CORE
Metadata, citation and similar papers at core.ac.uk
Provided by IntechOpen

We are IntechOpen, the world's leading publisher of Open Access books
Built by scientists, for scientists

4,800
Open access books available

122,000
International authors and editors

135M
Downloads

154
Countries delivered to

Our authors are among the
TOP 1%
most cited scientists

12.2%
Contributors from top 500 universities

WEB OF SCIENCE™
Selection of our books indexed in the Book Citation Index
in Web of Science™ Core Collection (BKCI)

Interested in publishing with us?
Contact book.department@intechopen.com

Numbers displayed above are based on latest data collected.
For more information visit www.intechopen.com

Chapter

Introductory Chapter: Ticks and Tick-Borne Pathogens

Muhammad Abubakar, Piyumali K. Perera, Abdullah Iqbal and Shumaila Manzoor

1. Introduction

Ticks are obligate ectoparasites that feed on the blood of their hosts. Ticks belong to the phylum Arthropoda, class Arachnida, subclass Acari, order Parasitiformes, and suborder Ixodida [1, 2]. There are three families of ticks classified as Ixodidae (hard ticks), Argasidae (soft ticks), and Nuttalliellidae (limited to Tanzania and South Africa) [3, 4]. More than 900 species of ticks have been classified in the world. Ticks not only cause physical damage to their hosts by sucking blood and injuring skin, but many of these tick species also have the ability to transmit pathogens to their host. The population of ticks in any region depends upon various factors such as climate, the presence of predators, and competitor species [5].

According to an estimate, every year, ticks and tick-borne pathogens cause the US $13.9–18.7 billion loss. Annually, tick infestations result in a loss of almost 3 billion hides of cattle [6]. Ticks transfer pathogens from their gut to host bloodstream by their saliva [7]. Ticks transmit a range of pathogens including viruses, bacteria, and protists to vertebrate hosts, including humans, domestic, and wild animals. These pathogens cause many viral diseases (e.g., Crimean-Congo hemorrhagic fever, West Nile fever, Omsk hemorrhagic fever, and Colorado tick fever), bacterial diseases (Lyme disease, Q fever, borreliosis, and relapsing fever), fungal diseases (dermatophilosis), protozoal diseases (theileriosis and babesiosis), and rickettsial diseases (anaplasmosis, ehrlichiosis, Brazilian spotted fever, and Rocky Mountain spotted fever) [7–11]. Tick-borne diseases (TBDs) of domestic animals (e.g., cattle, sheep, and goats) can substantially affect livestock production, food supply, and economy of many regions worldwide. TBDs cause production losses mainly as a consequence of infertility, abortions, reduced weight gain, decreased milk production, lower quality of milk, and mortality. In addition, costs associated with control and preventive measures, such as dipping with acaricides, vaccination, chemotherapy, veterinary services, and monitoring, also contribute considerably to economic losses (Brown, 1997). In addition, most of these pathogens are very serious zoonotic threats due to the worldwide distribution of ticks and lack of vaccine availability against these viruses and other pathogens [12].

Tick-borne pathogens are not the only problem due to tick infestation. When ticks feed on their host, they draw blood and cause damage to the skin. Injury of skin and subcutaneous tissues leads to edema, pruritus, erythema, scaling, and ulceration [13]. Excoriation can result in secondary bacterial infections. Along with these physical damages, ticks affect the productivity of animals by disturbing their normal behavior [14].

IntechOpen

2. Tick-borne viruses

Tick-borne viruses (TBV) are specifically named as tiboviruses, and all of them belong to a group of arboviruses [15]. These viruses require ticks and vertebrate host to complete their life cycle. Combined evolution of ticks and tiboviruses results in the development of such a life cycle that totally matches the feeding cycle of ticks. These viruses belong to nine families of viruses. Among nine tiboviruses families, eight are RNA families (Flaviviridae, Reoviridae, Rhabdoviridae, Orthomyxoviridae, Nyamiviridae, Phenuiviridae, Nairoviridae, and Peribunyaviridae) and one DNA family (Asfarviridae) [13, 16].

To date, almost 19 diseases of livestock and 16 diseases of humans have been reported by TBV [17, 18]. Flaviviridae viruses are most common tiboviruses that include tick-borne encephalitis virus, West Nile virus, louping ill virus, Powassan virus, and Kyasanur Forest disease virus that are transmitted by *Dermacentor reticulatus*, *Ornithodoros moubata*, *Ixodes ricinus*, *Ixodes scapularis*, and *Haemaphysalis punctata*, respectively [19, 20]. West Nile virus is endemic in many African and European countries [21]. African swine fever virus is also a tick-borne virus that belongs to family Asfarviridae and transmitted by *Ornithodoros porcinus*. African swine fever disease is a very serious threat for pigs due to its high mortality rate [22]. Thogoto virus of family Orthomyxoviridae is transmitted by tick species such as *Rhipicephalus appendiculatus*, *Boophilus microplus*, *Hyalomma dromedarii*, *Rhipicephalus evertsi*, and *Amblyomma variegatum* [23].

Two major tick-borne viruses of Nyamiviridae are Nyamanini virus and Midway nyavirus. Reoviruses include tiboviruses such as Colorado tick fever virus, Great Island virus, and Chobar Gorge virus. Colorado tick fever virus is prevalent in the United States and Canada. This virus is transmitted to mammals by a tick *Dermacentor andersoni*. Fever, meningitis, rash, and conjunctivitis are typical clinical signs of Colorado tick fever [9].

Rhabdoviridae includes tick-borne viruses such as Isfahan vesiculovirus, Connecticut virus, and Barur ledantevirus [13]. Nairoviridae contains two major tick-borne viruses; those are Crimean-Congo hemorrhagic fever virus and Nairobi sheep disease virus. Crimean-Congo hemorrhagic fever outbreaks have been reported from many African, Asian, and European countries in the last two decades. This virus is mainly transmitted by *Hyalomma marginatum*, *H. lusitanicum*, *H. truncatum*, *Rhipicephalus bursa*, and *Dermacentor marginatus* [24].

3. Tick-borne bacteria

Tick-borne bacterial (TBB) diseases not only affect the productivity of animals but also have zoonotic importance. Lyme disease is one of the major tick-borne bacterial diseases that is caused by *Borrelia burgdorferi* [25]. These bacteria are transmitted to mammal host by *I. ricinus*, *I. hexagonus*, *I. pacificus*, *I. scapularis*, and *I. persulcatus*. Lyme disease is rapidly spreading in Europe. It is estimated that about 10% of the total population of ticks are positive for *B. burgdorferi* in Europe, and annually more than 85,000 human cases of Lyme are reported from the European countries [26]. Lyme disease also affects domestic animals. Clinical signs and symptoms of Lyme disease in animals include lethargy, anorexia, lameness, and urinary disorder [25].

Another TBB is *Francisella tularensis* that causes tularemia. Ticks of species *I. ricinus*, *D. andersoni*, *D. variabilis*, *D. marginatus*, and *A. americanum* act as biological vectors for *Francisella tularensis*. These bacteria can cause disease in humans, rodents, rabbits, and rarely sheep [27]. Q fever is also a tick-borne zoonotic bacterial disease that is caused by *Coxiella burnetii*. Ticks of species *Haemaphysalis bispinosa* and *I. holocyclus* can also act as reservoir hosts and biological vectors [28].

4. Tick-borne Rickettsiae

Tick-borne Rickettsiae (TBR) can spread to new geographic areas and susceptible population by ticks. Anaplasmosis is an eminent tick-borne rickettsial disease of cattle that is caused by *Anaplasma marginale*. This is transmitted by *Rhipicephalus microplus*. The mortality rate of anaplasmosis in cattle varies from 30 to 50%. Another tick-borne rickettsia is *Rickettsia rickettsii* that causes spotted fever [29]. In the USA, *R. rickettsii* causes Rocky Mountain spotted fever, and in Brazil, it causes Brazilian spotted fever. Rocky Mountain spotted fever spreads mainly by ticks of species *Amblyomma americanum*, *A. cajennense*, *D. andersoni*, *D. variabilis*, and *R. sanguineus sensu lato* [30]. Medically significant vectors of Brazilian spotted fever include *A. aureolatum* and *A. cajennense*. The mortality rate of Rocky Mountain spotted fever in the USA and Brazil has been reported 10% and 30–40%, respectively. African tick bite fever is another tick-borne rickettsial disease that is caused by *Rickettsia africae*. Major vectors of *Rickettsia africae* are ticks of *A. variegatum* and *A. hebraeum* species [31].

Heartwater or cowdriosis is another tick-borne rickettsial disease that is caused by *Ehrlichia ruminantium*. *E. ruminantium* is mainly transmitted by *Amblyomma variegatum*, *A. pomposum*, and *A. hebraeum* [32]. This disease is limited to Africa and South Africa. Cowdriosis is a serious threat to ruminants in sub-Saharan Africa, where up to 90% mortality rate has been reported [33]. In dogs, *Ehrlichia canis* causes Ehrlichiosis. *E. canis* has been reported from the many Asian, European, and American countries and transmitted from one dog to another dog by *Rhipicephalus sanguineus sensu lato*. Clinical signs of this disease include high fever, lethargy, anemia, and nose bleeding [34].

5. Tick-borne fungi

Ticks are also involved in the transmission of a fungal pathogen, *Dermatophilus congolensis*, to mammals. *Dermatophilus congolensis* causes a skin disease Dermatophilosis [35]. This pathogenic fungus is transmitted by a tick vector *A. variegatum*. Dermatophilosis causes exudative dermatitis in sheep and cattle which leads to significant economic loss due to the devaluation of hide quality [36].

6. Tick-borne protozoa

Ticks can transmit many blood protozoan parasites to their vertebrate hosts. Among these, two main groups of TBDs are of importance to the livestock: theileriosis (i.e., tropical theileriosis and East Coast fever (ECf)) and babesiosis, posing major health and management problems to cattle and small ruminants, mainly in tropical and subtropical regions worldwide. The most pathogenic species are *T. annulata* and *T. parva*, the causative agents of tropical or Mediterranean theileriosis and ECf, respectively. Other species, such as *Theileria mutans*, *Theileria taurotragi*, and members of the *T. orientalis* complex, are usually considered to cause asymptomatic infections in livestock. *Theileria parva* is transmitted to cattle by *Rhipicephalus appendiculatus* (East Africa) or *R. zambeziensis* (South Africa) and causes ECf [35]. Tropical theileriosis is caused by *Theileria annulata* and transmitted by *Hyalomma* spp. It is characterized by lymph nodes swelling, high fever, and dyspnea [37].

Babesiosis is another tick-borne protozoal disease. Bovine babesiosis is caused by *Babesia bovis* and *B. bigemina*. These protozoans are transmitted by *Rhipicephalus microplus* and *R. annulatus*. In bovines, animals having babesiosis show clinical signs including hemoglobinuria, jaundice, rapid breathing, and high fever [38]. In canines, *Babesia canis* causes piroplasmosis. *B. canis* is transmitted to dogs by *R. sanguineus* and *D. reticulatus*. In humans, *B. microti* and *B. divergens* are responsible for babesiosis [39].

7. Conclusion

Ticks prevalent in the dairy or poultry industries lead to economic losses either by direct damage to hide and stress to animals or indirectly by pathogens that they transmit to animals and humans. Prevalence of ticks and tick-borne pathogens is influenced by environmental factors and quarantine measures. Tick control at any level can prevent the outbreak of diseases caused by tick-borne pathogens.

Author details

Muhammad Abubakar[1*], Piyumali K. Perera[2], Abdullah Iqbal[1] and Shumaila Manzoor[1]

1 National Veterinary Laboratory, Islamabad, Pakistan

2 Faculty of Science, Department of Zoology, University of Peradeniya, Peradeniya, Sri Lanka

*Address all correspondence to: mabnvl@gmail.com

IntechOpen

© 2018 The Author(s). Licensee IntechOpen. This chapter is distributed under the terms of the Creative Commons Attribution License (http://creativecommons.org/licenses/by/3.0), which permits unrestricted use, distribution, and reproduction in any medium, provided the original work is properly cited.

References

[1] Estrada-Peña A, Mangold AJ, Nava S, Venzal JM, Labruna MB, Guglielmone AA. A review of the systematics of the tick family Argasidae (Ixodida). Acarologia. 2010;**50**(3):317-333

[2] Nava S, Guglielmone AA, Mangold AJ. An overview of systematics and evolution of ticks. Frontiers in Bioscience. 2009;(14):2857-2877

[3] Krantz GW, Walter DE. A Manual of Acarology. 3rd ed. Lubbock, Texas: Texas Tech University Press; 2009

[4] Shi J, Hu Z, Deng F, Shen S. Tick-borne viruses. Virologica Sinica. 2018;**33**(1):21-43. DOI: 10.1007/s12250-018-0019-0

[5] Bartíková P, Holíková V, Kazimírová M, Štibrániová I. Tick-borne viruses. Acta Virologica. 2017;**61**(04):413-427. DOI: 10.4149/av_2017_403

[6] Karim S, Budachetri K, Mukherjee N, Williams J, Kausar A, Hassan MJ, et al. A study of ticks and tick-borne livestock pathogens in Pakistan. PLoS Neglected Tropical Diseases. 2017;**11**(6). https://doi.org/10.1371/journal.pntd.0005681

[7] Chmelař J, Kotál J, Kopecký J, Pedra JH, Kotsyfakis M. All for one and one for all on the tick-host battlefield. Trends in Parasitology. 2016;**32**:368-377. DOI: 10.1016/j.pt.2016.01.00

[8] Socolovschi C, Mediannikov O, Raoult D, Parola P. The relationship between spotted fever group Rickettsiae and ixodid ticks. Veterinary Research. 2009;**40**:34

[9] Pujalte GGA, Chua JV. Tick-borne infections in the United States. Primary Care; Clinics in Office Practice. 2013;**40**:619-635

[10] Bente DA, Forrester NL, Watts DM, McAuley AJ, Whitehouse CA, Bray M. Crimean-Congo hemorrhagic fever: History, epidemiology, pathogenesis, clinical syndrome and genetic diversity. Antiviral Research. 2013;**100**:159-189

[11] Ebel GD. Update on Powassan virus: Emergence of a North American tick-borne flavivirus. Annual Review of Entomology. 2010;**55**:95-110

[12] Clow KM, Ogden NH, Lindsay LR, Michel P, Pearl DL, Jardine CM. Distribution of ticks and the risk of lyme disease and other tick-borne pathogens of public health significance in Ontario, Canada. Vector Borne and Zoonotic Diseases. 2016;**16**(4):215-222. DOI: 10.1089/vbz.2015.1890

[13] Kazimírová M, Thangamani S, Bartíková P, Hermance M, Holíková V, Štibrániová I, et al. Tick-borne viruses and biological processes at the tick-host-virus interface. Frontiers in Cellular and Infection Microbiology. 2017;7:339. Published 2017 Jul 26. DOI: 10.3389/fcimb.2017.00339

[14] Mapholi NO, Marufu MC, Maiwashe A, Banga CB, Muchenje V, MacNeil MD, et al. Towards a genomics approach to tick (Acari: Ixodidae) control in cattle: A review. Ticks and Tick-borne Diseases. 2014;**5**:475-483

[15] Hubálek Z, Rudolf I. Tick-borne viruses in Europe. Parasitology Research. 2012;**111**:9-36. DOI: 10.1007/s00436-012-2910-1

[16] Kuhn JH, Wiley MR, Rodriguez SE, Bao Y, Prieto K, Travassos da Rosa AP, et al. Genomic characterization of the genus Nairovirus (Family Bunyaviridae). Viruses. 2016;**8**:164. DOI: 10.3390/v8060164

[17] Nicholson WL, Sonenshine DE, Lane RS, Uilenberg G. Ticks (Ixodida). In: Mullen GR, Durden LA, editors. Medical and Veterinary Entomology. Burlington, NJ: Academic Press; 2009. pp. 493-542

[18] Sonenshine DR, Roe RM. Overview. Ticks, people, and animals. In: Sonenshine DE, Roe RM, editors. Biology of Ticks. Vol. 1. New York, NY: Oxford University Press; 2014. pp. 3-17

[19] Labuda M, Nuttall PA. Viruses transmitted by ticks. In: Bowman AS, Nuttall PA, editors. Ticks: Biology, Disease and Control. Cambridge: Cambridge University Press; 2008. pp. 253-280

[20] Dobler G. Zoonotic tick-borne flaviviruses. Veterinary Microbiology. 2010;**140**:221-228

[21] Lawrie CH, Uzcátegui NY, Gould EA, Nuttall PA. Ixodid and argasid tick species and West Nile virus. Emerging Infectious Diseases. 2004;**10**(4):653-657

[22] Dantas-Torres F, Chomel BB, Otranto D. Ticks and tick-borne diseases: A one health perspective. Trends in Parasitology. 2012;**28**(10):437-446

[23] Costard S, Mur L, Lubroth J, Sanchez-Vizcaino JM, Pfeiffer DU. Epidemiology of African swine fever virus. Virus Research. 2013;**173**:191-197

[24] Mertens M, Schmidt K, Ozkul A, Groschup MH. The impact of Crimean-Congo hemorrhagic fever virus on public health. Antiviral Research. 2013;**98**:248-260

[25] Stanek G, Wormser GP, Gray J, Strle F. Lyme borreliosis. Lancet. 2012;**379**:461-473

[26] Stanek G, Fingerle V, Hunfeld KP, Jaulhac B, Kaiser R, Krause A, et al. Lyme borreliosis: Clinical case definitions for diagnosis and management in Europe. Clinical Microbiology and Infection. 2011;**17**:69-79

[27] Gyuranecz M, Rigó K, Dán Á, Földvári G, Makrai L, Dénes B, et al. Investigation of the ecology of *Francisella tularensis* during an inter-epizootic period. Vector Borne and Zoonotic Diseases. 2011;**11**(8):1031-1035

[28] Angelakis E, Raoult D. Q fever. Veterinary Microbiology. 2010;**140**:297-309

[29] Parola P, Paddock CD, Socolovschi C, Labruna MB, Mediannikov O, Kernif T, et al. Update on tick-borne rickettsioses around the world: A geographic approach. Clinical Microbiology Reviews. 2013;**26**(4):657-702

[30] Blanton LS. Rickettsial infections in the tropics and in the traveler. Current Opinion in Infectious Diseases. 2013;**26**:435-440

[31] Labruna MB, Santos FCP, Ogrzewalska M, Nascimento EMM, Colombo S, Marcili A, et al. Genetic identification of rickettsial isolates from fatal cases of Brazilian spotted fever and comparison with *Rickettsia rickettsii* isolates from the American continents. Journal of Clinical Microbiology. 2014;**52**(10):3788-3791

[32] Ibrahim MB, Saeed EMA, Hassan SM, Gameel AA, Suleiman KM, Zaki AZSA. Diagnosis of *Ehrlichia ruminantium* in ruminants in Central Sudan using polymerase chain reaction. Journal of Agriculture and Veterinary Sciences. 2013;**6**(2):59-68

[33] Allsopp BA. Natural history of *Ehrlichia ruminantium*. Veterinary Parasitology. 2010;**167**:123-135

[34] Vieira RFC, Biondo AW, Guimarães AMS, Santos AP, Santos RP, Dutra LH, et al. Ehrlichiosis in Brazil. Revista Brasileira de Parasitologia Veterinária. 2011;**20**(1):1-12

[35] Brites-Neto J, Duarte KMR, Martins TF. Tickborne infections in human and animal population worldwide. Veterinary World. 2015;**8**(3):301-315

[36] Dalis JS, Kazeem HM, Kwaga JKP, Kwanashie CN. Generalized skin lesions due to mixed infection with *Sporothrix schenkii* and *Dermatophilus congolensis* in a bull from Jos, Nigeria. Veterinary Microbiology. 2014;**172**:475-478

[37] Colwell DD, Dantas-Torres F, Otranto D. Vector-borne parasitic zoonoses: Emerging scenarios and new perspectives. Veterinary Parasitology. 2011;**182**:14-21

[38] Schnittger L, Rodriguez AE, Florin-Christensen M, Morrison DA. Babesia: A world emerging. Infection, Genetics and Evolution. 2012;**12**:1788-1809

[39] Chaudhry ZI. Vector identification and their role in epidemiology of canine babesiosis. Indian Journal of Canine Practice. 2012;**4**(1):70-75