered and occur on common hosts, it seems likely that less abundant species with patchy distributions, particularly those found only on islands and that do not parasitize migratory birds, may well represent species complexes. The elucidation of such complexes is of obvious importance when considering the potential role of particular tick species in pathogen transmission.

### 8.3 Tick Genetic Diversity

Investigations of the genetic diversity of Southeast Asian ticks have largely focused on Malaysia, where the molecular phylogeny of *Ixodes granulatus* was described based on the mitochondrial CO1 sequence (Lah et al. 2014) and subsequently used to

**Fig. 8.4** *Ixodes kopsteini* female collected from a wrinkle-lipped free-tailed bat (*Chaerephon plicatus*, family Molossidae) from Phaya cave, Loei Province, Thailand (Photo by Weerachi Saijuntha)



identify the different life history stages of this tick (Lah et al. 2016). Additionally, the cattle tick *Rhipicephalus microplus* in Malaysia was characterized using 16S rRNA and CO1 sequences, revealing four genetically divergent groups within Malaysian *R. microplus* and the identification of three principal genetic assemblages worldwide (Low et al. 2015). More recently, CO1 sequence variation of Malaysian *Haemaphysalis* species has been investigated (Ernieenor et al. 2017). Of 19 immature tick specimens collected from four localities, 16 were molecularly identified as *Haemaphysalis hystricis*, and three as *H. humerosa*, with sequence homologies of 97–99% and 86–87%, respectively. Low intraspecific variation (<0.3%) but high interspecific value (>15%) among *H. hystricis* was also observed (Ernieenor et al. 2017).

Some investigations of Southeast Asian tick genetic diversity have been conducted in areas outside Malaysia, such as a study of Bm86 mRNA sequence variation among *R. microplus* populations collected from cattle across Thailand, which revealed the presence of 6–9 genetically distinct groups related to Thai geography, all clearly separable from Neotropical *R. microplus* (Kaewmongkol et al. 2015). In Vietnam, Hornok et al. (2015) presented molecular evidence to show that more than one species may exist under the names *Ixodes simplex* and *Ixodes vespertilionis*. And most recently, high genetic diversity has been reported in six species of hard ticks—*Haemaphysalis kitaokai*, *H. longicornis*, *H. shimoga*, *Ixodes ovatus*, *Rhipicephalus haemaphysaloides*, and *R. microplus*—from a China-Myanmar border county, where specimens were analyzed using 16S rRNA and CO1 sequences. New species or subspecies closely related to *H. kitaokai*, *H. shimoga*, *I. ovatus*, and *R. haemaphysaloides* probably exist in this area (Li et al. 2018).

## 8.4 Tick Biodiversity on Host Species

Individual hosts or host populations commonly harbor a number of tick species. Intensive studies of such on-host communities have been conducted throughout southern Africa, where tick-borne diseases of livestock are a major veterinary problem (MacLeod 1970; Horak et al. 1979, 2001; Smith and Parker 2010; Nyangiwe et al. 2011). The veterinary concerns caused by ticks and their economic impact led directly to investigations of southern African ticks and tick-borne diseases (De Kock 1945; Horak et al. 2018). Communities of different tick species also occur on wildlife and companion animals (Petney and Horak 1997; Neves et al. 2004; Mathee et al. 2010; Anderson et al. 2013). Such communities can influence the potential transmission dynamics of pathogens when more than one species can act as a vector for the same disease-causing agent (Pfäffle et al. 2013). If two or more species that transmit different pathogens occur on a host, then infection with multiple pathogens can occur, leading to greater morbidity or mortality (Petney and Andrews 1998).

Perhaps due to a lack of perceived medical and veterinary significance of ticks in Southeast Asia, relatively little research has been carried out on tick communities in this area. Tanskul et al. (1983) provide a tick-host list for Thailand, unfortunately without listing the number of hosts examined. Of the 39 bird species listed, a single tick species was found on 33, and 2 tick species were found on 6 bird species. Eight tick species were found on domestic cattle (*Bos* spp.), while 8 wild artiodactyl species were infested with an average of 3.6 tick species. Wild carnivores were found with an average of 2.6 tick species, insectivores with 3.0 (the common tree shrew, *Tupaia glis*, had 7 species), bats with an average of 1 species, lagomorphs with 3, tapir (*Perissodactyla*) with 4, pangolins with 1, and rodents with 2.3. Reptiles averaged 1.7 tick species/host species.

Such figures are all likely to be underestimates due to generally low host sample sizes and recent additions to the number of tick species known to be present. For example, humans, who are not natural hosts for ticks, were found to be parasitized by 15 tick species. Tanskul et al. (1983) list seven species from dogs in Thailand, whereas for mainland Southeast Asia 18 tick species have been recorded (Petney et al. 2019). Even given these caveats, the data clearly show that individual host species harbor tick communities with potential interactions between species.

There are numerous small-scale surveys, also often with low sample sizes, that nonetheless provide an indication of the potentially interactive tick community on individual host species. Robbins et al. (1997) identified three species of tick from an Asian golden cat (*Catopuma temminckii*), including adults of *Haemaphysalis asiatica* and *Rhipicephalus haemaphysaloides*, as well as nymphs of an undetermined *Amblyomma* species. Grassman Jr et al. (2004) collected six species of ticks from eight species of carnivore, finding four tick species on *Prionailurus bengalensis* (leopard cat), three on *Martes flavigula* (yellow-throated marten), *Neofelis nebulosa* (clouded leopard) and *Cuon alpinus* (dhole), two on *Catopuma temminckii*, and a single species on *Pardofelis marmorata* (marbled cat), *Arctictis*



*binturong* (binturong), and *Viverra zibetha* (large Indian civet). Other Southeast Asian studies of ticks on wildlife include Audy et al. (1960), Munaf (1978), and Madinah et al. (2011).

Sahara et al. (2019) identified 1575 ticks on 26 cattle from five different areas of Indonesia. They found infestations with *Rhipicephalus microplus*, *Haemaphysalis bispinosa*, and *Rhipicephalus pilans*, with the cattle from three areas infested by both *R. microplus* and *R. pilans*. A survey within the Myanmar-Chinese border area of Yunnan Province (which is biogeographically related to mainland Southeast Asia, Yang et al. 2004, Zhu 2017) revealed that goats harbored four tick species (*R. microplus*, *R. haemaphysaloides*, *I. ovatus*, and *H. longicornis*) and cattle two (*R. microplus* and *R. haemaphysaloides*). The taxonomic situation was complicated because *R. haemaphysaloides* and *I. ovatus* each fell into three phylogenetic groups, with intergroup genetic distances higher than is normal between tick species. *Haemaphysalis longicornis* ticks also clustered into two separate clades, indicating that more than one species group could be present (Li et al. 2018).

Movement of hosts can also lead to the simultaneous transmission of one or more tick species. For example, a king cobra (*Ophiophagus hannah*) exported from Malaysia to Taiwan was infested with *Amblyomma cordiferum* and *A. varanense*, with females of both species being present (Norval et al. 2009). And the dramatic increase in commerce and communication between Southeast Asia and the rest of the world is almost certain to result in the importation of exotic tick species, as in the case of two male specimens of the Neotropical sloth tick *Amblyomma varium* collected from a male and female of the southern two-toed sloth (*Choloepus didactylus*) that were shipped to Wildlife Reserves Singapore in 2012 (both tick specimens, identified by RGR, have been deposited in the permanent research collections of the Peabody Museum of Natural History at Yale University, accession numbers YPM-ENT 300786–300787).

Very few tick species are specific parasites of a single host species. Most species have some preference for a group of hosts. Thus, a number of *Dermacentor* species occur most commonly on wild boar (Vongphayloth et al. 2018), while others prefer bats, tortoises, snakes and lizards, and particular mammal species (e.g., *Amblyomma javanense* on pangolins, *Manis* spp.) (Kwak et al. 2018; Petney et al. 2019). In addition, the immature stages of some tick species may have host preferences that differ from those of the adults (Petney et al. 2019). This mixture of hosts and life history stages complicates efforts to define tick communities (Petney and Horak 1997), requiring a knowledge of host species utilization by both adults and immatures in order to ascertain potential pathogen transmission pathways. Bats (Chiroptera) are unusual as they can act as hosts for both argasid and ixodid ticks, potentially allowing for the transfer of pathogens between these two families (Table 8.4).

**Table 8.4** Argasid and ixodid tick species recorded from bats in Southeast Asia. *Ixodes simplex* and *I. vespertilionis* may be species complexes (Guglielmone et al. 2020). *Ixodes kopsteini*, an unusual species in which the eggs hatch in the dead body of the female, is shown in Fig. 8.4

Family	Tick species
Argasidae	<i>Argas pusillus</i>
	<i>Argas vespertilionis</i>
	<i>Ornithodoros batuensis</i>
Ixodidae	<i>Ixodes kopsteini</i>
	<i>Ixodes simplex</i>
	<i>Ixodes vespertilionis</i>

## 8.5 Ticks as Vectors

Ticks are known to be major vectors of human and animal viral, bacterial, and protozoan diseases worldwide (de la Fuente et al. 2008; Guglielmone and Robbins 2018). Although this is also the case for Southeast Asia, comparatively little large-scale work has been done in this region (Petney et al. 2019). However, with the advent of molecular taxonomic methods, local studies have revealed a large number of hitherto unknown pathogenic agents, particularly members of the Rickettsiaceae (*Rickettsia*, *Ehrlichia*, and *Anaplasma*) (Petney et al. 2019; Low et al. 2020), the pathogenic potentials of which remain to be determined.

Petney et al. (2019) list a single argasid (20% of the known total number of Southeast Asian species) and 25 ixodids (26%) as potential vectors for human pathogens: one *Argas* species, three *Amblyomma*, five *Dermacentor*, one *Ixodes*, 13 *Haemaphysalis*, and three *Rhipicephalus*. This contrasts with potential vectors of pathogens of wildlife, stock and companion animals, with three (60%) argasids, all belonging to the genus *Argas*, and 14 ixodids (14%) (three *Amblyomma*, two *Dermacentor*, seven *Haemaphysalis*, and two *Rhipicephalus*). In both cases, a large number of unidentified tick species were associated with potential pathogens. Low et al. (2020) list 14 species of ixodid tick associated with rickettsiae in Southeast Asia (we know of no record of *Amblyomma integrum* from this region) from a variety of wild, companion and stock animals as well as humans.

## 8.6 Pathogen Identification

The advent of molecular methods has made pathogen identification relatively rapid and precise (Solano-Gallego et al. 2016; Lempereur et al. 2017; Seesao et al. 2017). It has, however, led to the discovery of a large number of pathogen species that have yet to be taxonomically defined, i.e., agents lacking a binomial name. Thus, in continental Southeast Asia, Petney et al. (2019) listed 14 known bacterial pathogens or potential pathogens of humans and 17 species with no biologically correct designation. For vertebrate animals the situation was slightly better for bacteria,

with 16 known and 16 unnamed species, while there were eight species in each category for protozoa. Most of the publications commenting on unnamed microbial species are very recent, and the ticks or hosts in which the potential pathogens were discovered represent a minuscule subset of those that occur in the region. We therefore expect a large increase in the number of undescribed pathogen species as more tick species and hosts are examined.

## 8.7 Pathogen Diversity

Wild animals are a potential source of a variety of bacterial and protozoan pathogens in Southeast Asia. Kho et al. (2015) examined 12 *Amblyomma varanense* and nine *Amblyomma helvolum* from seven *Python molurus* (Indian rock python) and six *A. helvolum* from a single *Naja sumatrana* (equatorial spitting cobra) from Johore, Malaysia. They found two potentially novel spotted fever group rickettsiae in the ticks: *Candidatus Rickettsia sepangensis* was determined from an engorged *A. varanense* with a high sequence similarity to *Rickettsia tamurae*. *Candidatus Rickettsia johorensis* was present in two samples from *A. helvolum* and two *A. varanense* ticks; it is closely related to *Rickettsia raoultii*. *Anaplasma* and *Ehrlichia* DNA was also found in seven and two ticks, respectively. Thus, four potentially new pathogens were found in a small sample of ticks from two host snake species.

In a similar study, Sumrandee et al. (2014b) examined five *A. helvolum* from single specimens of *Python bivittatus bivittatus* (Burmese python), *Xenochrophis piscator* (Asiatic water snake), and *Ptyas korros* (Indo-Chinese rat snake) and found that all ticks contained rickettsia, while an additional four *Ophiophagus hannah* (king cobra) infested with 19 ticks were again all infected with rickettsia. Five potentially novel species of rickettsia were found, with some isolates sequencing close to *Rickettsia belli* and *R. raoultii*. In addition, ticks from the same snakes yielded *Francisella*-like species (Sumrandee et al. 2014a) and *Hepatozoon* species (Sumrandee et al. 2015). In their 2015 study, Sumrandee et al. found *Theileria* species in *Haemaphysalis lagrangei*, *Ha. obesa*, and *Rhipicephalus microplus* from sambar deer (*Rusa unicolor*) and *Hepatozoon* species in *Dermacentor auratus* and *D. atrosignatus* from wild boar.

Domestic and stray dogs also harbor a number of tick-borne pathogens throughout Southeast Asia, including *Babesia vogeli*, *B. canis*, *Ehrlichia canis*, and *Hepatozoon canis*, with multiple species infections possible (Irwin and Jefferies 2004; Inpankaew et al. 2016; Petney et al. 2019). The vectors potentially include 18 species of ticks that have been found infesting dogs (Petney et al. 2019).

There is also considerable scope for potential human infection. Fever of unknown origin is commonplace in Southeast Asia, and some infections are probably caused by tick-borne pathogens (Aung et al. 2014; Kho et al. 2016).

Parola et al. (2003a) tested ticks collected from animals, people, and vegetation on the Thai-Myanmar border and from Vietnam. Six hundred and fifty specimens

representing 13 species were collected and analyzed for *Anaplasma*, *Ehrlichia*, and *Rickettsia* species. Three species each of *Anaplasma* and *Ehrlichia* were found, as well as two species of *Rickettsia*. They then examined the blood of 46 patients with fever for rickettsial infection and found that eight were infected with spotted fever group rickettsia, of which only one, an infection with *R. felis*, does not have a tick-host cycle (Parola et al. 2003b).

## 8.8 Dynamic Changes in Tick and Tick-Borne Pathogen Communities

Southeast Asia is undergoing a period of major change, including massive increases in the human population (Jones 2013), changes in land-use away from natural habitats to urban, suburban, and agricultural land (Zhao et al. 2006), and climate change (Petney et al. this volume). During the nineteenth century, European travelers, such as Mouhot (1863, 1864) Wallace (1869) and Warrington-Smyth (1895), described Southeast Asian countries as having limited access to rural areas, with natural vegetation predominating over agricultural land. The same situation was reported in the 1930s by May (1949). Now, much of Southeast Asia is connected by roads, aviation, and marine and freshwater navigation (Bowen Jr 2016; Kaffashi et al. 2016). The transition from natural habitats to human-influenced environments has a number of implications for the tick fauna of this region:

1. Reduction in natural habitats will reduce the number of potential tick host species, particularly the larger species that require larger territories to survive. In many areas, this will reduce and potentially eliminate hosts for ticks with a limited host range.
2. Habitat fragmentation will have the same effect unless large enough areas are preserved (Lynam and Billick 1999; Trisurat et al. 2010; Gibson et al. 2013).
3. Removal of natural habitats will bring humans into potential contact with tick species transmitting novel pathogens (Estrada-Peña et al. 2014; Loh et al. 2016).
4. Increases in urban and peri-urban environments will lead to increases in synanthropic vertebrate species that will act as hosts for their own tick faunas (Klimant et al. 2015; Hassell et al. 2017; Morand et al. 2019).
5. A spectrum of tick-borne diseases will emerge in these altered environments (Rizzoli et al. 2014; Noden et al. 2017).
6. Increases in grazing and pasture land for stock animals will lead to increased populations of those tick species that feed on these hosts, with consequent increases in tick-transmitted diseases.
7. There will be a consequent increased need for tick control and for greater knowledge of tick-borne diseases by physicians and veterinarians.

## 8.9 Conclusions

Ticks are common parasites of wild, stock, and companion animals in Southeast Asia, where there is an increasing recognition of their medical and veterinary significance. This has led to a number of studies that show the complexity of the tick communities inhabiting different ecosystems and infesting different hosts, as well as to recognition of the potential pathogens that they do or could transmit. Although the tick fauna is relatively well known, little information is available concerning interactions within tick communities and their relation to the epidemiology of tick-borne diseases.

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